

STIC-Biotech/ChemLib

160288

From: Vivlmore, Tracy
Sent: Friday, July 22, 2005 4:57 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request, application 10/698,070

Hello,

For application 10/698,070, please perform the following searches. For SEQ ID NO: 1, a score over length search with a length of 17-35 and a cutoff of 80%. For SEQ ID NO: 2, a standard search.

Thank you,

Tracy Vivlmore PhD
Remsen 2B-02, AU 1635
Mailbox: 2C-18
Tel: 571-272-2914

STAFF USE ONLY

Searcher: Noble
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: 10
Online Time: 40

Type of Search

NA#: 2+10 AA#: _____
Interference: _____ SPDI: _____
S/L: ✓ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: compugen
WWW/Internet: _____
Other(Specify): _____

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SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 60. $\text{min len} = 17$
 $\text{max len} = 35$

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2005, 13:10:46 ; Search time 6 Seconds
(without alignments)
3.170 Million cell updates/sec

Title: US-10-698-070-1

Perfect score: 3763

Sequence: 1 aggtggcgccgagaagatgg.....taacaaaaatatagctg 3763

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 132 seqs, 2527 residues

Total number of hits satisfying chosen parameters: 264

Minimum DB seq length: 17

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 141 summaries

Database : fetchlrni.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	32	0.9	33	1	US-08-863-639A-29
C 2	30.4	0.8	33	1	US-09-475-947A-251
C 3	30	0.8	30	1	US-08-068-747-6
C 4	30	0.8	30	1	US-08-068-747-11
C 5	30	0.8	30	1	US-08-863-639A-30
C 6	30	0.8	30	1	US-09-135-934-4
C 7	30	0.8	30	1	US-09-684-843A-4
C 8	30	0.8	31	1	US-08-570-155-14
C 9	30	0.8	31	1	PCT-US95-02861-14
C 10	25.4	0.7	29	1	US-09-304-232-152
C 11	24	0.6	24	1	US-08-863-639A-94
C 12	21	0.6	21	1	US-08-267-803B-66
C 13	21	0.6	21	1	US-08-863-639A-28
C 14	21	0.6	21	1	US-08-863-639A-40
C 15	21	0.6	21	1	US-08-863-639A-60
C 16	21	0.6	21	1	US-08-863-639A-66
C 17	21	0.6	21	1	US-08-863-639A-69
C 18	21	0.6	21	1	US-08-863-639A-87
C 19	20.2	0.5	25	1	US-09-396-196G-74107
C 20	19	0.5	20	1	US-09-198-452A-6476
C 21	18.8	0.5	23	1	US-09-633-098-24
C 22	18.8	0.5	23	1	US-10-177-308-24
C 23	18.4	0.5	20	1	US-08-568-271-1
C 24	18.4	0.5	21	1	US-08-863-639A-35
C 25	18.4	0.5	21	1	US-08-863-639A-47
C 26	18.4	0.5	21	1	US-08-863-639A-89
C 27	18.4	0.5	21	1	US-08-863-639A-92
C 28	18	0.5	18	1	US-08-863-639A-17
C 29	18	0.5	18	1	US-09-205-995-48
C 30	17.8	0.5	21	1	US-08-863-639A-14
C 31	17.8	0.5	21	1	US-08-863-639A-77
C 32	17.4	0.5	19	1	US-08-410-540-5
C 33	17.4	0.5	20	1	US-08-914-961-6

17.4	0.5	20	1	US-09-723-368-5	Sequence 5, Appli
17	0.5	18	1	US-08-970-369A-2	Sequence 2, Appli
17	0.5	18	1	US-09-407-562-2	Sequence 2, Appli
17	0.5	21	1	US-08-628-540-8	Sequence 8, Appli
17	0.5	21	1	US-08-941-100-3	Sequence 3, Appli
16.8	0.4	20	1	US-09-043-303-8	Sequence 8, Appli
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16.4	0.4	18	1	US-08-863-639A-15	Sequence 15, Appli
16.4	0.4	18	1	US-08-863-639A-16	Sequence 16, Appli
16.4	0.4	18	1	US-09-487-444-11	Sequence 11, Appli
16.4	0.4	20	1	US-09-657-042A-39	Sequence 39, Appli
16	0.4	20	1	US-09-907-843-23	Sequence 23, Appli
15.8	0.4	19	1	US-09-696-791-203	Sequence 203, App
15.6	0.4	33	1	US-09-475-947A-251	Sequence 251, App
15.4	0.4	17	1	US-08-985-162-175	Sequence 175, App
15.4	0.4	17	1	US-08-584-040-5601	Sequence 5601, Ap
15.4	0.4	17	1	US-09-371-772B-2491	Sequence 2491, Ap
15.4	0.4	17	1	US-09-401-063-175	Sequence 175, App
15.4	0.4	17	1	US-09-685-664B-2491	Sequence 2491, Ap
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15.4	0.4	19	1	US-09-696-791-323	Sequence 323, App
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15	0.4	31	1	PCT-US95-02861-14	Sequence 14, Appli
15	0.4	33	1	US-08-863-639A-29	Sequence 29, Appli
15	0.4	33	1	US-08-317-431A-11	Sequence 11, Appli
14.8	0.4	18	1	US-09-106-038A-24	Sequence 24, Appli
14.8	0.4	18	1	US-09-106-038A-25	Sequence 25, Appli
14.8	0.4	18	1	US-09-255-911-31	Sequence 31, Appli
14.8	0.4	18	1	US-08-961-810-60	Sequence 60, Appli
14.8	0.4	18	1	US-08-352-902D-60	Sequence 60, Appli
14.8	0.4	18	1	US-08-748-073-3	Sequence 3, Appli
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14.8	0.4	18	1	US-09-475-947A-340	Sequence 340, App
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14.8	0.4	18	1	US-09-371-772B-2184	Sequence 2184, Ap
14.8	0.4	18	1	US-09-685-664B-2184	Sequence 2184, Ap
14.8	0.4	18	1	US-10-272-865-14	Sequence 14, Appli
14.8	0.4	18	1	US-10-272-865-34	Sequence 34, Appli
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14.4	0.4	17	1	US-09-371-772B-1755	Sequence 1755, Ap
14.4	0.4	17	1	US-09-371-772B-6407	Sequence 6407, Ap
14.4	0.4	17	1	US-09-866-108A-7202	Sequence 7202, Ap
14.4	0.4	17	1	US-09-866-108A-8467	Sequence 8467, Ap
14.4	0.4	17	1	US-09-866-108A-8468	Sequence 8468, Ap
14.4	0.4	17	1	US-09-685-664B-1755	Sequence 1755, Ap
14.4	0.4	18	1	US-09-212-771-18	Sequence 18, Appli
14.4	0.4	18	1	US-09-205-143-19	Sequence 19, Appli
14	0.4	30	1	US-08-068-747-6	Sequence 6, Appli
14	0.4	30	1	US-08-068-747-11	Sequence 11, Appli
14	0.4	30	1	US-08-863-639A-30	Sequence 30, Appli
14	0.4	30	1	US-09-135-994-4	Sequence 4, Appli
14	0.4	30	1	US-09-684-843A-4	Sequence 4, Appli
13.8	0.4	17	1	US-08-390-850-438	Sequence 438, App
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c 132 13.8 0.4 17 1 US-09-866-108A-7803
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c 135 13.8 0.4 17 1 US-09-685-664B-25
c 136 13.8 0.4 17 1 US-09-685-664B-26
c 137 13.8 0.4 17 1 US-09-685-664B-414
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c 139 13.8 0.4 17 1 US-09-685-664B-1095
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ALIGNMENTS

RESULT 1
US-08-863-639A-29/c
; Sequence 29, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000

; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-29
Query Match 0.9%; Score 32; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 1440
Db 33 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 2
RESULT 2
US-09-475-947A-251
; Sequence 251, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 251
; LENGTH: 33
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-251
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Best Local Similarity 96.9%; Pred. No. 3.6;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 1440
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCA 32
RESULT 3
US-08-068-747-6
; Sequence 6, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747

FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-08-068-747-6

Query Match 0.8% Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 4
US-08-068-747-11/c
Sequence 11, Application US/08068747
Patent No. 5695933
GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Houseman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-08-068-747-11

Query Match 0.8% Score 30; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 30 CAGCAGCAGCAGCAGCAGCAGCAGCAG 1

RESULT 5
US-08-863-639A-30
Sequence 30, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C.T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueh
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 795-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-30

Query Match 0.8% Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 6
US-09-135-994-4
Sequence 4, Application US/09135994A
Patent No. 6280938
GENERAL INFORMATION:
APPLICANT: Ranum et al.
TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-994-4

Query Match          0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
      |||||||||||||||||||||||||||||||
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 7
US-09-684-843A-4
; Sequence 4, Application US/09684843A
; Patent No. 6514755
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/684,843A
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-684-843A-4

Query Match          0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
      |||||||||||||||||||||||||||||||
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 8
US-08-570-155-14
; Sequence 14, Application US/08570155
; Patent No. 5962332
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.
; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE REPEATS
; TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,155
; FILING DATE: 08/08/2005
```

```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/399,499
; FILING DATE: 07 March 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,823
; FILING DATE: 17 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06353/011001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-570-155-14

Query Match          0.8%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
      |||||||||||||||||||||||||||||||
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 9
PCT-US95-02861-14
; Sequence 14, Application PC/TUS9502861
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.
; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE
; TITLE OF INVENTION: REPEATS
; TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version
; SOFTWARE: #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02861
; FILING DATE: 08 March 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,823
; FILING DATE: 17 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Creason, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 06353/010W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US95-02861-14

Query Match      0.8%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2; Mismatches 0; Indels 0; Gaps 0;
Matches 30; Conservative 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 10
US-09-304-232-152
; Sequence 152, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304,232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084,641
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APOA4 3058
US-09-304-232-152

Query Match      0.7%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;
Matches 26; Conservative 1;

Qy 1400 CAGCAGCAACAGCAGCAGCAGCAGCAGCAGCA 1428
Db 1 CAGCAGGAACAGCAKAGCAGGAGCAGCAGCA 29

RESULT 11
US-08-863-639A-94
; Sequence 94, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
```

```
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel Wordperfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-94

Query Match      0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.7; Mismatches 24; Conservative 0; Indels 0; Gaps 0;
Matches 24;

Qy 1411 GCAGCAGCAGCAGCAGCAGCAGCA 1434
Db 1 GCAGCAGCAGCAGCAGCAGCAGCA 24

RESULT 12
US-08-267-803B-66/c
; Sequence 66, Application US/08267803B
; Patent No. 5834183
; GENERAL INFORMATION:
; APPLICANT: Orr, Harry T.
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Chung, Ming-yi
; APPLICANT: Zoghbi, Huda Y.
; TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
; Patent No. 5834183
; TITLE OF INVENTION: Type 1 and Method for Diagnosis
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/267,803B
; FILING DATE: 28-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H.
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 110.00030120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

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;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-267-803B-66

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1410 AGCAGCAGCAGCAGCAGCAGC 1430
Db 21 AGCAGCAGCAGCAGCAGCAGC 1

RESULT 13
US-08-663-639A-28
; Sequence 28, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-28

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 1 CAGCAGCAGCAGCAGCAGCAG 21

RESULT 14
US-08-863-639A-40
; Sequence 40, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-28
```

```
;
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-40

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1410 AGCAGCAGCAGCAGCAGCAGC 1430
Db 1 AGCAGCAGCAGCAGCAGCAGC 21

RESULT 15
US-08-863-639A-60/C
; Sequence 60, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
```


REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-60

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
DB 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 16
US-08-863-639A-66
Sequence 66, Application US/08863639A
Patent No. 5981185

GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-66

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAGCA 1431
DB 1 GCAGCAGCAGCAGCAGCAGCA 21

RESULT 17
US-08-863-639A-69/c
Sequence 69, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-69

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGC 1430
DB 21 AGCAGCAGCAGCAGCAGCAGC 1

RESULT 18
US-08-863-639A-87/c
Sequence 87, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA: 08/863.639A
; APPLICATION NUMBER: US/08/863.639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-87

Query Match      0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAGCA 1431
Db 21 GCAGCAGCAGCAGCAGCAGCA 1

RESULT 19
US-09-396-196G-74107
; Sequence 74107, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
; US-09-396-196G-74107

Query Match      0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 34;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1597 GCAGCAGCAGCAGCAACCACTCT 1621
Db 1 GCAGCAGCAGCAGCAGCAACCTCT 25

RESULT 20
US-09-198-452A-6476/c
; Sequence 6476, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffa, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention
```

```
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6476
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; US-09-198-452A-6476

Query Match      0.5%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1454 CAGCAACAGCAACAGCAAC 1472
Db 19 CAGCAACAGCAACAGCAAC 1

RESULT 21
US-09-632-098-24/c
; Sequence 24, Application US/09632098
; Patent No. 6420154
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/09/632,098
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ologonucleotide ZC21.076
; US-09-632-098-24

Query Match      0.5%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1421 CAGCAGCAGCAGCAGCAAC 1442
Db 23 CAGTAGTAGCAGCAGCAGCAAC 2

RESULT 22
US-10-177-308-24/c
; Sequence 24, Application US/10177308
; Patent No. 6762044
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/10/177,308
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/632,098
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ologonucleotide ZC21.076
```

Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Watson, Robert S.
APPLICANT: Coasasin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95

```
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-47
Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1574 CAACAACAACAGCAACAACA 1593
Db 1 CAACAACAACAACAACAACA 20

RESULT 26
US-08-863-639A-89/c
; Sequence 89, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863.639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-89
Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1574 CAACAACAACAGCAACAACA 1593
Db 20 CAACAACAACAACAACAACA 1

RESULT 27
```

```
US-08-863-639A-92/c
; Sequence 92, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863.639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-92
Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1574 CAACAACAACAGCAACAACA 1593
Db 21 CAACAACAACAACAACAACA 2

RESULT 28
US-08-863-639A-17/c
; Sequence 17, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
```

```
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 17:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-17

Query Match          0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCA 1428
Db 18 GCAGCAGCAGCAGCAGCA 1

RESULT 29
US-09-205-995-48/c
; Sequence 48, Application US/09205995
; Patent No. 6368855
; GENERAL INFORMATION:
; APPLICANT: Xu, Minzhen
; APPLICANT: Qiu, Gang
; TITLE OF INVENTION: CANCER CELL VACCINE
; FILE REFERENCE: U.S. Application 09/205,995, (CIP)
; CURRENT APPLICATION NUMBER: US/09/205,995
; CURRENT FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 09/036,746
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: 08/661,627
; PRIOR FILING DATE: 1996-06-11
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: oligonucleotide corresponding to a specific region
; OTHER INFORMATION: of the mouse II gene.
US-09-205-995-48

Query Match          0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAG 1417
Db 18 CAGCAGCAACAGCAGCAG 1

RESULT 30
US-08-863-639A-14
; Sequence 14, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
```

```
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-14

Query Match          0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1572 AGCAACAACAACAACAACAAC 1592
Db 1 AACACAACAACAACAACAACAAC 21

RESULT 31
US-08-863-639A-77/c
; Sequence 77, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-77

Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1572 AGCAACACACACACACAC 1592
Db 21 AACCAACACACACACACAC 1

RESULT 32
US-08-410-540-5
; Sequence 5, Application US/08410540
; Patent No. 5807678
; GENERAL INFORMATION:
; APPLICANT: Miller, Walter L.
; APPLICANT: Lin, Dong
; APPLICANT: Strauss III, Jerome F.
; TITLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
; TITLE OF INVENTION: ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 23-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-238/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 853 5070
; TELEFAX: 415 857 0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-410-540-5

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 31;
```

```
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAG 1429
Db 1 GCAGCAGCAGCAGCAGCAG 19

RESULT 33
US-08-914-961-6/C
; Sequence 6, Application US/08914961
; Patent No. 6018042
; GENERAL INFORMATION:
; APPLICANT: Mett, Helmut
; APPLICANT: Haner, Robert
; APPLICANT: Dean, Nicholas Mark
; TITLE OF INVENTION: Antitumor Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,961
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/287,753
; FILING DATE: 09-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 4-20047/P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8615
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; POSITION IN GENOME:
; MAP POSITION: 979
; UNITS: bp
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..20
; OTHER INFORMATION: /note= "All nucleotides are of the
; OTHER INFORMATION: phosphorothioate type"
US-08-914-961-6

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1545 AGCAGCAGCAGCAGCAGCA 1563
Db 19 AGAAGCAGCAGCAGCAGCA 1

RESULT 34
US-09-723-368-5
; Sequence 5, Application US/09723368
```

Patent No. 6641818
GENERAL INFORMATION:
APPLICANT: NORTHWESTERN UNIVERSITY
APPLICANT: SPEAR, Patricia G.
APPLICANT: WARNER, Morgyn S.
APPLICANT: GERAGHTY, Robert G.
APPLICANT: MARTINEZ, Wanda M.
APPLICANT: MONTGOMERY, Rebecca I.
APPLICANT: COHEN, Gary H.
APPLICANT: EISENBERG, Roselyn J.
APPLICANT: WHITBECK, Charles J.
APPLICANT: KRUMENACHER, Claude
APPLICANT: UNIVERSITY OF PENNSYLVANIA
TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
FILE REFERENCE: 200290.0050/2U1
CURRENT APPLICATION NUMBER: US/09/723,368
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. 60/087,862
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: PCT/US99/12235
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Primer PRR2A8
US-09-723-368-5

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 973 GATCAGCAGCACCAGCAG 991
Db 2 GAAGCAGCAGCACCAGCAG 20

RESULT 35
US-08-970-269A-2
Sequence 2, Application US/08970269A
Patent No. 5976803
GENERAL INFORMATION:
APPLICANT: Kathryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,269A
FILING DATE: No. 5976803ember 14, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-08-970-269A-2
Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 255 GGGAGAATCTCTCTGCA 271
Db 1 GGGAGAATCTCTCTGCA 17
RESULT 36
US-09-407-562-2
Sequence 2, Application US/09407562
Patent No. 6294334
GENERAL INFORMATION:
APPLICANT: Kathryn Meek
TITLE OF INVENTION: Genetic Test For Equine Severe
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Benjamin A. Adler
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,562
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/970,269
FILING DATE: No. 6294334ember 14, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
FEATURE:
US-09-407-562-2
Query Match 0.5%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 GGGAGAAATCTCTGCA 271
Db 1 GGGAGAAATCTCTGCA 17

RESULT 37
US-08-628-540-8/c
; Sequence 8, Application US/08628540
; Patent No. 6022951
; GENERAL INFORMATION:
; APPLICANT: SANO, Takeshi
; APPLICANT: CANTOR, Charles R.
; APPLICANT: VAJDA, Sandor
; APPLICANT: REZNIK, Gabriel O.
; APPLICANT: SMITH, Cassandra L.
; APPLICANT: PANDORI, Mark W.
; TITLE OF INVENTION: STREPTAVIDIN MUTANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,540
; FILING DATE: 10-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/420,010
; FILING DATE: 11-APR-1995
; APPLICATION NUMBER: 60/003,687
; FILING DATE: 18-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 016865-0244
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-628-540-8

Query Match 0.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1425 AGCAGCAGCAGCAGCAA 1441
Db 19 AGCAGCAGCAGCAGCAA 3

RESULT 38
US-08-628-540-8/c
; Sequence 8, Application US/08941100B
; Patent No. 6207390
; GENERAL INFORMATION:
; APPLICANT: Sano, Takeshi
; APPLICANT: Cantor, Charles R.
; TITLE OF INVENTION: Reduced Affinity Streptavidin
; FILE REFERENCE: BU-03165
; CURRENT APPLICATION NUMBER: US/08/941,100B
; CURRENT FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: 08/469,353
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/420,010
; PRIOR FILING DATE: 1995-04-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Streptomyces avidinii
US-08-941-100-3

Query Match 0.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1425 AGCAGCAGCAGCAGCAA 1441
Db 19 AGCAGCAGCAGCAGCAA 3

RESULT 39
US-09-043-303-8
; Sequence 8, Application US/09043303
; Patent No. 6251589
; GENERAL INFORMATION:
; APPLICANT: TSUJI, Shoji
; APPLICANT: SANPEI, Kazuhiro
; TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Alaxia Type 2 and
; TITLE OF INVENTION: Primers Therefor
; FILE REFERENCE: 0760-0241P
; CURRENT APPLICATION NUMBER: US/09/043,303
; CURRENT FILING DATE: 1998-05-18
; EARLIER APPLICATION NUMBER: PCT/JP96/01999
; EARLIER FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-043-303-8

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1448 CAGCAGCAGCAGCAACA 1467
Db 1 CACCACCAGCAACAACA 20

RESULT 40
US-09-661-753-35
; Sequence 35, Application US/09661753
; Patent No. 6436909
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
; FILE REFERENCE: ISPH-0498

; CURRENT APPLICATION NUMBER: US/09/661,753
; CURRENT FILING DATE: 2000-09-14
; EARLIER APPLICATION NUMBER: 60/154,546
; EARLIER FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-661-753-35

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 90.4%; Pred. No. 44;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGC 1430
Db 1 GTAGCAGCAGCGGCAGCAGC 20

RESULT 41

US-08-863-639A-15
; Sequence 15, Application US/08863639A
; Patent No. 5981185

; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-15

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1576 ACAACAACAGCAACAA 1593
Db 1 ACAACAACAGCAACAA 18

RESULT 42

US-08-863-639A-16
; Sequence 16, Application US/08863639A
; Patent No. 5981185

; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-16

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1574 CAACAACAGCAACAA 1591
Db 1 CAACAACAGCAACAA 18

RESULT 43

US-09-487-444-11
; Sequence 11, Application US/09487444
; Patent No. 6159697

; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD7 EXPRESSION
; FILE REFERENCE: RTS-0133
; CURRENT APPLICATION NUMBER: US/09/487,444
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-487-444-11

```
Query Match      0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1406 CAACAGCAGCAGCAGCAG 1423
Db 1 CGACAGCAGCAGCAGCAG 18

RESULT 44
US-09-657-042A-39/c
; Sequence 39, Application US/09657042A
; Patent No. 6329203
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRESSION
; FILE REFERENCE: RTS-0148
; CURRENT APPLICATION NUMBER: US/09/657,042A
; CURRENT FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-657-042A-39

Query Match      0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 976 GCAGCAGCAGCAGCAGCA 993
Db 19 GCAGCAGCTCCAGCAGCA 2

RESULT 45
US-09-907-843-23/c
; Sequence 23, Application US/09907843
; Patent No. 6440739
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSION
; FILE REFERENCE: RTS-0279
; CURRENT APPLICATION NUMBER: US/09/907,843
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-907-843-23

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1427 CAGCAGCAGCAGCAAC 1442
Db 17 CAGCAGCAGCAGCAAC 2

RESULT 46
US-09-696-791-203/c
; Sequence 203, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
```

```
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdk2 ribozyme binding site
US-09-696-791-203

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAACACAGATAGC 948
Db 19 AGCAGCTGGAACAGATAGC 1

RESULT 47
US-09-475-947A-251/c
; Sequence 251, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 251
; LENGTH: 33
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-251

Query Match      0.4%; Score 15.6; DB 1; Length 33;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTACTGCTGCTGCTGCTGCTGCTG 1

RESULT 48
US-08-985-162-175
; Sequence 175, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
```

```
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985.162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036.476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-985-162-175

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 38;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3633 GAGAACCTGAGAAACAT 3649
Db 1 GAGAACCUAGAAAUCAU 17
|||||:|||||:|

RESULT 49
US-08-584-040-5601/c
; Sequence 5601, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584.040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005.974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5601:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-5601

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 326 TTGCCTATGAGCCCAAGC 342
Db 17 TTGCCTGTGAGCCAAGC 1
|||||:|||||:|

RESULT 50
US-09-371-772B-2491/c
; Sequence 2491, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2491
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
; US-09-371-772B-2491

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 326 TTGCCTATGAGCCCAAGC 342
Db 17 TTGCCTGTGAGCCAAGC 1
|||||:|||||:|

RESULT 51
US-09-401-063-175
; Sequence 175, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
```

```

, TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
, TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
, TITLE OF INVENTION: FACTOR RECEPTORS
, NUMBER OF SEQUENCES: 1877
, CORRESPONDENCE ADDRESS:
, ADDRESSEE: Lyon & Lyon
, STREET: 633 West Fifth Street
, STREET: Suite 4700
, CITY: Los Angeles
, STATE: California
, COUNTRY: U.S.A.
, ZIP: 90071-2066
, COMPUTER READABLE FORM:
, MEDIUM TYPE: 3.5" diskette, 1.44 Mb
, MEDIUM TYPE: storage
, COMPUTER: IBM Compatible
, OPERATING SYSTEM: IBM P.C. DOS 5.0
, SOFTWARE: FastSeq For Windows 2.0
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/09/401,063
, FILING DATE:
, CLASSIFICATION:
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 08/985,162
, FILING DATE: 04 December 1997
, APPLICATION NUMBER: 60/036,476
, FILING DATE: 31 January 1997
, ATTORNEY/AGENT INFORMATION:
, NAME: Warburg, Richard J.
, REGISTRATION NUMBER: 32,327
, REFERENCE/DOCKET NUMBER: 230/107
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (213) 489-1600
, TELEFAX: (213) 955-0440
, TELEX: 67-3510
, INFORMATION FOR SEQ ID NO: 175:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 17 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, US-09-401-063-175

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```

; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2491
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2491

Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred.No.38;
Matches 16; Conservative 0; Mismatches 1; Indels

QY      326 TTGCCTATGAGCCCAAGC 342
        |||||:|||||
Db       17 TTGCCTGTGAGCCCAAGC 1

RESULT 53
US-08-758-306-519
; Sequence 519, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 519:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-758-306-519

Query Match      0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 88.2%; Pred.No.47;
Matches 15; Conservative 1; Mismatches 1; Indels

QY      993 AGCACCAACGCTTACCAAC 1009
        |||||:|||||

```

Db 1 AGCCCCAGCCUACCAAC 17

RESULT 54
US-08-647-144-10/c
; Sequence 10, Application US/08647144
; Patent No. 5858728
; GENERAL INFORMATION:
; APPLICANT: Gram, Hermann
; APPLICANT: Di Padova, Franco
; APPLICANT: Barclay, George R.
; APPLICANT: Poxtton, Ian R.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST LPS CORE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; CITY: Charlotte
; STATE: No. 5858728th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,144
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/119,046
; FILING DATE: 10-SEP-1993
; APPLICATION NUMBER: EP 92/00380
; FILING DATE: 22-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 1749-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: YES
US-08-647-144-10

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 593 AGTCACTTGAACCTGGA 609
Db 17 AGTGACCTTGACCTGGA 1

RESULT 55
US-09-255-912-14/c
; Sequence 14, Application US/09255912
; Patent No. 6037142
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTS-0044
; CURRENT APPLICATION NUMBER: US/09/255,912
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-912-14

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 73 GAACGACGCGGAGGAGA 89
Db 18 GGACGACGCGGAGGAGA 2

RESULT 56
US-09-696-791-323
; Sequence 323, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 323
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdk3 ribozyme binding site
US-09-696-791-323

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2942 TTGACTTCTCTCAGCCA 2958
Db 3 TTGAGTTCTCTCAGCCA 19

RESULT 57
US-09-696-791-324
; Sequence 324, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
; APPLICANT: Robbins, Joan M.
; APPLICANT: Tritz, Richard
; TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 480124.407
; CURRENT APPLICATION NUMBER: US/09/696,791
; CURRENT FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4523
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 324
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cdk3 ribozyme binding site
US-09-696-791-324

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2942 TTTGACTTCTCAGCCA 2958
Db 2 TTTGAGTTCTCAGCCA 18

RESULT 58
US-08-570-155-14/c
; Sequence 14, Application US/08570155
; Patent No. 5962332
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.
; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE REPEATS
; TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570.155
; FILING DATE: 17 March 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/399,499
; FILING DATE: 07 March 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,823
; FILING DATE: 17 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06353/011001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US95-02861-14/c
; Sequence 14, Application PC/TUS9502861
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.
; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE REPEATS
; TITLE OF INVENTION: REPEATS

Query Match 0.4%; Score 15; DB 1; Length 31;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1924 ACAGCAACTTCTCTCCAGCAGCAGATGCTG 1954
Db 31 ACTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 59
PCT-US95-02861-14/c
; Sequence 14, Application PC/TUS9502861
; GENERAL INFORMATION:
; APPLICANT: Singer, Robert H.
; APPLICANT: Taneja, Krishan L.
; TITLE OF INVENTION: DETECTION OF TRINUCLEOTIDE REPEATS
; TITLE OF INVENTION: REPEATS

; TITLE OF INVENTION: BY IN SITU HYBRIDIZATION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version
; SOFTWARE: #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02861
; FILING DATE: 08 March 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/214,823
; FILING DATE: 17 March 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Creason, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 06353/010W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US95-02861-14

Query Match 0.4%; Score 15; DB 1; Length 31;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1924 ACAGCAACTTCTCTCCAGCAGCAGATGCTG 1954
Db 31 ACTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 60
US-08-863-639A-29
; Sequence 29, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:

```
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Joseph E. Mueth
;   REGISTRATION NUMBER: 20,532
;   REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (626) 796-4000
;   TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 33 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: Other nucleic acid
US-08-863-639A-29

Query Match      0.4%; Score 15; DB 1; Length 33;
Best Local Similarity 67.7%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGC 1439
Db 1 CTGCTGCTGCTGCTGCTGCTGCTGCTGTC 31

RESULT 61
US-08-317-431A-11
; Sequence 11, Application US/08317431A
; Patent No. 5650277
; GENERAL INFORMATION:
; APPLICANT: Nir Navot and Nurit Eyal
; TITLE OF INVENTION: A method of determining the presence and
; TITLE OF INVENTION: quantifying the number of di- and
; TITLE OF INVENTION: trinucleotide repeats and instrument and
; TITLE OF INVENTION: kits therefore
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
; STREET: 2940 Birchtree space lane
; CITY: Silver Spring
; STATE: Maryland
; COUNTRY: United States of America
; ZIP: 20906
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Chicony NB5500/386SX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.1
; SOFTWARE: Word for Windows version 2.0
; SOFTWARE: Conv. to ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,431A
; FILING DATE: 4-Oct-94
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/084,505
; APPLICATION NUMBER: 08/084,505
; FILING DATE: 1-Jul-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedmam, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 128/8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-6938541
; TELEFAX: 972-3-6938542
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 18
;   TYPE: nucleic acid
;   STRANDEDNESS: single
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; TOPOLOGY: linear
US-08-317-431A-11
; Query Match      0.4%; Score 14.8; DB 1; Length 18;
; Best Local Similarity 88.9%; Pred. No. 56;
; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1448 CAGCAGCAGCAGCAGCAGCAGCAGCAG 1465
Db 1 CACCACCAGCAGCAGCAGCAGCAGCAGCAG 18

RESULT 62
US-09-106-038A-24
; Sequence 24, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 18
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-09-106-038A-24

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1406 CAACAGCAGCAGCAGCAGCAGCAGCAG 1423
Db 1 CACCAGCGGCAGCAGCAGCAGCAGCAGCAG 18

RESULT 63
US-09-106-038A-25
; Sequence 25, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
```



```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/352,902D
; FILING DATE: 09-Dec-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Ryselberghe, Pierre C.
; REGISTRATION NUMBER: 33,557
; REFERENCE/DOCKET NUMBER: OHSU 306B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 224-6655
; TELEFAX: (503) 295-6679
; TELEX: 360619
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "primers directed to genomic
; intron DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-08-352-902D-60

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1223 CAAAAGCTTCAGATCTC 1240
Db 1 CAAAAGCTTCAGATCTC 18

RESULT 67
US-08-748-073-3
; Sequence 3, Application US/08748073
; Patent No. 6204008
; GENERAL INFORMATION:
; APPLICANT: Borneman, W. Scott
; APPLICANT: Goyal, Anil
; APPLICANT: Conder, Michael J.
; APPLICANT: Vinci, Victor A.
; TITLE OF INVENTION: BIOPROCESS FOR PRODUCTION OF DIPEPTIDE
; TITLE OF INVENTION: BASED COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,073
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: MK-19147F
```

```
;
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732/594-3905
; TELEFAX: 732/594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
US-08-748-073-3

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 983 CACCAGCAGCAGCACCAG 1000
Db 1 CACCAGCTCCAGCACCAG 18

RESULT 68
US-08-584-040-4471
; Sequence 4471, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4471:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4471
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Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1094 ACATTGAGCCACAGAGC 1111
DB 1 ACAUGCAGCCACUGAGC 18

RESULT 69
US-09-475-947A-340
; Sequence 340, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS00867
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 340
; LENGTH: 18
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-340

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428
DB 1 GCAGCAGCAGCAGCAGCA 18

RESULT 70
US-09-280-030-28/c
; Sequence 28, Application US/09280030A
; Patent No. 6506595
; GENERAL INFORMATION:
; APPLICANT: Sato, Seiji
; APPLICANT: Higashikuni, Naohiko
; APPLICANT: Kudo, Toshiyuki
; APPLICANT: Kondo, Masaaki
; TITLE OF INVENTION: DNAs ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
; TITLE OF INVENTION: PREPARING USEFUL POLYPEPTIDES THROUGH EXPRESSION OF THE
; FILE REFERENCE: DNAs
; FILE REFERENCE: 382.1026
; CURRENT APPLICATION NUMBER: US/09/280,030A
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: JP10-87339/1998
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designated is
; OTHER INFORMATION: a reverse primer for PCR amplification of
; OTHER INFORMATION: MWPp-MWPmp5 DNA
US-09-280-030-28

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428

Db 18 GCAGCAGCAGCAGCAGCA 1

RESULT 71
US-09-265-503B-60
; Sequence 60, Application US/09265503B
; Patent No. 6538108
; GENERAL INFORMATION:
; APPLICANT: Liskay, Robert M.
; APPLICANT: Bronner, C. Eric
; APPLICANT: Baker, Sean M.
; APPLICANT: Bollag, Roni J.
; APPLICANT: Kolodner, Richard D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: RELATING TO DNA MISMATCH REPAIR GENES
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack & Heuser
; STREET: 520 S.W. Yamhill Street, Suite 200
; CITY: Portland
; STATE: Oregon
; COUNTRY: U.S.A.
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/265,503B
; FILING DATE: March 10, 1999
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Rysselberghe, Pierre C.
; REGISTRATION NUMBER: 33,557
; REFERENCE/DOCKET NUMBER: OHSU 306D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 224-6655
; TELEFAX: (503) 295-6679
; TELEX: 360619
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "primers directed to genomic
; OTHER INFORMATION: intron DNA"
US-09-265-503B-60

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1223 CAAAAGCCTCAGATCTC 1240
DB 1 CAAAAGCCTCAGATCTC 18

RESULT 72
US-09-371-772B-2184
; Sequence 2184, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

```
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2184
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2184

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1094 ACATTCAGCCCAAGC 1111
    |||: ||||| |||||
Db 1 ACAUGCAGCCCAAGC 18

RESULT 73
US-09-685-664B-2184
; Sequence 2184, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2184
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-2184

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1094 ACATTCAGCCCAAGC 1111
    |||: ||||| |||||
Db 1 ACAUGCAGCCCAAGC 18

RESULT 74
US-10-272-865-14
; Sequence 14, Application US/10272865
; Patent No. 6828105
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
```

```
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for Treating sRNA Viral Infection
; FILE REFERENCE: 50450-8046.US00
; CURRENT APPLICATION NUMBER: US/10/272,865
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/329,815
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-272-865-14

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1271 GCCATGGAGCCCGTCAG 1288
    ||||| ||||| |||||
Db 1 GCCATGGAGCCCGTCAG 18

RESULT 75
US-10-272-865-34/C
; Sequence 34, Application US/10272865
; Patent No. 6828105
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for Treating sRNA Viral Infection
; FILE REFERENCE: 50450-8046.US00
; CURRENT APPLICATION NUMBER: US/10/272,865
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/329,815
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antisense oligomer
US-10-272-865-34

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1271 GCCATGGAGCCCGTCAG 1288
    ||||| ||||| |||||
Db 18 GCCATGGAGCCCGTCAG 1

RESULT 76
US-08-292-620A-1659
; Sequence 1659, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF INTRACELLULAR ADHESION
```


COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.845
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/292.620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008.895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989.849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1659:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1659

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2349 GGCACCTACTCTAGG 2364
DB 1 GGGCCCUACCUAGG 16

RESULT 80
US-08-584-040-3988
Sequence 3988, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3988:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-3988

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 52;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3494 AATTGCTCTAATAGA 3509
DB 1 AAUUGCUCUUAUGA 16

RESULT 81
US-09-371-772B-1755
Sequence 1755, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MEHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371.772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1755
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-1755

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 52;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3494 AATTGCTCTAATAGA 3509
DB 1 AAUUGCUCUUAUGA 16

RESULT 82
US-09-371-772B-6407
Sequence 6407, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam

```
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6407
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6407

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 52;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy      3494 AATTGCTCTAATAGA 3509
      ||::||:|:|:|:|:|
Db      2 AAUUGCUCUAUUGA 17

RESULT 83
US-09-866-108A-7201
; Sequence 7201, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7201
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7202

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      322 GACCTTGCCCTATGAGC 337
      |||||
Db      1 GACCTTGCCGATGAGC 16

RESULT 84
US-09-866-108A-7202
; Sequence 7202, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7202
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7202

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 52;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      322 GACCTTGCCCTATGAGC 337
      |||||
Db      1 GACCTTGCCGATGAGC 16

RESULT 85
US-09-866-108A-8467
; Sequence 8467, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
```

; PRIOR APPLICATION NUMBER: PCT/US01/006667

; GENERAL INFORMATION:

```
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-212-771-18

Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 73 GAAGCAGCGGAGGAG 88
Db 18 GAAGCAGCGGAGGAG 3

RESULT 89
US-09-205-143-19
; Sequence 19, Application US/09205143
; Patent No. 6107091
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-16 EXPRESSION
; FILE REFERENCE: RTS-0032
; CURRENT APPLICATION NUMBER: US/09/205,143
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-143-19

Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1532 GCCCAACGACGACG 1547
Db 3 GCCCAAAAGCAGCAGC 18

RESULT 90
US-08-068-747-6/c
; Sequence 6, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Houseman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/068,747
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
US-08-068-747-6

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCACTTCTTCTCCAGCAGCAGCTG 1954
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 91
US-08-068-747-11
; Sequence 11, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Houseman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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; DESCRIPTION: /desc = "Synthetic"
US-08-068-747-11

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred.No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 1 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 30

RESULT 92
US-08-639A-30/c
; Sequence 30, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel Wordperfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863.639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muech
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-639A-30

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred.No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 93
US-09-135-994-4/c
; Sequence 4, Application US/09135994A
; Patent No. 6280938
; GENERAL INFORMATION:
; APPLICANT: Rannum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/135,994A
```

```
; CURRENT FILING DATE: 1998-08-18
; EARLIER APPLICATION NUMBER: 60/056,170
; EARLIER FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-994-4

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred.No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 94
US-09-684-843A-4/c
; Sequence 4, Application US/09684843A
; Patent No. 6514755
; GENERAL INFORMATION:
; APPLICANT: Rannum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/09/684,843A
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-684-843A-4

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred.No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 95
US-08-390-850-438/c
; Sequence 438, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
```


; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1513:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-1513

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 62;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 3008 GATTCTTTATTGAGAC 3024
Db 1 GAUUCUUCUUGAACAC 17

RESULT 98
; Sequence 2, Application US/08158352
; Patent No. 5700922
; GENERAL INFORMATION:
; APPLICANT: Philip Dan Cook
; TITLE OF INVENTION: PNA-DNA-PNA Chimeric
; TITLE OF INVENTION: Macromolecules
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
; ADDRESSEE: No. 5700922ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/158,352
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US92/11339
; FILING DATE: December 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-1236
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes

US-08-158-352-2
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 38 CGGAATTCAGCGAGAA 54
Db 17 CTGAATTCAGCGAGAA 1

RESULT 99
US-08-435-634-438/c
; Sequence 438, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggan, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 438:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-634-438

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 560 AATGAAGTACCAACAT 576
Db 17 ACTGAAGTACCAACAT 1

RESULT 100
US-08-435-634-452/c
; Sequence 452, Application US/08435634
; Patent No. 5731295
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela

```

; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435.634
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/390,850
; FILING DATE: February 17, 1995
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: No. 5731295ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 211/084
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 452:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-634-452

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1432 GCAGCAGACAGCAGC 1448
Db 17 GCAGCATCAACAGCATC 1

RESULT 101
US-08-758-306-903/c
; Sequence 903, Application US/08/58306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

```

; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 903:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-903

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 252 TTGGGGAGATCTCTCT 268
Db 17 TTGGGGGGAATCTGCT 1

RESULT 102
US-08-435-628-1513
; Sequence 1513, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628

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; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1513:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-1513

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 62;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 3008 GATCTTTATTCAGAC 3024
Db 1 GAUCUUCUUGAACAC 17

RESULT 103
US-09-050-159-45
; Sequence 45, Application US/09050159A
; Patent No. 6197505
; GENERAL INFORMATION:
; APPLICANT: No. 6197505berg, Leif T
; APPLICANT: Andersson, Maria K
; APPLICANT: Linstrom, Per H
; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
; FILE REFERENCE: 1248/1D042
; CURRENT APPLICATION NUMBER: US/09/050,159A
; CURRENT FILING DATE: 1998-03-27
; EARLIER APPLICATION NUMBER: 60/042,930
; EARLIER FILING DATE: 1987-04-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
US-09-050-159-45

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1427 CAGCAGCAGCAGCAACA 1443
Db 1 CGGCGGCAGCAGCAACA 17

RESULT 104

US-09-050-159-51
; Sequence 51, Application US/09050159A
; Patent No. 6197505
; GENERAL INFORMATION:
; APPLICANT: No. 6197505berg, Leif T
; APPLICANT: Andersson, Maria K
; APPLICANT: Linstrom, Per H
; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
; FILE REFERENCE: 1248/1D042
; CURRENT APPLICATION NUMBER: US/09/050,159A
; CURRENT FILING DATE: 1998-03-27
; EARLIER APPLICATION NUMBER: 60/042,930
; EARLIER FILING DATE: 1987-04-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
US-09-050-159-51

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1427 CAGCAGCAGCAGCAACA 1443
Db 1 CGGCGGCAGCAGCAACA 17

RESULT 105
US-09-108-911-2/c
; Sequence 2, Application US/09108911
; Patent No. 6277603
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; TITLE OF INVENTION: PNA-DNA-PNA Chimeric Macromolecules
; FILE REFERENCE: ISIS3102
; CURRENT APPLICATION NUMBER: US/09/108,911
; CURRENT FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 08/877,317
; PRIOR FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Antisense Sequence
US-09-108-911-2

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 38 CGGAAATTCAGCGAGAA 54
Db 17 CTGAAATGCAGCGAGAA 1

RESULT 106
US-08-584-040-1480
; Sequence 1480, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.


```

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1869:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-1869

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 430 GGAGCCAGGAGACTC 446
Db 17 GGAGCCAGGAGAGCTC 1

RESULT 109
US-08-584-040-1870/c
; Sequence 1870, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2571:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2571

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

; INFORMATION FOR SEQ ID NO: 1870:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-1870

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 429 AGGAGCCAGGAGACT 445
Db 17 AGGAGCCAGGAGAGCT 1

RESULT 110
US-08-584-040-2571
; Sequence 2571, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2571:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-2571

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
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QY      224 TCATTCTTGATACAA 240
      :||: :||: :||: :||:
Db      1 UCAUGUCUUAUUUCAA 17

RESULT 111
US-08-584-040-4365/c
; Sequence 4365, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4365:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-4365

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1509 AACAGCAGCAGAGTCA 1525
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Db      17 AACAGGAGGAGAGTCA 1

RESULT 112
US-08-584-040-7233
; Sequence 7233, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4365:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7233

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2166 TGTCTACTTCTCAGGG 2182
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Db      1 UGUCUGUCUUCACAGG 17

RESULT 113
US-08-584-040-7234
; Sequence 7234, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7233

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 62;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      2166 TGTCTACTTCTCAGGG 2182
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Db      1 UGUCUGUCUUCACAGG 17

RESULT 113
US-08-584-040-7234
; Sequence 7234, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7233:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7233

```


CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7234:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-7234

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 62;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2167 GTCTACTTCTCAGCGGA 2183
|.:|.:|.:|.:|.:|
Db 1 GUCUGUCUCACAGGA 17

RESULT 114
US-08-584-040-7450
; Sequence 7450, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7450:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-7450

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 62;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2757 GTCTGAATCTCAGACCC 2773
|.:|.:|.:|.:|.:|
Db 1 GCGUGACUCACAGACC 17

RESULT 115
US-09-612-555-13/c
; Sequence 13, Application US/09612555
; Patent No. 6528257
; GENERAL INFORMATION:
; APPLICANT: Sharma, Vishva M
; APPLICANT: Ganesan, Kallanman
; TITLE OF INVENTION: A Method for the Simultaneous Monitoring of Individual
; TITLE OF INVENTION: Mutants in Mixed Populations
; FILE REFERENCE: Method for Simultaneous Monitoring
; CURRENT APPLICATION NUMBER: US/09/612,555
; CURRENT FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tag1 adapters
US-09-612-555-13

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2753 AGGGTCTGAATCTCAG 2769
|.:|.:|.:|.:|.:|
Db 17 AGGGTCTGAGCTCAG 1

RESULT 116
US-09-371-772B-25
; Sequence 25, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-25

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 62;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TGTCTACTTCTCAGGG 2182
:|:|:|:|:|:|
Db 1 UGUCGUUCUCACAGG 17

RESULT 117
US-09-371-772B-26
; Sequence 26, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-26

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 62;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2167 GTCTACTTCTCAGGGA 2183
|:|:|:|:|:|
Db 1 GUCUGUUCUCACAGGA 17

RESULT 118
US-09-371-772B-414/c
; Sequence 414, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)

; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 414
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-414

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 GGAGCCAGGAGAGACTC 446
|:|:|:|:|:|:|
Db 17 GGAGCCAGGAGAGACTC 1

RESULT 119
US-09-371-772B-415/c
; Sequence 415, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 415
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-415

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 429 AGGAGCCAGGAGAGACT 445
|:|:|:|:|:|:|
Db 17 AGGAGCCAGGAGAGACT 1

RESULT 120
US-09-371-772B-1095
; Sequence 1095, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1095
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1095

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 62;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
QY 224 TCATTCTTGATATCAA 240
DB 1 UCAUGUCUUGAUUCAA 17

RESULT 121
US-09-371-772B-2132/c
; Sequence 2132, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-2132

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1509 AACAGCAGCAGCTCA 1525
DB 17 AACAGGAGGAGCTCA 1

RESULT 122
US-09-371-772B-3256
; Sequence 3256, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3256
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3256

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 62;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2757 GTCGAATCTCAGACCC 2773
DB 1 GGCUGACUCUCAGACCC 17

RESULT 123
US-09-371-772B-4212
; Sequence 4212, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4212
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4212

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 62;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 2165 CTGCTACTTCTCAGG 2181
DB 1 CUGUCUGUCUCACAG 17

RESULT 124
US-09-371-772B-6437
; Sequence 6437, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974

```
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6437
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6437

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 62;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1095 CATTGAGCCACAGAGC 1111
||: ||||| |||||
Db 1 CAUGCAGCCACAGAGC 17

RESULT 125
US-09-827-998-524
; Sequence 524, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 524
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-524

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 473 CAATGACCCCAAGAGAA 489
|||| || ||||| |||||
Db 1 CAAAGGAACCAAGAGAA 17

RESULT 126
US-09-866-108A-664
; Sequence 664, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
```

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 664
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-664

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 664 TCAGCAAAGCCAGAGGA 680
||||| ||||| |||||
Db 1 TCAGCCAAAGCCAGAGAA 17

RESULT 127
US-09-866-108A-665
; Sequence 665, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
```

```

; SOFTWARE: Aecomica Sequence Listing Engine
;
; Patent NO. 6686188
; SEQ ID NO 665
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-665

```

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 665 CAGCAAAGCCAGAGGAG 681
Db 1 CAGCCAAAGCCAGAGAAG 17

```

RESULT 128
US-09-866-108A-1872
; Sequence 1872, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOICA-7

```

CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: GB 24263.6

; PRIORITY APPLICATION NUMBER: US 60/
; PRIORITY APPLICATION NUMBER: US 60/
; PRIORITY FILING DATE: 2000-09-27
; PRIORITY APPLICATION NUMBER: PCT/US

```

/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/006654
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/006659
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/006665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/006668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/006663
/ PRIOR FILING DATE: 2001-01-30
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 15755
/ SOFTWARE: Aemica Sequence Listing Engine
/

```

SEQ ID NO 1672
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens

Query Match	0.4%	S
Best Local Similarity	88.2%	P
Matches	15:	Conservative

Qy	1022	CCCCCTCCTCTGGACC	1038
Db	1	CCCTCCTGAGCTGGACC	17
RESULT 129			

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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2733
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2733

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 765 CTCCTCAGCTGAGGCC 781
DB 1 CTACGACGCTGAGGCC 17

RESULT 131
US-09-866-108A-7802
; Sequence 7802, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7803
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7803

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCAA 1441
DB 1 AGCAGCAGCTGAAGCAA 17
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; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7802
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7802

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1425
DB 1 CAGCAGCAGCTGAAGCA 17

RESULT 132
US-09-866-108A-7803
; Sequence 7803, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ACOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7803
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7803

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCAA 1441
DB 1 AGCAGCAGCTGAAGCAA 17
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RESULT 133
US-09-866-108A-10247
; Sequence 10247, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10247
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10247

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1187 TCAGCCAGGTTGGGCA 1203
Db      1 TCAGCCAAAGTTGGGCA 17

RESULT 134
US-09-866-108A-10747
; Sequence 10747, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10247
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10247

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1187 TCAGCCAGGTTGGGCA 1203
Db      1 TCAGCCAAAGTTGGGCA 17

RESULT 135
US-09-685-664B-25
; Sequence 25, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-25

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 62;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy      2166 TGCTACTTCTCAGGG 2182
Db      1 UGUCGUCUCACAGG 17
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RESULT 136
US-09-866-108A-10747
; Sequence 10747, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10747
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10747

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1771 TGTGTTAGGCCAGAAC 1787
Db      1 TGTGTTGGCCTGAACA 17

RESULT 137
US-09-685-664B-25
; Sequence 25, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBH00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-685-664B-25

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 62;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy      2166 TGCTACTTCTCAGGG 2182
Db      1 UGUCGUCUCACAGG 17
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US-09-685-664B-3256

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 62;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2757 GTCTGAATCTCAGACCC 2773
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Db      1 GGCUGACUCUCAGACCC 17

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Job time : 6 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)

3.607 Million cell updates/sec

Title: US-10-698-070-1

Perfect score: 3763

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Searched: 492 seqs, 10066 residues

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Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 496 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 108	21	0.6	21	1	US-10-831-778-780	Sequence 780, App	c 181	17.4	0.5	19	1	US-10-922-544-29	Sequence 29, Appl
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c 111	20.8	0.6	24	1	US-10-433-561-46	Sequence 46, Appl	c 184	17.4	0.5	20	1	US-09-563-728A-16	Sequence 16, Appl
c 112	20.8	0.6	24	1	US-10-477-726-46	Sequence 46, Appl	c 185	17.4	0.5	20	1	US-10-145-493B-52	Sequence 52, Appl
c 113	20.8	0.6	24	1	US-10-500-175A-46	Sequence 46, Appl	c 186	17.4	0.5	20	1	US-10-315-962-67	Sequence 67, Appl
c 114	20.8	0.6	24	1	US-10-311-019B-46	Sequence 46, Appl	c 187	17.4	0.5	21	1	US-09-946-374-105	Sequence 105, App
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c 123	20.2	0.5	25	1	US-10-719-900-833923	Sequence 833923, A	c 196	17.4	0.5	21	1	US-10-006-116A-105	Sequence 105, App
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c 129	20.2	0.5	25	1	US-10-719-956-149049	Sequence 149049, A	c 202	17.4	0.5	21	1	US-10-011-671A-105	Sequence 105, App
c 130	20.2	0.5	25	1	US-10-719-956-174059	Sequence 174059, A	c 203	17.4	0.5	21	1	US-10-012-755A-105	Sequence 105, App
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c 135	20.2	0.5	25	1	US-10-719-956-576463	Sequence 576463, A	c 208	17.4	0.5	21	1	US-10-006-063A-105	Sequence 105, App
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c 140	20	0.5	20	1	US-10-371-474-63	Sequence 63, Appl	c 213	17.4	0.5	21	1	US-10-006-041A-105	Sequence 105, App
c 141	20	0.5	20	1	US-10-032-585-4667	Sequence 4667, App	c 214	17.4	0.5	21	1	US-10-015-822A-105	Sequence 105, App
c 142	20	0.5	20	1	US-10-032-585-5708	Sequence 5708, App	c 215	17.4	0.5	21	1	US-10-015-387A-105	Sequence 105, App
c 143	20	0.5	25	1	US-10-494-343-533	Sequence 533, App	c 216	17.4	0.5	21	1	US-10-006-130A-105	Sequence 105, App
c 144	20	0.5	25	1	US-10-494-343-540	Sequence 540, App	c 217	17.4	0.5	21	1	US-10-006-172A-105	Sequence 105, App
c 145	19.4	0.5	21	1	US-10-215-432-37	Sequence 37, Appl	c 218	17.4	0.5	21	1	US-10-017-253A-105	Sequence 105, App
c 146	19.4	0.5	21	1	US-10-215-432-44	Sequence 44, Appl	c 219	17.4	0.5	21	1	US-10-015-392A-105	Sequence 105, App
c 147	19.4	0.5	21	1	US-10-418-182-96	Sequence 96, Appl	c 220	17.4	0.5	21	1	US-10-017-306A-105	Sequence 105, App
c 148	19.4	0.5	21	1	US-10-418-182-114	Sequence 114, Appl	c 221	17.4	0.5	21	1	US-10-012-064A-105	Sequence 105, App
c 149	19.4	0.5	21	1	US-10-418-182-132	Sequence 132, App	c 222	17.4	0.5	21	1	US-10-013-909A-105	Sequence 105, App
c 150	19.4	0.5	21	1	US-10-418-182-132	Sequence 132, App	c 223	17.4	0.5	21	1	US-10-013-912A-105	Sequence 105, App
c 151	19.4	0.5	22	1	US-10-751-736-39220	Sequence 39220, A	c 224	17.4	0.5	21	1	US-10-015-653A-105	Sequence 105, App
c 152	19	0.5	22	1	US-10-728-131-125	Sequence 125, App	c 225	17.4	0.5	21	1	US-10-015-610A-105	Sequence 105, App
c 153	19	0.5	19	1	US-10-698-070-8	Sequence 8, Appl	c 226	17.4	0.5	21	1	US-10-012-137A-105	Sequence 105, App
c 154	19	0.5	19	1	US-10-922-544-26	Sequence 26, Appl	c 227	17.4	0.5	21	1	US-10-012-752A-105	Sequence 105, App
c 155	19	0.5	19	1	US-10-922-544-200	Sequence 200, App	c 228	17.4	0.5	21	1	US-10-012-754A-105	Sequence 105, App
c 156	19	0.5	20	1	US-10-289-762-6476	Sequence 6476, App	c 229	17.4	0.5	21	1	US-10-013-910A-105	Sequence 105, App
c 157	19	0.5	23	1	US-10-728-131-124	Sequence 124, App	c 230	17.4	0.5	21	1	US-10-013-911A-105	Sequence 105, App
c 158	18.8	0.5	22	1	US-09-888-615-120	Sequence 120, App	c 231	17.4	0.5	21	1	US-10-013-912A-105	Sequence 105, App
c 159	18.8	0.5	22	1	US-10-295-942-16	Sequence 16, Appl	c 232	17.4	0.5	21	1	US-10-015-653A-105	Sequence 105, App
c 160	18.8	0.5	23	1	US-10-177-308-24	Sequence 24, Appl	c 233	17.4	0.5	21	1	US-10-012-101B-105	Sequence 105, App
c 161	18.8	0.5	23	1	US-09-861-893-15	Sequence 15, Appl	c 234	17.4	0.5	21	1	US-10-015-480A-105	Sequence 105, App
c 162	18.4	0.5	20	1	US-09-563-728A-6	Sequence 6, Appl	c 235	17.4	0.5	21	1	US-10-015-715A-105	Sequence 105, App
c 163	18.4	0.5	20	1	US-09-563-728A-15	Sequence 15, Appl	c 236	17.4	0.5	21	1	US-10-012-237A-105	Sequence 105, App
c 164	18.4	0.5	20	1	US-10-145-493B-51	Sequence 51, Appl	c 237	17.4	0.5	21	1	US-10-013-906A-105	Sequence 105, App
c 165	18.4	0.5	20	1	US-10-315-962-46	Sequence 46, Appl	c 238	17.4	0.5	21	1	US-10-015-388A-105	Sequence 105, App
c 166	18.4	0.5	20	1	US-10-296-263-15	Sequence 15, Appl	c 239	17.4	0.5	21	1	US-10-012-753A-105	Sequence 105, App
c 167	18.4	0.5	20	1	US-10-751-736-8810	Sequence 8810, App	c 240	17.4	0.5	21	1	US-10-015-385A-105	Sequence 105, App
c 168	18.4	0.5	18	1	US-10-054-387-48	Sequence 48, Appl	c 241	17.4	0.5	21	1	US-10-007-236A-105	Sequence 105, App
c 169	18	0.5	18	1	US-10-321-039-541	Sequence 541, App	c 242	17.4	0.5	21	1	US-10-015-389A-105	Sequence 105, App
c 170	18	0.5	18	1	US-10-360-854-11	Sequence 11, Appl	c 243	17.4	0.5	21	1	US-10-013-915A-105	Sequence 105, App
c 171	18	0.5	18	1	US-10-479-472A-11	Sequence 11, Appl	c 244	17.4	0.5	21	1	US-10-015-394A-105	Sequence 105, App
c 172	18	0.5	18	1	US-09-888-361-152	Sequence 152, App	c 245	17.4	0.5	21	1	US-10-015-390A-105	Sequence 105, App
c 173	18	0.5	20	1	US-10-705-715-152	Sequence 152, App	c 246	17.4	0.5	21	1	US-10-006-746A-105	Sequence 105, App
c 174	18	0.5	21	1	US-10-479-510-11	Sequence 11, Appl	c 247	17.4	0.5	21	1	US-10-226-254A-105	Sequence 105, App
c 175	18	0.5	21	1	US-10-380-195A-15	Sequence 15, Appl	c 248	17.4	0.5	21	1	US-10-011-795A-105	Sequence 105, App
c 176	17.8	0.5	21	1	US-10-751-736-11486	Sequence 11486, A	c 249	17.4	0.5	21	1	US-10-012-231A-105	Sequence 105, App
c 177	17.8	0.5	21	1	US-10-751-736-19232	Sequence 19232, A	c 250	17.4	0.5	21	1	US-10-015-395A-105	Sequence 105, App
c 178	17.8	0.5	21	1	US-10-764-730-11	Sequence 11, Appl	c 251	17.4	0.5	21	1	US-10-751-736-8809	Sequence 8809, App
c 179	17.8	0.5	21	1			c 252	17.4	0.5	21	1		

253	17.4	0.5	21	1	US-10-751-736-39221	Sequence 39221, A	326	15	0.4	18	1	US-10-498-848-6	Sequence 6, Appli
c 254	17.4	0.5	21	1	US-10-012-149A-105	Sequence 105, App	c 327	14.8	0.4	18	1	US-09-280-030-28	Sequence 28, Appl
255	17.4	0.5	21	1	US-10-730-771-62	Sequence 62, Appl	328	14.8	0.4	18	1	US-09-426-548-43	Sequence 43, Appl
256	17	0.5	17	1	US-10-494-343-167	Sequence 167, App	329	14.8	0.4	18	1	US-09-861-893-11	Sequence 11, Appl
257	17	0.5	17	1	US-10-494-343-168	Sequence 168, App	330	14.8	0.4	18	1	US-10-272-865-14	Sequence 14, Appl
258	17	0.5	17	1	US-10-494-343-169	Sequence 169, App	c 331	14.8	0.4	18	1	US-10-272-865-34	Sequence 34, Appl
259	17	0.5	17	1	US-10-494-343-170	Sequence 170, App	c 332	14.8	0.4	18	1	US-10-422-671-14	Sequence 14, Appl
260	17	0.5	17	1	US-10-494-343-171	Sequence 171, App	c 333	14.8	0.4	18	1	US-10-422-671-34	Sequence 34, Appl
261	17	0.5	17	1	US-10-494-343-172	Sequence 172, App	334	14.8	0.4	18	1	US-10-349-607-60	Sequence 60, Appl
262	17	0.5	18	1	US-09-933-638A-9	Sequence 9, Appli	c 335	14.8	0.4	18	1	US-10-317-444-47	Sequence 47, App
c 263	17	0.5	18	1	US-09-933-638A-10	Sequence 10, Appl	336	14.8	0.4	18	1	US-10-317-444-448	Sequence 448, App
c 264	17	0.5	18	1	US-10-194-584-1	Sequence 1, Appli	c 337	14.8	0.4	18	1	US-10-317-444-449	Sequence 449, App
c 265	17	0.5	18	1	US-10-194-584-2	Sequence 2, Appli	338	14.8	0.4	18	1	US-10-317-444-450	Sequence 450, App
266	17	0.5	18	1	US-10-436-231-1	Sequence 1, Appli	339	14.8	0.4	18	1	US-10-138-674-2184	Sequence 2184, App
c 267	17	0.5	18	1	US-10-436-231-2	Sequence 2, Appli	340	14.8	0.4	18	1	US-10-287-949A-2184	Sequence 2184, App
268	16.8	0.4	20	1	US-09-948-002-35	Sequence 35, Appl	341	14.8	0.4	18	1	US-10-702-817-24	Sequence 24, Appl
269	16.8	0.4	20	1	US-09-920-033-22	Sequence 22, Appl	342	14.8	0.4	18	1	US-10-702-817-25	Sequence 25, Appl
270	16.8	0.4	20	1	US-10-060-301-43	Sequence 43, Appl	343	14.8	0.4	18	1	US-10-296-263-11	Sequence 11, Appl
271	16.8	0.4	20	1	US-10-147-196-22	Sequence 22, Appl	344	14.4	0.4	17	1	US-09-866-108-7201	Sequence 7201, App
272	16.8	0.4	20	1	US-10-388-263-554	Sequence 554, App	345	14.4	0.4	17	1	US-09-866-108-7202	Sequence 7202, App
c 273	16.8	0.4	20	1	US-10-210-479-79	Sequence 79, Appl	346	14.4	0.4	17	1	US-09-866-108-8467	Sequence 8467, App
274	16.8	0.4	20	1	US-10-633-163-35	Sequence 35, Appl	347	14.4	0.4	17	1	US-09-866-108-8468	Sequence 8468, App
275	16.8	0.4	20	1	US-10-712-795-22	Sequence 22, Appl	348	14.4	0.4	17	1	US-09-780-533A-234	Sequence 234, App
276	16.8	0.4	20	1	US-10-920-612-22	Sequence 22, Appl	349	14.4	0.4	17	1	US-09-780-533A-235	Sequence 235, App
277	16.8	0.4	20	1	US-10-831-901A-11559	Sequence 11559, A	350	14.4	0.4	17	1	US-09-848-754A-1158	Sequence 1158, App
278	16.8	0.4	20	1	US-10-831-901A-11560	Sequence 11560, A	351	14.4	0.4	17	1	US-09-848-754A-3275	Sequence 3275, App
279	16.8	0.4	21	1	US-09-906-419-91	Sequence 91, Appl	c 352	14.4	0.4	17	1	US-09-827-395A-505	Sequence 505, App
280	16.8	0.4	21	1	US-10-119-136-91	Sequence 91, Appl	c 353	14.4	0.4	17	1	US-09-827-395A-765	Sequence 765, App
281	16.8	0.4	21	1	US-10-430-195A-2	Sequence 2, Appli	c 354	14.4	0.4	17	1	US-09-740-332-2661	Sequence 2661, App
282	16.8	0.4	21	1	US-10-380-195A-46	Sequence 46, Appl	355	14.4	0.4	17	1	US-09-792-818-524	Sequence 524, App
c 283	16.8	0.4	21	1	US-10-380-195A-46	Sequence 46, Appl	356	14.4	0.4	17	1	US-09-792-818-524	Sequence 524, App
c 284	16.8	0.4	21	1	US-10-751-736-10540	Sequence 10540, A	c 357	14.4	0.4	17	1	US-09-817-879-2661	Sequence 2661, App
c 285	16.8	0.4	21	1	US-10-751-736-10541	Sequence 10541, A	358	14.4	0.4	17	1	US-10-061-201-574	Sequence 574, App
c 286	16.8	0.4	21	1	US-10-751-736-18508	Sequence 18508, A	359	14.4	0.4	17	1	US-10-061-201-575	Sequence 575, App
c 287	16.8	0.4	21	1	US-10-751-736-18509	Sequence 18509, A	c 360	14.4	0.4	17	1	US-10-430-882-505	Sequence 505, App
c 288	16.8	0.4	21	1	US-10-751-736-49304	Sequence 49304, A	c 361	14.4	0.4	17	1	US-10-430-882-765	Sequence 765, App
289	16.8	0.4	21	1	US-10-847-918-3217	Sequence 3217, App	362	14.4	0.4	17	1	US-10-138-674-1755	Sequence 1755, App
290	16.4	0.4	18	1	US-10-181-603-11	Sequence 11, Appl	363	14.4	0.4	17	1	US-10-138-674-6407	Sequence 6407, App
291	16.4	0.4	18	1	US-10-730-771-206	Sequence 206, Appl	364	14.4	0.4	17	1	US-10-138-674-8510	Sequence 8510, App
c 292	16.4	0.4	20	1	US-09-865-866-61	Sequence 61, Appl	365	14.4	0.4	17	1	US-10-287-949A-1755	Sequence 1755, App
c 293	16.4	0.4	20	1	US-10-186-157-17	Sequence 17, Appl	366	14.4	0.4	17	1	US-10-287-949A-6407	Sequence 6407, App
c 294	16.4	0.4	20	1	US-10-380-126-39	Sequence 39, Appl	367	14.4	0.4	17	1	US-10-287-949A-8510	Sequence 8510, App
295	16.4	0.4	20	1	US-10-831-901A-11557	Sequence 11557, A	c 368	14.4	0.4	17	1	US-10-712-672-2609	Sequence 2609, App
296	16.4	0.4	20	1	US-10-831-901A-11558	Sequence 11558, A	c 369	14.4	0.4	17	1	US-10-669-841-5254	Sequence 5254, App
297	16.4	0.4	20	1	US-10-643-038-61	Sequence 61, Appl	c 370	14.4	0.4	17	1	US-10-723-361-7201	Sequence 7201, App
298	16	0.4	17	1	US-09-792-818-608	Sequence 608, App	371	14.4	0.4	17	1	US-10-723-361-7202	Sequence 7202, App
299	16	0.4	17	1	US-10-494-343-166	Sequence 166, App	372	14.4	0.4	17	1	US-10-723-361-8467	Sequence 8467, App
300	16	0.4	17	1	US-10-494-343-173	Sequence 173, App	373	14.4	0.4	17	1	US-10-723-361-8468	Sequence 8468, App
301	16	0.4	18	1	US-10-436-231-5	Sequence 5, Appli	374	14.4	0.4	17	1	US-10-712-633-3573	Sequence 3573, App
c 302	16	0.4	18	1	US-10-436-231-6	Sequence 6, Appli	375	14.4	0.4	17	1	US-10-494-343-175	Sequence 175, App
c 303	16	0.4	20	1	US-10-148-835-86	Sequence 86, Appl	c 376	14.4	0.4	18	1	US-10-388-263-343	Sequence 343, App
c 304	16	0.4	20	1	US-10-704-263-201	Sequence 201, App	c 377	14.4	0.4	18	1	US-10-468-655-42	Sequence 42, Appl
c 305	15.8	0.4	19	1	US-10-923-329-8	Sequence 8, Appli	378	14.4	0.4	26	1	US-10-467-019-7	Sequence 7, Appli
c 306	15.8	0.4	19	1	US-10-923-329-204	Sequence 204, App	c 379	14	0.4	17	1	US-10-376-770-220	Sequence 220, App
c 307	15.6	0.4	30	1	US-10-215-432-43	Sequence 43, Appl	c 380	14	0.4	17	1	US-10-661-165-220	Sequence 220, App
c 308	15.4	0.4	17	1	US-09-848-754A-175	Sequence 175, App	381	14	0.4	17	1	US-10-494-343-164	Sequence 164, App
309	15.4	0.4	17	1	US-09-792-818-360	Sequence 360, App	c 382	14	0.4	30	1	US-10-011-993-35	Sequence 35, Appl
310	15.4	0.4	17	1	US-09-792-818-361	Sequence 361, App	c 383	14	0.4	30	1	US-10-357-322-4	Sequence 42, Appli
311	15.4	0.4	17	1	US-09-792-818-362	Sequence 362, App	384	13.8	0.4	17	1	US-09-179-536B-90	Sequence 90, Appli
312	15.4	0.4	17	1	US-09-792-818-363	Sequence 363, App	385	13.8	0.4	17	1	US-09-866-108-664	Sequence 664, App
313	15.4	0.4	17	1	US-09-792-818-609	Sequence 609, App	386	13.8	0.4	17	1	US-09-866-108-665	Sequence 665, App
c 314	15.4	0.4	17	1	US-10-138-674-2491	Sequence 2491, App	387	13.8	0.4	17	1	US-09-866-108-1872	Sequence 1872, App
c 315	15.4	0.4	17	1	US-10-287-949A-2491	Sequence 2491, App	388	13.8	0.4	17	1	US-09-866-108-1873	Sequence 1873, App
316	15.4	0.4	17	1	US-10-494-343-174	Sequence 174, App	389	13.8	0.4	17	1	US-09-866-108-2733	Sequence 2733, App
c 317	15.4	0.4	18	1	US-09-968-122-9	Sequence 9, Appli	390	13.8	0.4	17	1	US-09-866-108-7802	Sequence 7802, App
c 318	15.4	0.4	18	1	US-10-432-422-27	Sequence 27, Appl	391	13.8	0.4	17	1	US-09-866-108-7803	Sequence 7803, App
319	15.4	0.4	19	1	US-10-444-925-183	Sequence 183, App	392	13.8	0.4	17	1	US-09-866-108-10247	Sequence 10247, A
320	15.4	0.4	19	1	US-10-883-218-297	Sequence 297, App	393	13.8	0.4	17	1	US-09-866-108-10747	Sequence 10747, A
c 321	15.4	0.4	19	1	US-10-883-218-699	Sequence 699, App	394	13.8	0.4	17	1	US-09-827-998-524	Sequence 524, App
c 322	15.4	0.4	19	1	US-10-893-010-278	Sequence 39, Appl	395	13.8	0.4	17	1	US-09-872-462-243	Sequence 243, App
323	15.4	0.4	19	1	US-10-893-010-278	Sequence 278, App	396	13.8	0.4	17	1	US-09-872-462-244	Sequence 244, App
324	15	0.4	17	1	US-09-880-313A-228	Sequence 228, App	397	13.8	0.4	17	1	US-09-872-462-245	Sequence 245, App
325	15	0.4	17	1	US-10-494-343-165	Sequence 165, App	398	13.8	0.4	17	1	US-09-872-462-246	Sequence 246, App

; Sequence 4, Application US/10357322
; Publication No. US20030180768A1
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/10/357,322
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/684,843
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-322-4

Query Match 0.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 3
US-09-801-274-1530
; Sequence 1530, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1530
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1530

Query Match 0.8%; Score 29; DB 1; Length 31;
Best Local Similarity 93.5%; Pred. No. 22;
Matches 29; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1561 GCACGACGAGCAGCAACCAACGACGACAA 1591
Db 1 GCACGACGAGCAGCAGCAACCAACCAACAA 31

RESULT 4
US-10-215-432-43
; Sequence 43, Application US/10215432
; Publication No. US20030109476A1
; GENERAL INFORMATION:
; APPLICANT: Eric B. Kmiec
; APPLICANT: Hetal Parekh-Olmedo
; TITLE OF INVENTION: Composition and methods for the
; TITLE OF INVENTION: prevention and treatment of Huntington's disease

; FILE REFERENCE: Napro-10
; CURRENT APPLICATION NUMBER: US/10/215,432
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Converted HD sequence
US-10-215-432-43

Query Match 0.8%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 23;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCTGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 5
US-10-479-546-11/c
; Sequence 11, Application US/10479546
; Publication No. US20040180349A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J
; APPLICANT: Tonon, Giovanni
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER INVOLVING THE NOTCH PATHWAY
; FILE REFERENCE: 225402
; CURRENT APPLICATION NUMBER: US/10/479,546
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/US02/21344
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,788
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-479-546-11

Query Match 0.7%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 CTCCTGCCACAGCAGCAGCCCAATGG 210
Db 28 CTCCTGCCACAGCAGCAGCCCAATGG 1

RESULT 6
US-10-698-070-5/c
; Sequence 5, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiva, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 28
; TYPE: DNA

; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: fragment of Mectl-MAML2 sequence
US-10-698-070-5

Query Match 0.7%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 AACAGGTAGTTAACTATCTCTGCAA 192
DB 28 AACAGGTAGTTAACTATCTCTGCAA 1

RESULT 7
US-10-698-070-6/c
; Sequence 6, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiyu, Taketumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: fragment of Mectl-MAML2 sequence
US-10-698-070-6

Query Match 0.7%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTGAGCGAGAAGATCGCGTGCACAAT 70
DB 28 ATTGAGCGAGAAGATCGCGTGCACAAT 1

RESULT 8
US-10-418-182-174
; Sequence 174, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-174

Query Match 0.7%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTGAGCGAGAAGATCGCGTGCACAAT 70
DB 28 ATTGAGCGAGAAGATCGCGTGCACAAT 1

RESULT 9
US-10-698-070-7
; Sequence 7, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiyu, Taketumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: fragment of Mectl-MAML2 sequence
US-10-698-070-7

Query Match 0.7%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1418 CAGCAGCAGCAGCAGCAGCAGCAGCAG 1444
DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 29

Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 27

RESULT 10
US-10-336-638-152
; Sequence 152, Application US/10336638
; Publication No. US20030170699A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; TITLE OF INVENTION: Hypertension
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/10/336,638
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US/09/304,232
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/084,641
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APOA4 3058
US-10-336-638-152

Query Match 0.7%; Score 27; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ATTGAGCGAGAAGATCGCGTGCACA 69
DB 1 ATTGAGCGAGAAGATCGCGTGCACA 27

RESULT 11
US-10-336-638-152
; Sequence 152, Application US/10336638
; Publication No. US20030170699A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; TITLE OF INVENTION: Hypertension
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/10/336,638
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US/09/304,232
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/084,641
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: APOA4 3058
US-10-336-638-152

Query Match 0.7%; Score 25.4; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 49;
Matches 26; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGCAGCAGCAGCA 1428
DB 1 CAGCAGCAACAGCAGCAGCAGCAGCAGCA 29

RESULT 11


```

US-10-956-157-111930
; Sequence 111930, Application US/10956157
; Publication NO. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031895-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: FatcatIn version 3.2
; SEQ ID NO 111930
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111930

```

Query Match	0.7%	Score 25;	DB 1;	Length 25;
Best Local Similarity	100.0%	Pred. No. 38;		
Matches 25;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

Qy 3347 AGAACTGTGGTGTCAATGTGTAATT 3371
|||
Db 1 AGAACTGTGGTGTCAATGTGTAATT 25

```

RESULT 12
US-10-956-157-111931
; Sequence 111931, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 101018)
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11931
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111931

```

Query Match	0.78;	Score 25;	DB 1;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 38;		
Matches 25;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

Qy	3346	CAGAACTGTGGTGTCAATGTGTAAT	3370
Db	1	CAGAACTGTGGTGTCAATGTGTAAT	25

```

RESULT 13
US-10-956-157-111932
; Sequence 111932, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: HUMAN OSTEOARTHRIT
; FILE REFERENCE: 031896-043000 (AM 10108
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111932
; LENGTH: 25

```

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*      ;      TYPE: DNA
      ;      ORGANISM: Probe Sequence
      US-10-956-157-111932

```

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels

Qy 3178 CAGGTGGACTACATGAAGATAACAT 3202
 Db 1 CAGGTGGACTACATGAAGATAACAT 25

```

RESULT 14
US-10-956-157-111933
; Sequence 111933, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mynths, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 10108)
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111933
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111933

```

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels

QY 3348 GAAC TGTGGTGTCAATGTGTAATTA 3372
|||||
Db 1 GAAC TGTGGTGTCAATGTGTAATTA 25

```

RESULT 15
US-10-956-157-111934
; Sequence 111934, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS
; FILE REFERENCE: 031896-043000 (AM 10108)
; CURRENT APPLICATION NUMBER: US/10/956,1
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111934
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111934

```

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels

QY 3349 AACTGTGGTGTCAATGTGTAATTAA 3373
|||||
Db 1 AACTGTGGTGTCAATGTGTAATTAA 25

RESULT 16
US-10-956-157-111935

```
; Sequence 111935, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111935
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111935

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3350 ACTGTGGTCAATGCTGAATTAAT 3374
      |||
Db 1 ACTGTGGTCAATGCTGAATTAAT 25

RESULT 17
US-10-956-157-111936
; Sequence 111936, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111936
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111936

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3177 TCAGTGGACTACATGAAGATAACA 3201
      |||
Db 1 TCAGTGGACTACATGAAGATAACA 25

RESULT 18
US-10-956-157-111937
; Sequence 111937, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111937
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; ORGANISM: Probe Sequence
US-10-956-157-111937

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3474 TTCCAAGCAACAACCTCTTAATTT 3498
      |||
Db 1 TTCCAAGCAACAACCTCTTAATTT 25

RESULT 19
US-10-956-157-111938
; Sequence 111938, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111938
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111938

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3473 GTTCCAAGCAACAACCTCTTAATTT 3497
      |||
Db 1 GTTCCAAGCAACAACCTCTTAATTT 25

RESULT 20
US-10-956-157-111939
; Sequence 111939, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111939
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111939

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3165 AACTGTTGATGTTTCAGGTGACTAC 3189
      |||
Db 1 AACTGTTGATGTTTCAGGTGACTAC 25

RESULT 21
US-10-956-157-111940
; Sequence 111940, Application US/10956157
```

Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2.
; SEQ ID NO 111940
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111940

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3724 GGGATGCTGCTCTAGTGAATTAAC 3748
Db 1 GGGATGCTGCTCTAGTGAATTAAC 25

RESULT 22

US-10-956-157-111941
; Sequence 111941, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111941
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111941

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3517 GGTTAATCTTCCATGTGCTTT 3541
Db 1 GGTTAATCTTCCATGTGCTTT 25

RESULT 23

US-10-956-157-111942
; Sequence 111942, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111942
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence

US-10-956-157-111942

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3325 ACAGTATCCAATTATCCAAACAGA 3349
Db 1 ACAGTATCCAATTATCCAAACAGA 25

RESULT 24

US-10-956-157-111943
; Sequence 111943, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111943
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111943

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3723 TGGGATGCTGCTCTAGTGAATTA 3747
Db 1 TGGGATGCTGCTCTAGTGAATTA 25

RESULT 25

US-10-956-157-111944
; Sequence 111944, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111944
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111944

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3726 GATGCTGTGCTCTAGTGAATTAAC 3750
Db 1 GATGCTGTGCTCTAGTGAATTAAC 25

RESULT 26

US-10-956-157-111945
; Sequence 111945, Application US/10956157
; Publication No. US20050118625A1


```
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111950

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3344 AACAGAACTGGTGTCAATGTGTA 3368
Db 1 AACAGAACTGGTGTCAATGTGTA 25

RESULT 32
US-10-956-157-111951
; Sequence 111951, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111951

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3176 TTCAGGTGGACTACATGAAGATAAC 3200
Db 1 TTCAGGTGGACTACATGAAGATAAC 25

RESULT 33
US-10-956-157-111952
; Sequence 111952, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111952
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111952
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Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3175 GTTCAGGTGGACTACATGAAGATAA 3199
Db 1 GTTCAGGTGGACTACATGAAGATAA 25

RESULT 34
US-10-956-157-111953
; Sequence 111953, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111953
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-111953

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3174 TGTTCAAGTGGACTACATGAAGATA 3198
Db 1 TGTTCAAGTGGACTACATGAAGATA 25

RESULT 35
US-10-956-157-122224
; Sequence 122224, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122224
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-122224

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3290 ATTGGGATCACTTTTCCCTGTCTAA 3314
Db 1 ATTGGGATCACTTTTCCCTGTCTAA 25

RESULT 36
US-10-956-157-136916
; Sequence 136916, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

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; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136916
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-136916

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3721 AGTGGGATGCTGCTGTAGTGATTA 3745
Db 1 AGTGGGATGCTGCTGTAGTGATTA 25

RESULT 37
US-10-956-157-137818
; Sequence 137818, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137818
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-137818

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3224 AGTAACTGCAGTGATGAACATTTG 3248
Db 1 AGTAACTGCAGTGATGAACATTTG 25

RESULT 38
US-10-956-157-141744
; Sequence 141744, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141744
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-141744

Query Match      0.7%; Score 25; DB 1; Length 25;
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Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3347 AGAACTGTGTGTCGAATGTGAATT 3371
Db 1 AGAACTGTGTGTCGAATGTGAATT 25

RESULT 39
US-10-956-157-148286
; Sequence 148286, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148286
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-148286

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3166 ACTGTTGATGTTCCAGGTGGACTACA 3190
Db 1 ACTGTTGATGTTCCAGGTGGACTACA 25

RESULT 40
US-10-956-157-148714
; Sequence 148714, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148714
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-148714

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3469 ACTAGTTCCCAAGCAACAACACTCCTT 3493
Db 1 ACTAGTTCCCAAGCAACAACACTCCTT 25

RESULT 41
US-10-956-157-149958
; Sequence 149958, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
```

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; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 149958
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-149958

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3298 CACTTTCCCTGCTAAACTCCAGG 3322
      |||||
Db 1 CACTTTCCCTGCTAAACTCCAGG 25

RESULT 42
US-10-956-157-151079
; Sequence 151079, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 151079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-151079

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3716 ACTTCAGTGGGATGCTGTCTAGT 3740
      |||||
Db 1 ACTTCAGTGGGATGCTGTCTAGT 25

RESULT 43
US-10-956-157-152079
; Sequence 152079, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152079
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-152079

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3716 ACTTCAGTGGGATGCTGTCTAGT 3740
      |||||
Db 1 ACTTCAGTGGGATGCTGTCTAGT 25

RESULT 44
US-10-956-157-156478
; Sequence 156478, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 156478
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-156478

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3447 AAACCCCATGTCATGAGGAGTACT 3471
      |||||
Db 1 AAACCCCATGTCATGAGGAGTACT 25

RESULT 45
US-10-956-157-160387
; Sequence 160387, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160387
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-160387

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3486 AACTCCTTAATTTGCTCTAATAGAT 3510
      |||||
Db 1 AACTCCTTAATTTGCTCTAATAGAT 25

RESULT 46
US-10-956-157-164546
; Sequence 164546, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3646 ACATCCAGTGGATTACAGAAATTTCT 3670
      |||||
Db 1 ACATCCAGTGGATTACAGAAATTTCT 25

RESULT 44
US-10-956-157-156478
; Sequence 156478, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 156478
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-156478

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3447 AAACCCCATGTCATGAGGAGTACT 3471
      |||||
Db 1 AAACCCCATGTCATGAGGAGTACT 25

RESULT 45
US-10-956-157-160387
; Sequence 160387, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160387
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-160387

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3486 AACTCCTTAATTTGCTCTAATAGAT 3510
      |||||
Db 1 AACTCCTTAATTTGCTCTAATAGAT 25

RESULT 46
US-10-956-157-164546
; Sequence 164546, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
```

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 51
US-10-956-157-217246
; Sequence 217246, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217246
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-217246

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3480 GCAACAACTCTTAATTGCTCTA 3504
Db 1 GCAACAACTCTTAATTGCTCTA 25

RESULT 52
US-10-956-157-221650
; Sequence 221650, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 221650
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-221650

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3557 GAAGCTTCAGGATAGTGAATG 3581
Db 1 GAAGCTTCAGGATAGTGAATG 25

RESULT 53
US-10-956-157-222074
; Sequence 222074, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 222074
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-222074

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3635 GAACCTAGAAAACATCCAGTGGATT 3659
Db 1 GAACCTAGAAAACATCCAGTGGATT 25

RESULT 54
US-10-956-157-225637
; Sequence 225637, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225637
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-225637

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3576 GAAATGTTATAGTTTGTGGAGT 3600
Db 1 GAAATGTTATAGTTTGTGGAGT 25

RESULT 55
US-10-956-157-235078
; Sequence 235078, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 235078
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-235078

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3464 GAGTACTAGTTCACGCAACAAAC 3488
Db 1 GAGTACTAGTTCACGCAACAAAC 25

RESULT 56
US-10-956-157-236490
; Sequence 236490, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 236490
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-236490

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3461 GAGGAGGTACTAGTTCNAGCAACA 3485
Db 1 GAGGAGGTACTAGTTCNAGCAACA 25

RESULT 57

US-10-956-157-238283
; Sequence 238283, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 238283
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-238283

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3172 GATGTTGAGTGGACTACATGAAGA 3196
Db 1 GATGTTGAGTGGACTACATGAAGA 25

RESULT 58

US-10-956-157-238612
; Sequence 238612, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 238612
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-238612

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3726 GATGCTGTCTAGTGATTAACAA 3750

Db 1 GATGCTGTCTAGTGATTAACAA 25

RESULT 59

US-10-956-157-239925
; Sequence 239925, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239925
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-239925

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3508 GATAGGTATCGTTTAATCTTTCCAT 3532
Db 1 GATAGGTATCGTTTAATCTTTCCAT 25

RESULT 60

US-10-956-157-240345
; Sequence 240345, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 240345
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-240345

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3322 GATACAGTATCCCAATTTATCCAAAC 3346
Db 1 GATACAGTATCCCAATTTATCCAAAC 25

RESULT 61

US-10-956-157-243640
; Sequence 243640, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 243640
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-243640

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3473 GTTCCAAGCAACAACCTCTTAATT 3497
|||||
Db 1 GTTCCAAGCAACAACCTCTTAATT 25

RESULT 62
US-10-956-157-245055
; Sequence 245055, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 245055
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-245055

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3439 GTTTATTAAACCCCATGTCATGAG 3463
|||||
Db 1 GTTTATTAAACCCCATGTCATGAG 25

RESULT 63
US-10-956-157-251464
; Sequence 251464, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 251464
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-251464

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3309 GTCTAAACTCCAGGATACAGTATCC 3333
|||||

Db 1 GTCTAAACTCCAGGATACAGTATCC 25

RESULT 64
US-10-956-157-260477
; Sequence 260477, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 260477
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-260477

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3724 GGGATGCTGTCTCTAGTGATTAAAC 3748
|||||
Db 1 GGGATGCTGTCTCTAGTGATTAAAC 25

RESULT 65
US-10-956-157-278616
; Sequence 278616, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278616
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-278616

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3292 TGGATCACATTTCCCTGTCTAAAC 3316
|||||
Db 1 TGGATCACATTTCCCTGTCTAAAC 25

RESULT 66
US-10-956-157-290105
; Sequence 290105, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-290105

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3710 TCCTCTACTTCAGTGGGATGCTGTG 3734
|||||
Db 1 TCCTCTACTTCAGTGGGATGCTGTG 25

RESULT 67

US-10-956-157-299227
; Sequence 299227, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 299227
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-299227

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3371 TAAATGTGTAAATAGCCTTCCCAA 3395
|||||
Db 1 TAAATGTGTAAATAGCCTTCCCAA 25

RESULT 68

US-10-956-157-306169
; Sequence 306169, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 306169
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-306169

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3514 TATGGTTTAATCTTCCATTGTGC 3538
|||||
Db 1 TATGGTTTAATCTTCCATTGTGC 25

RESULT 69

US-10-956-157-308532
; Sequence 308532, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 308532
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-308532

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3302 TTTCCCTGTCTAACTCCAGGATAC 3326
|||||
Db 1 TTTCCCTGTCTAACTCCAGGATAC 25

RESULT 70

US-10-956-157-311335
; Sequence 311335, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 311335
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-311335

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3546 TTAATTTTCTGAAGCTTGCGAGAT 3570
|||||
Db 1 TTAATTTTCTGAAGCTTGCGAGAT 25

RESULT 71

US-10-956-157-312666
; Sequence 312666, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 312666
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-312666

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3337 TTATCCAAACAGAACTGGTGTCGA 3361
Db 1 TTATCCAAACAGAACTGGTGTCGA 25

RESULT 72
US-10-956-157-317093
; Sequence 317093, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 317093
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-317093

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3701 TTCCCAACAATCCTTACTTCAGTGG 3725
Db 1 TTCCCAACAATCCTTACTTCAGTGG 25

RESULT 73
US-10-956-157-319547
; Sequence 319547, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 319547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-319547

Query Match      0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3594 TTGGAGTAACCAACAGATGCAAA 3618
Db 1 TTGGAGTAACCAACAGATGCAAA 25
```

```
RESULT 74
US-09-885-441-42
; Sequence 42, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-885-441-42

Query Match      0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 AGCAGCAGCAGCAGCAACAAAC 1583
Db 1 AGCAGCAGCAGCAGCAACAAAC 24

RESULT 75
US-10-424-836-42
; Sequence 42, Application US/10424836
; Publication No. US20030224430A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/10/424,836
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/885,441
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-424-836-42

Query Match      0.6%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1560 AGCAGCAGCAGCAGCAACAAAC 1583
Db 1 AGCAGCAGCAGCAGCAACAAAC 24
```

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; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 10/846,770
; PRIOR FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: 09/997,059
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic probe
; NAME/KEY: misc feature
; LOCATION: (1)..(29)
US-10-967-592-8

Query Match          0.6%; Score 23.4; DB 1; Length 29;
Best Local Similarity 96.0%; Pred. No. 83;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1424 CAGCAGCAGCAGCAGCAACAGCAGC 1448
      |||||||||||||||||||||
Db 29 CAGCAGCAGCAGCAGCAACAGCAGC 5

RESULT 79
US-09-848-754A-9122
; Sequence 9122, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9122
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-9122

Query Match          0.6%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGCAG 1432
      |||||||||||||||||||
Db 1 AGCAGCAGCAGCAGCAGCAGCAG 23

RESULT 80
US-10-479-546-10
; Sequence 10, Application US/10479546
; Publication No. US20040180349A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J
; APPLICANT: Tonon, Giovanni
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER INVOLVING THE NOTCH PATHWAY
; FILE REFERENCE: 225402
; CURRENT APPLICATION NUMBER: US/10/479,546
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/US02/21344
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,788
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 12

```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-479-546-10

Query Match          0.6%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGAGAAGATGGCGACTTCGAACA 32
      |||||
Db 1 CGAGAAGATGGCGACTTCGAACA 23

RESULT 81
US-09-848-754A-9375/c
; Sequence 9375, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9375
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; NAME/KEY: misc feature
; LOCATION: (2)..(8)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (18)..(24)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (9)..(17)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
US-09-848-754A-9375

Query Match          0.6%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1410 AGCAGCAGCAGCAGCAGCAGCAG 1432
      |||||
Db 24 AGCAGCAGCAGCAGCAGCAGCAG 2

RESULT 82
US-10-719-900-7258
; Sequence 7258, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
```

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; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 7258
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-7258

Query Match          0.6%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 76;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1331 AACGACGACGATGCTTCTGTTTG 1354
      |||||
Db 2 AACGACGACGATGCTTCTGTTTG 25

RESULT 83
US-10-719-956-496780
; Sequence 496780, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE OF INVENTION: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 496780
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-496780

Query Match          0.6%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 76;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2126 GTTCAACACACACACCATTTAACT 2149
      |||||
Db 1 GTTCAACACACACACCATTTAACT 24

RESULT 84
US-10-418-182-156/c
; Sequence 156, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-156

Query Match          0.6%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1450 GCAGCAGCAACAGCAACAGCAACAGCA 1476
||||| ||||| ||||| ||||| |||||
Db 27 GCAGCAACAACAACAACAACAACAACA 1

RESULT 85

US-10-738-642-25
; Sequence 25, Application US/10738642
; Publication No. US20040241854A1
; GENERAL INFORMATION:
; APPLICANT: Paulson, Henry
; APPLICANT: Miller, Victor
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: siRNA-Mediated Gene Silencing
; FILE REFERENCE: 875.101US1
; CURRENT APPLICATION NUMBER: US/10738,642
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 10/212,322
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/322,086
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/430,351
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/US03/16887
; PRIOR FILING DATE: 2003-05-26
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-738-642-25

Query Match 0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGC 1430
||||| ||||| ||||| ||||| |||||
Db 1 CAGCAGCAGCAGCAGCAGCAGC 22

RESULT 86

US-10-738-642-26/c
; Sequence 26, Application US/10738642
; Publication No. US20040241854A1
; GENERAL INFORMATION:
; APPLICANT: Paulson, Henry
; APPLICANT: Miller, Victor
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: siRNA-Mediated Gene Silencing
; FILE REFERENCE: 875.101US1
; CURRENT APPLICATION NUMBER: US/10738,642
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 10/212,322
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/322,086
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/430,351
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: PCT/US03/16887
; PRIOR FILING DATE: 2003-05-26
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-738-642-26

Query Match 0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 62;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1411 GCAGCAGCAGCAGCAGCAGCAG 1432
||||| ||||| ||||| ||||| |||||
Db 22 GCAGCAGCAGCAGCAGCAGCAG 1

RESULT 87

US-10-494-343-535
; Sequence 535, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10494,343
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 535
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-535

Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
||||| ||||| ||||| ||||| |||||
Db 4 GCAGCAGCAGCAACAGCAGCAG 25

RESULT 88

US-10-494-343-536
; Sequence 536, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 536
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-536

Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
||||| ||||| ||||| ||||| |||||
Db 3 GCAGCAGCAGCAACAGCAGCAG 24


```
RESULT 89
US-10-494-343-537
; Sequence 537, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 537
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-537

Query Match          0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGCAG 1450
Db 2 GCAGCAGCAGCAACAGCAGCAG 23

RESULT 90
US-10-494-343-538
; Sequence 538, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 538
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-538

Query Match          0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGCAG 1450
Db 1 GCAGCAGCAGCAACAGCAGCAG 22

RESULT 91
US-10-719-900-175878
; Sequence 175878, Application US/10719900
```

```
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 175878
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-175878

Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1299 AGCCTTTGTTTCATTTTAACCTCAGA 1323
Db 1 AGCCTTTGTTTCCTTTTAACTCAGA 25

RESULT 92
US-10-719-900-917073
; Sequence 917073, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 917073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-917073

Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1314 TTAAGTCAGATCAAGCGAACCGCA 1338
Db 1 TTAAGTCAGACCAAGCAACCGCA 25

RESULT 93
US-10-956-157-73632
; Sequence 73632, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73632
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
```

```
US-10-956-157-73632
Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1574 CAACAACACAGCAGCAACAGCAGC 1598
|||||
Db 1 CAACAACACACACACACACAGCAGC 25

RESULT 94
US-10-956-157-73633
; Sequence 73633, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73633
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-956-157-73633

Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1575 AACAAACACACACACACAGCAGCA 1599
|||||
Db 1 AACAAACACACACACACAGCAGCA 25

RESULT 95
US-10-956-157-73638
; Sequence 73638, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73638
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-956-157-73638

Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1576 ACAACAACACAGCAACACAGCAGCAG 1600
|||||
Db 1 ACAACAACACACACACACAGCAGCAG 25

RESULT 96
US-10-956-157-73638
; Sequence 73638, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73638
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-956-157-73638

Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1577 ACAACAACACAGCAACACAGCAGCAG 1600
|||||
Db 1 ACAACAACACACACACACAGCAGCAG 25

RESULT 97
US-10-956-422355/c
; Sequence 422355, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 422355
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-422355

Query Match          0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 89;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2219 ATGGGATGTATGGAATCTGCCTT 2243
|||||
Db 1 ATAGGGATGTATGGAACCTGCCTT 25

RESULT 98
US-10-719-956-576464
; Sequence 576464, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 576464
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-576464
```

RESULT 101
US-10-467-019-7/c
; Sequence 7, Application US/10467019
; Publication No. US20040048314A1

; APPLICANT: FOURCH, IVES
 ; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
 ; TITLE OF INVENTION: Treatment of Asthma and Allergy
 ; FILE REFERENCE: C1037/7013 (HCL/MAT)

; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-780

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 104

US-09-776-479-780/c
; Sequence 780, Application US/09/776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-780

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 105

US-10-112-653-753/c
; Sequence 753, Application US/10/112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 753
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-753

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 106

US-10-017-995-780/c
; Sequence 780, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-780

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 107

US-10-314-578-780/c
; Sequence 780, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-780

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 108

US-10-831-778-780/c
; Sequence 780, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 780
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-780

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 109

US-10-494-343-534
; Sequence 534, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 534
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-534

Query Match 0.6%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGCA 1449
Db 5 GCAGCAGCAGCAACAGCAGCA 25

RESULT 110

US-10-494-343-539
; Sequence 539, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 539
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-539

Query Match 0.6%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1430 CAGCAGCAGCAACAGCAGCAG 1450
Db 1 CAGCAGCAGCAACAGCAGCAG 21

RESULT 111

US-10-433-561-46
; Sequence 46, Application US/10433561
; Publication No. US20040029178A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: No. US20040029178A1el G Protein-Coupled Receptor Proteins and DNAs
; FILE REFERENCE: P01-0255PCT
; CURRENT APPLICATION NUMBER: US/10/433,561
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: JP 2000-364801
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: JP 2001-087482
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-145434
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: JP 2001-270838
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 191
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-433-561-46

Query Match 0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1418 CAGCAGCAGCAGCAGCAGCA 1441

```
; Sequence 46, Application US/10477726
; Publication No. US20040110231A1
; GENERAL INFORMATION:
; APPLICANT: TAKEDA Chemical Industries, Ltd.
; TITLE OF INVENTION: Screening method
; FILE REFERENCE: P02-0058PCT
; CURRENT APPLICATION NUMBER: US/10/477,726
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 2001-145411
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-477-726-46

Query Match          0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1418 CAGCAGCAGCAGCAGCAGCAGCAA 1441
      |||||
Db 1 CAGCGGCAGCAGCAGCAGCAGTAA 24

RESULT 113
US-10-500-175A-46
; Sequence 46, Application US/10500175A
; Publication No. US20050124539A1
; GENERAL INFORMATION:
; APPLICANT: Hirokazu Matsumoto
; APPLICANT: Jiro Noguchi
; APPLICANT: Mioko Harada
; APPLICANT: Masaaki Mori
; TITLE OF INVENTION: Body weight gain inhibitor
; FILE REFERENCE: 61536 (46342)
; CURRENT APPLICATION NUMBER: US/10/500,175A
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: PCT/JP01/13781
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: JP2001-403260
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: JP2002-93096
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 150
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-500-175A-46

Query Match          0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1418 CAGCAGCAGCAGCAGCAGCAGCAA 1441
      |||||
Db 1 CAGCGGCAGCAGCAGCAGCAGTAA 24

RESULT 114
US-10-311-019B-46
; Sequence 46, Application US/10311019B
; Publication No. US20050153391A1
; GENERAL INFORMATION:
; APPLICANT: MORI, Masaaki
; APPLICANT: SHIMOMURA, Yukio
; APPLICANT: HARADA, Mioko
; APPLICANT: ASAMI, Taiji
; APPLICANT: MATSUMOTO, Yoshio
; APPLICANT: ADACHI, Yuka
; APPLICANT: SUGO, Tsukasa
; APPLICANT: ABE, Michiko
; APPLICANT: GOTO, Mika nee KURIHARA
; APPLICANT: KITADA, Chieko
; APPLICANT: WATANABE, Takuya
; TITLE OF INVENTION: Ligand for GPR8 and its DNA
; FILE REFERENCE: 2739 USOP
; CURRENT APPLICATION NUMBER: US/10/311,019B
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: PCT/JP01/05257
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191089
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: JP 2000-275013
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: JP 2001-116000
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 125
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-311-019B-46

Query Match          0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1418 CAGCAGCAGCAGCAGCAGCAGCAA 1441
      |||||
Db 1 CAGCGGCAGCAGCAGCAGCAGTAA 24

RESULT 115
US-10-719-900-7257
; Sequence 7257, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 7257
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-7257

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1331 AACCCAGCAGATGCTTCTCTTTTG 1354
      |||||
Db 2 AACCCAGCAGATCCCTTCTCTTTTG 25
```

```
RESULT 116
US-10-719-900-13951
; Sequence 13951, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13951
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-13951

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1225 AAAGCCTCAGGATCTCAGTGAAG 1248
      ||||| ||||| ||||| |||||
Db 1 AAAGCCTCAGGACCTCAATCGAAG 24

RESULT 117
US-10-719-900-13952
; Sequence 13952, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13952
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-13952

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1225 AAAGCCTCAGGATCTCAGTGAAG 1248
      ||||| ||||| ||||| |||||
Db 1 AAAGCCTCAGGACCTCAATCGAAG 24

RESULT 118
US-10-719-900-132626/c
; Sequence 132626, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 132626
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-132626

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1571 CAGCAACAACAACAGCAACAGCAG 1594
      ||||| ||||| ||||| |||||
Db 25 CAGCAACAACGACGACGACGACGAG 2

RESULT 119
US-10-719-900-883394
; Sequence 883394, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 883394
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-883394

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1289 GGCAACACCAAGCCTTGTTTCAT 1312
      ||||| ||||| ||||| |||||
Db 2 GGCAATACCAAGCCTTGTTTCAT 25

RESULT 120
US-10-956-157-73631
; Sequence 73631, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73631
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-73631

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1574 CAACAACAACAGCAACAACAGCAG 1597
      ||||| ||||| ||||| |||||
Db 2 CAACAACAACAACATTAACAGCAG 25

RESULT 121
```

```
US-10-719-956-496781
; Sequence 496781, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 496781
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-496781

Query Match          0.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2126 GTTTCACACACACACATTTTAACT 2149
Db 1 GTCTCAACACACTCCATTTTAACT 24

RESULT 122
US-10-028-415-27/c
; Sequence 27, Application US/10028415
; Publication No. US20020151063A1
; GENERAL INFORMATION:
; APPLICANT: Lasham, Annette
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Methods for Modulating Apoptotic Cell
; TITLE OF INVENTION: Death
; FILE REFERENCE: 11000.1004c3
; CURRENT APPLICATION NUMBER: US/10/028,415
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/NZ01/00286
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 09/724,809
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/036,004
; PRIOR FILING DATE: 1998-03-04
; PRIOR APPLICATION NUMBER: US 08/713,557
; PRIOR FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Human
US-10-028-415-27

Query Match          0.5%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 95;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1397 CAACAGCAGCAACAGCAGCAGC 1418
Db 22 CACCAGCAGCAACAGCAGCAGC 1

RESULT 123
US-10-719-900-833923/c
; Sequence 833923, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
```

```
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 833923
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-833923

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3198 AACATGCTTAAAAATGGAAGCAGA 3222
Db 25 AACATGCATTAATAATGGACAGCAGA 1

RESULT 124
US-10-719-900-907760
; Sequence 907760, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 907760
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-907760

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1210 TGTCTTCATCGCAGCAAAAGCCTCAG 1234
Db 1 TGTGCTTCTCGCAGCAAAAGCCTCAG 25

RESULT 125
US-10-719-900-917074
; Sequence 917074, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 917074
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-917074

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1210 TGTCTTCATCGCAGCAAAAGCCTCAG 1234
Db 1 TGTGCTTCTCGCAGCAAAAGCCTCAG 25

RESULT 125
US-10-719-900-917074
; Sequence 917074, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 917074
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-917074

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```



```
Qy 1314 TTAACACAGATCAAGCGAACCAACGCA 1338
      ||||| ||||| ||||| ||||| |||||
Db 1 TTAACACAGACTAGCAAAACCAACGCA 25

RESULT 126
US-10-809-189-74107
; Sequence 74107, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-74107

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1597 GCAGCAGCAGCAGCAACACATCT 1621
      ||||| ||||| ||||| ||||| |||||
Db 1 GCAGCAGCAGCAGCAGCAACATCT 25

RESULT 127
US-10-719-956-24229
; Sequence 24229, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24229
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-24229

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2105 AACCCAGGCTTGGCAAAACCCAGTTT 2129
      ||||| ||||| ||||| ||||| |||||
Db 1 AACCCAGGCTTGACAAACCCAGTCT 25

RESULT 128
US-10-719-956-24230
; Sequence 24230, Application US/10719956
; Publication No. US20040146910A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24230
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-24230

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2105 AACCCAGGCTTGGCAAAACCCAGTTT 2129
      ||||| ||||| ||||| ||||| |||||
Db 1 AACCCAGGCTTGTCAAACCCAGTCT 25

RESULT 129
US-10-719-956-149049
; Sequence 149049, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 149049
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-149049

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2654 AGGCGAGTGGCTCTCTCAACCACT 2678
      ||||| ||||| ||||| ||||| |||||
Db 1 AGGCGAGTGGCTCTCTTGACCACT 25

RESULT 130
US-10-719-956-174099
; Sequence 174099, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 174099
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-174099
```

```
Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2219 ATGGGGATGTATGGAATCTGCCTT 2243
||| ||||| ||||| ||||| ||||| |||||
Db 1 ATAGGGATGTATCGAAACCTGCCTT 25

RESULT 131
US-10-719-956-222455
; Sequence 222455, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 222455
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-222455

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2133 CACACACATTTTAACCTCCCAATTC 2157
||| ||||| ||||| ||||| ||||| |||||
Db 1 CACACACATTTTAACCTCGAATC 25

RESULT 132
US-10-719-956-422354/c
; Sequence 422354, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 422354
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-422354

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2724 CACTAAATGGCAACCAATGGTGTC 2748
||| ||||| ||||| ||||| ||||| |||||
Db 25 CATTAAATGGGCTAACTTGCGTCC 1

RESULT 133
US-10-719-956-471981/c
; Sequence 471981, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 471981
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-471981

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2696 ATGAGACCCCATGAACCAATGAGCC 2720
||| ||||| ||||| ||||| ||||| |||||
Db 25 ATGAGACCTGTGAACCAATGAACC 1

RESULT 134
US-10-719-956-553657/c
; Sequence 553657, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 553657
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-553657

Query Match          0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1398 AACAGCAGCAACAGCAGCAGCA 1422
||| ||||| ||||| ||||| ||||| |||||
Db 25 AACAGCATAAACAGCAGCAGCAGTA 1

RESULT 135
US-10-719-956-576463
; Sequence 576463, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 576463
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-576463
```

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2326 TCAAAACACCTATGATGCCACGG 2350
Db 1 TCAGAACCAACCTGATGCCACGG 25

RESULT 136

US-10-719-956-585024/c
; Sequence 585024, Application US/10719956
; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 585024

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-585024

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3011 TCTTTATTGAACAGACGACCTGGTA 3035
Db 25 TCTTTATTGAACAGACGACGGGA 1

RESULT 137

US-10-719-956-627844

; Sequence 627844, Application US/10719956

; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 627844

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-627844

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2230 TGGAAATCTGCTTGAATCAACCT 2254
Db 1 TGGAAACCTGCTTGTATCAACGCT 25

RESULT 138

US-10-719-956-643296/c

; Sequence 643296, Application US/10719956

; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 643296
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-643296

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2566 AGGAGTCGGTTCCCAACAGGTACA 2590
Db 25 AGGAGTCGGTTCCCAACAGGTACA 1

RESULT 139

US-10-719-956-682691/c

; Sequence 682691, Application US/10719956

; Publication No. US20040146910A1

; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou

; TITLE OF INVENTION: Methods of Genetic Analysis of Rat

; FILE REFERENCE: 3527.1

; CURRENT APPLICATION NUMBER: US/10/719,956

; CURRENT FILING DATE: 2003-11-20

; PRIOR APPLICATION NUMBER: 60/427,836

; PRIOR FILING DATE: 2002 11 20

; NUMBER OF SEQ ID NOS: 699466

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 682691

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-10-719-956-682691

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2751 TCAGGGTCTGAATCTCAGACCCAA 2775
Db 25 TCAGGGTCTGAATCTCAGACCCAA 1

RESULT 140

US-10-371-474-63

; Sequence 63, Application US/10371474

; Publication No. US20030144242A1

; GENERAL INFORMATION:

; APPLICANT: Donna T. Ward

; APPLICANT: William Gaarde

; APPLICANT: Brett P. Monia

; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF MEK4 EXPRESSION

; FILE REFERENCE: RTS-0169

; CURRENT APPLICATION NUMBER: US/10/371,474

; CURRENT FILING DATE: 2003-02-21

; PRIOR APPLICATION NUMBER: US/09/676,436

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 89

; SEQ ID NO 63

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

```
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-371-474-63

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAGC 1430
Db 1 GCAGCAGCAGCAGCAGCAGC 20

RESULT 141
US-10-032-585-4667/c
; Sequence 4667, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4667
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-4667

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1553 CAACAACAGCAGCAGCAGCA 1572
Db 20 CAACAACAGCAGCAGCAGCA 1

RESULT 142
US-10-032-585-5708/c
; Sequence 5708, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5708
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-5708

Query Match          0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1555 ACAACAGCAGCAGCAGCAGC 1574
Db 20 ACAACAGCAGCAGCAGCAGC 1

RESULT 143
```

```
US-10-494-343-533
; Sequence 533, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 533
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-533

Query Match          0.5%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGC 1448
Db 6 GCAGCAGCAGCAACAGCAGC 25

RESULT 144
US-10-494-343-540
; Sequence 540, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 540
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-540

Query Match          0.5%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1431 AGCAGCAGCAACAGCAGCAG 1450
Db 1 AGCAGCAGCAACAGCAGCAG 20

RESULT 145
US-10-215-432-37
; Sequence 37, Application US/10215432
; Publication No. US20030109476A1
; GENERAL INFORMATION:
; APPLICANT: Eric B. Kniec
```

```
; APPLICANT: Hetal Parekh-Olmedo
; TITLE OF INVENTION: Composition and methods for the
; FILE REFERENCE: Napro-10
; CURRENT APPLICATION NUMBER: US/10/215,432
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Isolated clone of gene-alteration directed by a
US-10-215-432-37

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db      1 CAGCAGCAGTAGCAGCAGCAG 21

RESULT 146
US-10-215-432-44
; Sequence 44, Application US/10215432
; Publication No. US20030109476A1
; GENERAL INFORMATION:
; APPLICANT: Eric B. Kmiec
; TITLE OF INVENTION: Hetal Parekh-Olmedo
; TITLE OF INVENTION: Composition and methods for the
; FILE REFERENCE: Napro-10
; CURRENT APPLICATION NUMBER: US/10/215,432
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Converted HD sequence
US-10-215-432-44

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db      1 CAGCAGCAGTAGCAGCAGCAG 21

RESULT 147
US-10-418-182-96/c
; Sequence 96, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-132

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1576 ACAACACAGCAGCAACACAGCA 1596
Db      21 ACAACACAGCAACACACACA 1

RESULT 149
US-10-418-182-132
; Sequence 132, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-132

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1538 CAGCAGCAGCAGCAGCAACAA 1558
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-96

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1410 AGCAGCAGCAGCAGCAGCAGC 1430
Db      21 AGCAGCAGCGCAGCAGCAGCAGC 1

RESULT 148
US-10-418-182-114/c
; Sequence 114, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-114

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1576 ACAACACAGCAGCAACACAGCA 1596
Db      21 ACAACACAGCAACACACACA 1

RESULT 149
US-10-418-182-132
; Sequence 132, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-132

Query Match          0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1538 CAGCAGCAGCAGCAGCAACAA 1558
```

Db 1 CAGCAGCAACGACGACGACAA 21
|||||

RESULT 150
US-10-751-736-39220
; Sequence 39220, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751.736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39220
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-39220

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1427 CAGCAGCAGCAGCAGCAGCAG 1447
|||||

Db 1 CAGCAGCAGCAGCTACAGCAG 21
|||||

RESULT 151
US-10-728-131-125
; Sequence 125, Application US/10728131
; Publication No. US20050075303A1
; GENERAL INFORMATION:
; APPLICANT: Neeper, Michael P.
; APPLICANT: McClements, William L.
; APPLICANT: Jansen, Kathrin U.
; APPLICANT: Schultz, Loren D.
; APPLICANT: Chen, Ling
; APPLICANT: Wang, Xin-Min
; TITLE OF INVENTION: SYNTHETIC HUMAN PAPILLOMAVIRUS GENES
; FILE REFERENCE: 20413YCA
; CURRENT APPLICATION NUMBER: US/10/728,131
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 09/642,405
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: PCY/US00/22932
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 60/210,143
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/150,728
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon-Optimized HPV6 E2 fragment
US-10-728-131-125

Query Match 0.5%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1497 CTCAACAACGACGACGACG 1517
|

Db 2 CGCAACAACGACGACGACG 22
|||||

RESULT 152
US-10-698-070-8
; Sequence 8, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kave, Frederic J.
; APPLICANT: Komiya, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: siRNA #1
US-10-698-070-8

Query Match 0.5%; Score 19; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 97;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CCTATCTCTGCCCAACAGC 196
|||

Db 1 CCUAUCCUGCCCAACAGC 19
|||

RESULT 153
US-10-698-070-10
; Sequence 10, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kave, Frederic J.
; APPLICANT: Komiya, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: siRNA #2
US-10-698-070-10

Query Match 0.5%; Score 19; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 97;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 167 CAGTAGTTAACCTATCTC 185
|||||

Db 1 CAGUAGUUAACCUAUCUC 19
|||||

RESULT 154
US-10-922-544-26
; Sequence 26, Application US/10922544
; Publication No. US20050153915A1
; GENERAL INFORMATION:

```
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Usman, Naseem
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Early Growth Response
; FILE REFERENCE: 400/204 (MBH03-939-B)
; CURRENT APPLICATION NUMBER: US/10/922,544
; PENDING FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/512,701
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense 1
US-10-922-544-26

Query Match          0.5%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
Db 1 CAGCAGCAGCAGCAGCAGC 19

RESULT 155
US-10-922-544-200/c
; Sequence 200, Application US/10922544
; Publication No. US20050153915A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Usman, Naseem
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Early Growth Response
; FILE REFERENCE: 400/204 (MBH03-939-B)
; CURRENT APPLICATION NUMBER: US/10/922,544
; PENDING FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/512,701
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
```

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; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-922-544-200

Query Match          0.5%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
Db 19 CAGCAGCAGCAGCAGCAGC 1

RESULT 156
US-10-289-762-6476/c
; Sequence 6476, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6476
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6476

Query Match          0.5%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1454 CAGCAGCAGCAGCAGCAGC 1472
Db 19 CAGCAGCAGCAGCAGCAGC 1

RESULT 157
US-10-728-131-124/c
; Sequence 124, Application US/10728131
; Publication No. US20050075303A1
; GENERAL INFORMATION:
; APPLICANT: Neepser, Michael P.
; APPLICANT: McClements, William L.
; APPLICANT: Jansen, Kathrin U.
; APPLICANT: Schultz, Loren D.
; APPLICANT: Chen, Ling
; APPLICANT: Wang, Xin-Min
; TITLE OF INVENTION: SYNTHETIC HUMAN PAPILLOMAVIRUS GENES
; FILE REFERENCE: 20413YCA
; CURRENT APPLICATION NUMBER: US/10/728,131
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 09/642,405
; PRIOR FILING DATE: 2000-08-21
```

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; PRIOR APPLICATION NUMBER: PCr/US00/22932
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 60/210,143
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/150,728
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon-Optimized HPV6 E2 fragment
US-10-728-131-124

Query Match          0.5%; Score 19; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 CAACAACGACGACGACG 1517
Db 22 CAACAACGACGACGACG 4

RESULT 158
US-09-888-615-120/c
; Sequence 120, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-888-615-120

Query Match          0.5%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 980 CAGCACCAGCAGCAGCACCAGC 1001
Db 22 CTGCACCAGCAGCAGCAGCAGC 1

RESULT 159
US-10-295-942-16/c
; Sequence 16, Application US/10295942
; Publication No. US20030109480A1
; GENERAL INFORMATION:
; APPLICANT: Corder, Roger
; APPLICANT: Smith, Adrian
; APPLICANT: Higenbottam, Tim
; APPLICANT: Rothblatt, Martine
; APPLICANT: Vane, John
; APPLICANT: Jones, Delphine
; TITLE OF INVENTION: INHIBITORS OF ENDOTHELIN-1 SYNTHESIS
; FILE REFERENCE: 080618/0123
; CURRENT APPLICATION NUMBER: US/10/295,942

; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/09/527,240
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ASON
US-10-295-942-16

Query Match          0.5%; Score 18.8; DB 1; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 807 TGGCCAACTCTGCCCTCTCCAC 828
Db 22 TGGCCGACTCTGCACCTCTCCAC 1

RESULT 160
US-10-177-308-24/c
; Sequence 24, Application US/10177308
; Publication No. US20030175262A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/10/177,308
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/632,098
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ologonucleotide ZC21,076
US-10-177-308-24

Query Match          0.5%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1421 CAGCAGCAGCAGCAGCAGCAAC 1442
Db 23 CAGTAGTAGCAGCAGCAGCAGCAAC 2

RESULT 161
US-10-853-665-24/c
; Sequence 24, Application US/10853665
; Publication No. US20040259163A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Baidur, Nand
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: MAMMALIAN ADHESION PROTEASE PEPTIDES
; FILE REFERENCE: 99-39
; CURRENT APPLICATION NUMBER: US/10/853,665
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: US/10/177,308
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/632,098
; PRIOR FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
```



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; OTHER INFORMATION: oligonucleotide
US-09-563-728A-6

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1
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|||||

RESULT 164
US-09-563-728A-15/c
; Sequence 15, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 17-20 are modified
; OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-16 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-15

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1
|||||
|||||

RESULT 165
US-10-145-493B-51/c
; Sequence 51, Application US/10145493B
; Publication No. US2003009677A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-01SDV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer

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US-10-145-493B-51
Query Match          0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 166
US-10-315-962-46
; Sequence 46, Application US/10315962
; Publication No. US20040109848A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF AP-2 ALPHA EXPRESSION
; FILE REFERENCE: PTS-0046
; CURRENT APPLICATION NUMBER: US/10/315.962
; CURRENT FILING DATE: 2000-12-09
; NUMBER OF SEQ ID NOS: 126
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-315-962-46

Query Match          0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAGC 1430
Db 1 GCAGCAGCAGCAGCAGTAGC 20

RESULT 167
US-10-296-263-15/c
; Sequence 15, Application US/10296263
; Publication No. US20050153440A1
; GENERAL INFORMATION:
; APPLICANT: Feinberg, Andrew
; APPLICANT: Strichman-Almashanu, Liora
; APPLICANT: Jiang, Shan
; TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING AND
; TITLE OF INVENTION: METHYLATED CpG ISLANDS
; FILE REFERENCE: 01107.00128
; CURRENT APPLICATION NUMBER: US/10/296.263
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/206,158
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/206,161
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-263-15

Query Match          0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1430 CAGCAGCAGCAGCAGCAGCA 1449
Db 1 CAGCAGCAGCAGCAGCAGCA 1449

US-10-054-387-48/c
Query Match          0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1554 AACACAGCAGCAGCAGCAG 1573
Db 20 AAGACAGCAGCAGCAGCAG 1

RESULT 169
US-10-054-387-48/c
; Sequence 48, Application US/10054387
; Publication No. US20030054365A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Minzhen
; APPLICANT: Qiu, Gang
; APPLICANT: Humphreys, Robert
; TITLE OF INVENTION: CANCER CELL VACCINE
; FILE REFERENCE: U.S. Application 09/205,995, (CIP)
; CURRENT APPLICATION NUMBER: US/10/054,387
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 09/036,746
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: 08/661,627
; PRIOR FILING DATE: 1996-06-11
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: oligonucleotide corresponding to a specific region
; OTHER INFORMATION: of the mouse li gene.
US-10-054-387-48

Query Match          0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAGCAGCAGCAG 1417
Db 18 CAGCAGCAGCAGCAGCAG 1
```

RESULT 170
US-10-321-039-541
; Sequence 541, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 541
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-321-039-541

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCA 1428
Db 1 GCAGCAGCAGCAGCAGCA 18
|||||

RESULT 171
US-10-360-854-11
; Sequence 11, Application US/10360854
; Publication No. US20040157220A1
; GENERAL INFORMATION:
; APPLICANT: Kurnool, Purnima
; APPLICANT: Wo, Betty
; APPLICANT: Banks, Peter
; TITLE OF INVENTION: Method and Apparatus for Sample Tracking
; FILE REFERENCE: 10255-020-999
; CURRENT APPLICATION NUMBER: US/10/360,854
; CURRENT FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: mammalian
US-10-360-854-11

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAG 1426
Db 1 CAGCAGCAGCAGCAGCAG 18
|||||

RESULT 172
US-10-479-472A-11
; Sequence 11, Application US/10479472A
; Publication No. US20050118581A1
; GENERAL INFORMATION:
; APPLICANT: DEL-FAVERO, JURGEN PETER LODE

; APPLICANT: VAN BROECKHOVEN, CHRISTINE
; TITLE OF INVENTION: NOVEL BRAIN EXPRESSED GENE AND PROTEIN ASSOCIATED WITH
; FILE REFERENCE: JAB-1711
; CURRENT APPLICATION NUMBER: US/10/479,472A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/BP02/06316
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: EP 01202214.1
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Illustrative
; OTHER INFORMATION: oligonucleotide
US-10-479-472A-11

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAG 1426
Db 1 CAGCAGCAGCAGCAGCAG 18
|||||

RESULT 173
US-09-888-361-152/c
; Sequence 152, Application US/09888361
; Publication No. US2003006494A1
; GENERAL INFORMATION:
; APPLICANT: Susan Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR
; FILE REFERENCE: RTS-0158
; CURRENT APPLICATION NUMBER: US/09/888,361
; CURRENT FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 163
; SEQ ID NO 152
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-888-361-152

Query Match 0.5%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1602 AGCAGCAGCAACACCAT 1619
Db 20 AGCAGCAGCAACACCAT 3
|||||

RESULT 174
US-10-705-715-152/c
; Sequence 152, Application US/10705715
; Publication No. US20040147472A1
; GENERAL INFORMATION:
; APPLICANT: Susan Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR
; FILE REFERENCE: RTS-0158
; CURRENT APPLICATION NUMBER: US/10/705,715
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US/09/888,361

```
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 163
; SEQ ID NO 152
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-705-715-152

Query Match          0.5%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1602 AGCAGCAGCAACACCAT 1619
Db 20 AGCAGCAGCAACACCAT 3

RESULT 175
US-10-479-510-11/c
; Sequence 11, Application US/10479510
; Publication No. US20040157230A1
; GENERAL INFORMATION:
; APPLICANT: Cavidi Tech AB
; TITLE OF INVENTION: A method for measuring DNA polymerization and
; FILE REFERENCE: 110063501
; CURRENT APPLICATION NUMBER: US/10/479,510
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/297,773
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: template
US-10-479-510-11

Query Match          0.5%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAG 1426
Db 18 CAGCAGCAGCAGCAGCAG 1

RESULT 176
US-10-380-195A-15
; Sequence 15, Application US/10380195A
; Publication No. US20040072776A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Kiyama, Satoshi
; APPLICANT: Nelson, Colleen
; APPLICANT: Remnie, Paul
; TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
; FILE REFERENCE: Oligodeoxynucleotides for Prostate and Endocrine Tumor Therapy
; FILE REFERENCE: UBC-P-023
; CURRENT APPLICATION NUMBER: US/10/380,195A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: PCT/US01/28748
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: US 60/232,641
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 21

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IGFBP2 antisense
US-10-380-195A-15

Query Match          0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAG 1429
Db 1 CAGTAGCAGCAGCAGCAGCG 21

RESULT 177
US-10-751-736-11486/c
; Sequence 11486, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11486
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-11486

Query Match          0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1407 AACAGCAGCAGCAGCAGCAG 1427
Db 21 AACATCAGCAGCGCAGCAGC 1

RESULT 178
US-10-751-736-19232/c
; Sequence 19232, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19232
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-19232

Query Match          0.5%; Score 17.8; DB 1; Length 21;
```

```
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2146 AACTCCCAATTCAGCCTCCT 2166
DB 21 AATCTCAATTCAGCCTCCT 1

RESULT 179
US-10-764-730-11
; Sequence 11, Application US/10764730
; Publication No. US20050032134A1
; GENERAL INFORMATION:
; APPLICANT: Mueller-Hermelink, Hans Konrad
; APPLICANT: Vollmers, Heinz Peter
; APPLICANT: Hensel, Frank
; TITLE OF INVENTION: Neoplasm-Specific Polypeptides and Their
; TITLE OF INVENTION: Uses
; FILE REFERENCE: 50308/009002
; CURRENT APPLICATION NUMBER: US/10/764,730
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: PCT/DE02/02699
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: DE 10210425.5
; PRIOR FILING DATE: 2002-03-09
; PRIOR APPLICATION NUMBER: DE 10136009.6
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-764-730-11

Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1426 GCAGCAGCAGCAGCAACAGCA 1446
DB 1 GCAGCTTCAGCAGCAACAGCA 21

RESULT 180
US-09-263-959-793/c
; Sequence 793, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
```

```
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/POCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 793:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-793

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCA 1428
DB 19 AGCAGCAGCAGCAGCA 1

RESULT 181
US-10-922-544-29
; Sequence 29, Application US/10922544
; Publication No. US20050153915A1
; GENERAL INFORMATION:
; APPLICANT: Sitna Therapeutics, Inc.
; APPLICANT: Uman, Nassim
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Early Growth Response
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/204 (MBH03-939-B)
; CURRENT APPLICATION NUMBER: US/10/922,544
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/512,701
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-922-544-29

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 980 CAGCACCAGCAGCAGCACC 998
DB 19 CAGCACCAGCAGCAGCACC 1
```

Db 1 CAGCAGCAGCAGCAGCACC 19

RESULT 182

US-10-922-544-203/c
; Sequence 203, Application US/10922544
; Publication No. US20050153915A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Usman, Nasim
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Early Growth Response
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/204 (MBHB03-939-B)
; CURRENT APPLICATION NUMBER: US/10/922,544
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US 60/512,701
; PRIOR FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-11-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 203
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-922-544-203

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 980 CAGCAGCAGCAGCAGCACC 998

Db 19 CAGCAGCAGCAGCAGCACC 1

RESULT 183

US-09-563-728A-7/c
; Sequence 7, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: oligonucleotide
US-09-563-728A-7

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429

Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 184

US-09-563-728A-16/c
; Sequence 16, Application US/09563728A
; Publication No. US20030078216A1
; GENERAL INFORMATION:
; APPLICANT: MacLeod, Alan R
; APPLICANT: Li, Zoumei
; APPLICANT: Besterman, Jeffrey M
; TITLE OF INVENTION: Inhibition of Histone Deacetylase
; FILE REFERENCE: 106101.229
; CURRENT APPLICATION NUMBER: US/09/563,728A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/132,287
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified base
; LOCATION: 1-4 and 17-20 are modified
; OTHER INFORMATION: Positions 1-4 and 17-20 are 2'-methoxyribose
; OTHER INFORMATION: substituted nucleotides; positions 5-16 are
; OTHER INFORMATION: deoxyribonucleotides
US-09-563-728A-16

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429

Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 185

US-10-145-493B-52/c
; Sequence 52, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: MacLeod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-52

Query Match          0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAG 1429
Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 186
US-10-315-962-67
; Sequence 67, Application US/10315962
; Publication No. US20040109848A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF AP-2 ALPHA EXPRESSION
; FILE REFERENCE: PTS-0046
; CURRENT APPLICATION NUMBER: US/10/315,962
; CURRENT FILING DATE: 2000-12-09
; NUMBER OF SEQ ID NOS: 126
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-315-962-67

Query Match          0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAG 1429
Db 1 GCGGCAGCAGCAGCAGCAG 19

RESULT 187
US-09-946-374-105/c
; Sequence 105, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
```

```
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
```

; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401

; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| |||||
Db 20 CAGCAGCAACAGCAGCAGC 2

RESULT 188

US-10-006-856A-105/c
; Sequence 102, Application US/10006856A
; Publication No. US2003004841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Pao, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: Synthetic oligonucleotide probe
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e-02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 189

US-10-006-818A-105/c
; Sequence 105, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PLC4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-818A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e-02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 190

US-10-006-485A-105/c
; Sequence 105, Application US/10006485A
; Publication No. US20030064062A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PLC9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919

; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5% Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418

|||||

Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 191

US-10-013-907A-105/c

; Sequence 105, Application US/10013907A

; Publication No. US20030064925A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan I.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C34

; CURRENT APPLICATION NUMBER: US/10/013,907A

; PRIOR FILING DATE: 2001-12-10

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 105

```
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-907A-105
```

```
Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2
```

RESULT 192

```
US-10-015-499A-105/c
; Sequence 105, Application US/10015499A
; Publication No. US20030065142A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-499A-105
```

```
Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2
```

RESULT 193

```
US-10-015-393A-105/c
; Sequence 105, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
```

```
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-393A-105
```

```
Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2
```

RESULT 194

```
US-10-015-869A-105/c
; Sequence 105, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-869A-105
```

```
Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2
```

RESULT 195

```
US-10-012-121A-105/c
; Sequence 105, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-121A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 196
US-10-006-116A-105/c
; Sequence 105, Application US/10006116A
; Publication No. US20030082626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC15
; CURRENT APPLICATION NUMBER: US/10/006,116A
; CURRENT FILING DATE: 2001-12-16
; Prior Application Number: 60/098716
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098723
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098749
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098750
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098803
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/098821
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/098843
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/099536
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099596
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099598
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099602
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099642
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099741
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099754
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099763
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099792
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099808
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099812
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099815
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/099816
; Prior Filing Date: 1998-09-10
; Prior Application Number: 60/100385
; Prior Filing Date: 1998-09-15
; Prior Application Number: 60/100388
; Prior Filing Date: 1998-09-15
; Prior Application Number: 60/100390
; Prior Filing Date: 1998-09-15
; Prior Application Number: 60/100584
; Prior Filing Date: 1998-09-16
; Prior Application Number: 60/100627
; Prior Filing Date: 1998-09-16
; Prior Application Number: 60/100661
; Prior Filing Date: 1998-09-16
; Prior Application Number: 60/100662
; Prior Filing Date: 1998-09-16
; Prior Application Number: 60/100664
; Prior Filing Date: 1998-09-16
; Prior Application Number: 60/100683
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/100684
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/100710
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/100711
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/100848
; Prior Filing Date: 1998-09-18
; Prior Application Number: 60/100849
; Prior Filing Date: 1998-09-18
; Prior Application Number: 60/100919
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/100930
; Prior Filing Date: 1998-09-17
; Prior Application Number: 60/101014
; Prior Filing Date: 1998-09-18
; Prior Application Number: 60/101068
; Prior Filing Date: 1998-09-18
; Prior Application Number: 60/101071
; Prior Filing Date: 1998-09-18
; Prior Application Number: 60/101279
; Prior Filing Date: 1998-09-22
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; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-09-29
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; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
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; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
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; PRIOR APPLICATION NUMBER: 60/105807
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; PRIOR APPLICATION NUMBER: 60/105881
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; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
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Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 197

US-10-006-117A-105/c
; Sequence 105, Application US/10006117A
; Publication No. US20030082627A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C13
; CURRENT APPLICATION NUMBER: US/10/006,117A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-117A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACGACGACG 1418
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Db 20 CAGGAGCAACGACGACG 2

RESULT 198
US-10-017-527A-105/c
; Sequence 105, Application US/10017527A
; Publication No. US20030082628A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1CG3
; CURRENT APPLICATION NUMBER: US/10/017,527A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
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; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
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;; PRIOR APPLICATION NUMBER: 60/102487
;; PRIOR FILING DATE: 1998-09-30
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;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102571
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102684
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102687
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102965
;; PRIOR FILING DATE: 1998-10-02
;; PRIOR APPLICATION NUMBER: 60/103258
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103314
;; PRIOR FILING DATE: 1998-10-07
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;; PRIOR APPLICATION NUMBER: 60/103395
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;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/106023
;; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1400 CAGCAGCAACAGCAGCAGC 1418
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Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 199

US-10-013-913A-105/c
; Sequence 105, Application US/10013913A
; Publication No. US20030083462A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C40
; CURRENT APPLICATION NUMBER: US/10/013,913A
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-913A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1400 CAGCAGCAACAGCAGCAGC 1418
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Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 200
US-10-007-194A-105/c
; Sequence 105, Application US/10007194A
; Publication No. US20030092061A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C6
; CURRENT APPLICATION NUMBER: US/10/007,194A
; CURRENT FILING DATE: 2002-06-25
; Prior Application Number: 60/098716
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098723
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098749
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098750

1	PRIOR FILING DATE: 1998-09-01	2	PRIOR APPLICATION NUMBER: 60/101477
3	PRIOR APPLICATION NUMBER: 60/098803	4	PRIOR FILING DATE: 1998-09-23
5	PRIOR FILING DATE: 1998-09-02	6	PRIOR APPLICATION NUMBER: 60/101472
7	PRIOR APPLICATION NUMBER: 60/098821	8	PRIOR FILING DATE: 1998-09-23
9	PRIOR FILING DATE: 1998-09-02	10	PRIOR APPLICATION NUMBER: 60/101474
11	PRIOR APPLICATION NUMBER: 60/098843	12	PRIOR FILING DATE: 1998-09-23
13	PRIOR FILING DATE: 1998-09-02	14	PRIOR APPLICATION NUMBER: 60/101475
15	PRIOR APPLICATION NUMBER: 60/099536	16	PRIOR FILING DATE: 1998-09-09
17	PRIOR FILING DATE: 1998-09-09	18	PRIOR APPLICATION NUMBER: 60/099596
19	PRIOR APPLICATION NUMBER: 60/099596	20	PRIOR FILING DATE: 1998-09-09
21	PRIOR FILING DATE: 1998-09-09	22	PRIOR APPLICATION NUMBER: 60/099598
23	PRIOR APPLICATION NUMBER: 60/099602	24	PRIOR FILING DATE: 1998-09-09
25	PRIOR FILING DATE: 1998-09-09	26	PRIOR APPLICATION NUMBER: 60/099642
27	PRIOR APPLICATION NUMBER: 60/099642	28	PRIOR FILING DATE: 1998-09-09
29	PRIOR FILING DATE: 1998-09-09	30	PRIOR APPLICATION NUMBER: 60/099741
31	PRIOR APPLICATION NUMBER: 60/099741	32	PRIOR FILING DATE: 1998-09-10
33	PRIOR FILING DATE: 1998-09-10	34	PRIOR APPLICATION NUMBER: 60/099754
35	PRIOR APPLICATION NUMBER: 60/099754	36	PRIOR FILING DATE: 1998-09-10
37	PRIOR FILING DATE: 1998-09-10	38	PRIOR APPLICATION NUMBER: 60/099763
39	PRIOR APPLICATION NUMBER: 60/099763	40	PRIOR FILING DATE: 1998-09-10
41	PRIOR FILING DATE: 1998-09-10	42	PRIOR APPLICATION NUMBER: 60/099792
43	PRIOR APPLICATION NUMBER: 60/099792	44	PRIOR FILING DATE: 1998-09-10
45	PRIOR FILING DATE: 1998-09-10	46	PRIOR APPLICATION NUMBER: 60/099808
47	PRIOR APPLICATION NUMBER: 60/099808	48	PRIOR FILING DATE: 1998-09-10
49	PRIOR FILING DATE: 1998-09-10	50	PRIOR APPLICATION NUMBER: 60/099812
51	PRIOR APPLICATION NUMBER: 60/099812	52	PRIOR FILING DATE: 1998-09-10
53	PRIOR FILING DATE: 1998-09-10	54	PRIOR APPLICATION NUMBER: 60/099815
55	PRIOR APPLICATION NUMBER: 60/099815	56	PRIOR FILING DATE: 1998-09-10
57	PRIOR FILING DATE: 1998-09-10	58	PRIOR APPLICATION NUMBER: 60/099816
59	PRIOR APPLICATION NUMBER: 60/099816	60	PRIOR FILING DATE: 1998-09-10
61	PRIOR FILING DATE: 1998-09-10	62	PRIOR APPLICATION NUMBER: 60/100385
63	PRIOR APPLICATION NUMBER: 60/100385	64	PRIOR FILING DATE: 1998-09-15
65	PRIOR FILING DATE: 1998-09-15	66	PRIOR APPLICATION NUMBER: 60/100388
67	PRIOR APPLICATION NUMBER: 60/100388	68	PRIOR FILING DATE: 1998-09-15
69	PRIOR FILING DATE: 1998-09-15	70	PRIOR APPLICATION NUMBER: 60/100390
71	PRIOR APPLICATION NUMBER: 60/100390	72	PRIOR FILING DATE: 1998-09-15
73	PRIOR FILING DATE: 1998-09-15	74	PRIOR APPLICATION NUMBER: 60/100584
75	PRIOR APPLICATION NUMBER: 60/100584	76	PRIOR FILING DATE: 1998-09-16
77	PRIOR FILING DATE: 1998-09-16	78	PRIOR APPLICATION NUMBER: 60/100627
79	PRIOR APPLICATION NUMBER: 60/100627	80	PRIOR FILING DATE: 1998-09-16
81	PRIOR FILING DATE: 1998-09-16	82	PRIOR APPLICATION NUMBER: 60/100661
83	PRIOR APPLICATION NUMBER: 60/100661	84	PRIOR FILING DATE: 1998-09-16
85	PRIOR FILING DATE: 1998-09-16	86	PRIOR APPLICATION NUMBER: 60/100662
87	PRIOR APPLICATION NUMBER: 60/100662	88	PRIOR FILING DATE: 1998-09-16
89	PRIOR FILING DATE: 1998-09-16	90	PRIOR APPLICATION NUMBER: 60/100664
91	PRIOR APPLICATION NUMBER: 60/100664	92	PRIOR FILING DATE: 1998-09-16
93	PRIOR FILING DATE: 1998-09-16	94	PRIOR APPLICATION NUMBER: 60/100683
95	PRIOR APPLICATION NUMBER: 60/100683	96	PRIOR FILING DATE: 1998-09-17
97	PRIOR FILING DATE: 1998-09-17	98	PRIOR APPLICATION NUMBER: 60/100684
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101	PRIOR FILING DATE: 1998-09-17	102	PRIOR APPLICATION NUMBER: 60/100710
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107	PRIOR APPLICATION NUMBER: 60/100711	108	PRIOR FILING DATE: 1998-09-17
109	PRIOR FILING DATE: 1998-09-17	110	PRIOR APPLICATION NUMBER: 60/100848
111	PRIOR APPLICATION NUMBER: 60/100848	112	PRIOR FILING DATE: 1998-09-18
113	PRIOR FILING DATE: 1998-09-18	114	PRIOR APPLICATION NUMBER: 60/100849
115	PRIOR APPLICATION NUMBER: 60/100849	116	PRIOR FILING DATE: 1998-09-18
117	PRIOR FILING DATE: 1998-09-18	118	PRIOR APPLICATION NUMBER: 60/100919
119	PRIOR APPLICATION NUMBER: 60/100919	120	PRIOR FILING DATE: 1998-09-17
121	PRIOR FILING DATE: 1998-09-17	122	PRIOR APPLICATION NUMBER: 60/100930
123	PRIOR APPLICATION NUMBER: 60/100930	124	PRIOR FILING DATE: 1998-09-17
125	PRIOR FILING DATE: 1998-09-17	126	PRIOR APPLICATION NUMBER: 60/101014
127	PRIOR APPLICATION NUMBER: 60/101014	128	PRIOR FILING DATE: 1998-09-18
129	PRIOR FILING DATE: 1998-09-18	130	PRIOR APPLICATION NUMBER: 60/101068
131	PRIOR APPLICATION NUMBER: 60/101068	132	PRIOR FILING DATE: 1998-09-18
133	PRIOR FILING DATE: 1998-09-18	134	PRIOR APPLICATION NUMBER: 60/101071
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; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

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Query Match 0.5%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 1.9e+02; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1400 CAGCAGCAACAGCAGCAGC 1418
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Db 20 CAGGAGCAACAGCAGCAGC 2

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RESULT 201
US-10-013-430A-105/c
; Sequence 105, Application US/10013430A
; Publication No. US20030092883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PlC31
; CURRENT APPLICATION NUMBER: US/10/013,430A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-430A-105

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Query Match 0.5%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 1.9e+02; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1400 CAGCAGCAACAGCAGCAGC 1418
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Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 202
US-10-011-671A-105/c
; Sequence 105, Application US/10011671A
; Publication No. US20030096954A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PlC27
; CURRENT APPLICATION NUMBER: US/10/011,671A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15

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RESULT 203
US-10-012-755A-105/c

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US-10-015-386A-105

Query Match          0.5%;   Score 17.4;   DB 1;   Length 21;
Best Local Similarity 94.7%;   Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 205
US-10-011-692A-105/c
; Sequence 105, Application US/10011692A
; Publication No. US20030109672A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C30
; CURRENT APPLICATION NUMBER: US/10/011,692A
; CURRENT FILING DATE: 2001-12-07
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-011-692A-105

Query Match          0.5%;   Score 17.4;   DB 1;   Length 21;
Best Local Similarity 94.7%;   Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 206
US-10-006-768A-105/c
; Sequence 105, Application US/10006768A
; Publication No. US20030113793A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

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PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099754
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099763
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099792
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099808
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099812
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099815
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/099816
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/100385
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100388
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100390
PRIOR FILING DATE:	1998-09-15
PRIOR APPLICATION NUMBER:	60/100584
PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100627
PRIOR FILING DATE:	1998-09-16
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PRIOR FILING DATE:	1998-09-16
PRIOR APPLICATION NUMBER:	60/100662
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PRIOR APPLICATION NUMBER:	60/100683
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PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100711
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100848
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/100849
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/100919
PRIOR FILING DATE:	1998-09-17
PRIOR APPLICATION NUMBER:	60/100930
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PRIOR APPLICATION NUMBER:	60/101279
PRIOR FILING DATE:	1998-09-22
PRIOR APPLICATION NUMBER:	60/101014
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/101068
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/101071
PRIOR FILING DATE:	1998-09-18
PRIOR APPLICATION NUMBER:	60/101474
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101475
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101476
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101477
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101479
PRIOR FILING DATE:	1998-09-23
PRIOR APPLICATION NUMBER:	60/101738
PRIOR FILING DATE:	1998-09-24
PRIOR APPLICATION NUMBER:	60/101741
PRIOR FILING DATE:	1998-09-24

;; PRIOR APPLICATION NUMBER: 60/101743
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101915
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101916
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;; PRIOR FILING DATE: 1998-09-30
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;; PRIOR APPLICATION NUMBER: 60/102571
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102684
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102687
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102965
;; PRIOR FILING DATE: 1998-10-02
;; PRIOR APPLICATION NUMBER: 60/103258
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103314
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103315
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103328
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103395
;; PRIOR FILING DATE: 1998-10-07
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;; PRIOR APPLICATION NUMBER: 60/103401
;; PRIOR FILING DATE: 1998-10-07
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;; PRIOR FILING DATE: 1998-10-06
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;; PRIOR APPLICATION NUMBER: 60/103711
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/104257
;; PRIOR FILING DATE: 1998-10-14
;; PRIOR APPLICATION NUMBER: 60/104987
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104
;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807

;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105881
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105882
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/106023
;; PRIOR FILING DATE: 1998-10-28
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| |||||
Db 20 CAGCAGCAACAGCAGCAGC 2
RESULT 208
US-10-006-063A-105/c
; Sequence 105, Application US/10006063A
; Publication No. US20030114652A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C3
; CURRENT APPLICATION NUMBER: US/10/006.063A
; CURRENT FILING DATE: 2002-03-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-063A-105
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| |||||
Db 20 CAGCAGCAACAGCAGCAGC 2
RESULT 209
US-10-020-063A-105/c
; Sequence 105, Application US/10020063A
; Publication No. US20030119097A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey

```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C65
; CURRENT APPLICATION NUMBER: US/10/020,063A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-020-063A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 210
US-10-015-391A-105/c
; Sequence 105, Application US/10015391A
; Publication No. US20030120053A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C59
; CURRENT APPLICATION NUMBER: US/10/015,391A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-407A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 211
US-10-017-407A-105/c
; Sequence 105, Application US/10017407A
; Publication No. US20030125535A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C61
; CURRENT APPLICATION NUMBER: US/10/017,407A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-407A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 212
US-10-011-833A-105/c
; Sequence 105, Application US/10011833A
; Publication No. US20030129650A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
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; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-391A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 211
US-10-017-407A-105/c
; Sequence 105, Application US/10017407A
; Publication No. US20030125535A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C61
; CURRENT APPLICATION NUMBER: US/10/017,407A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-407A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 212
US-10-011-833A-105/c
; Sequence 105, Application US/10011833A
; Publication No. US20030129650A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
```

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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C22
; CURRENT APPLICATION NUMBER: US/10/011,833A
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-011-833A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 213
US-10-006-041A-105/c
; Sequence 105, Application US/10006041A
; Publication No. US20030130490A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C8
; CURRENT APPLICATION NUMBER: US/10/006,041A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-041A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 214
US-10-015-822A-105/c
; Sequence 105, Application US/10015822A
; Publication No. US20030130491A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C38
; CURRENT APPLICATION NUMBER: US/10/015,822A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-822A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 215
US-10-015-387A-105/c
; Sequence 105, Application US/10015387A
; Publication No. US20030135034A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C54
; CURRENT APPLICATION NUMBER: US/10/015,387A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
```

```
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-387A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 216
US-10-006-130A-105/c
; Sequence 105, Application US/10006130A
; Publication No. US20030148375A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-130A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 217
US-10-006-172A-105/c
; Sequence 105, Application US/10006172A
; Publication No. US20030153000A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
```

```
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006,172A
; CURRENT FILING DATE: 2002-03-19
; Prior Application NUMBER: 60/098716
; Prior Filing DATE: 1998-09-01
; Prior Application NUMBER: 60/098723
; Prior Filing DATE: 1998-09-01
; Prior Application NUMBER: 60/098749
; Prior Filing DATE: 1998-09-01
; Prior Application NUMBER: 60/098750
; Prior Filing DATE: 1998-09-01
; Prior Application NUMBER: 60/098803
; Prior Filing DATE: 1998-09-02
; Prior Application NUMBER: 60/098821
; Prior Filing DATE: 1998-09-02
; Prior Application NUMBER: 60/098843
; Prior Filing DATE: 1998-09-02
; Prior Application NUMBER: 60/099536
; Prior Filing DATE: 1998-09-09
; Prior Application NUMBER: 60/099596
; Prior Filing DATE: 1998-09-09
; Prior Application NUMBER: 60/099598
; Prior Filing DATE: 1998-09-09
; Prior Application NUMBER: 60/099602
; Prior Filing DATE: 1998-09-09
; Prior Application NUMBER: 60/099642
; Prior Filing DATE: 1998-09-09
; Prior Application NUMBER: 60/099741
; Prior Filing DATE: 1998-09-10
; Prior Application NUMBER: 60/099754
; Prior Filing DATE: 1998-09-10
; Prior Application NUMBER: 60/099763
; Prior Filing DATE: 1998-09-10
; Prior Application NUMBER: 60/099792
; Prior Filing DATE: 1998-09-10
; Prior Application NUMBER: 60/099808
; Prior Filing DATE: 1998-09-10
; Prior Application NUMBER: 60/099812
; Prior Filing DATE: 1998-09-10
; Prior Application NUMBER: 60/099815
; Prior Filing DATE: 1998-09-10
; Prior Application NUMBER: 60/099816
; Prior Filing DATE: 1998-09-10
; Prior Application NUMBER: 60/100385
; Prior Filing DATE: 1998-09-15
; Prior Application NUMBER: 60/100388
; Prior Filing DATE: 1998-09-15
; Prior Application NUMBER: 60/100390
; Prior Filing DATE: 1998-09-15
; Prior Application NUMBER: 60/100584
; Prior Filing DATE: 1998-09-16
; Prior Application NUMBER: 60/100627
; Prior Filing DATE: 1998-09-16
; Prior Application NUMBER: 60/100661
; Prior Filing DATE: 1998-09-16
; Prior Application NUMBER: 60/100662
; Prior Filing DATE: 1998-09-16
; Prior Application NUMBER: 60/100664
; Prior Filing DATE: 1998-09-16
; Prior Application NUMBER: 60/100683
; Prior Filing DATE: 1998-09-17
; Prior Application NUMBER: 60/100684
; Prior Filing DATE: 1998-09-17
; Prior Application NUMBER: 60/100710
; Prior Filing DATE: 1998-09-17
; Prior Application NUMBER: 60/100711
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; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 218
US-10-017-253A-105/c
; Sequence 105, Application US/10017253A
; Publication No. US20030166055A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

```
; FILE REFERENCE: P2830PIC62
; CURRENT APPLICATION NUMBER: US/10/017,253A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-253A-105
```

```
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2
```

```
RESULT 219
US-10-015-392A-105/c
; Sequence 105, Application US/10015392A
; Publication No. US20030166901A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC58
; CURRENT APPLICATION NUMBER: US/10/015,392A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
```

```
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-392A-105
```

```
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2
```

```
RESULT 220
US-10-017-306A-105/c
; Sequence 105, Application US/10017306A
; Publication No. US20030170718A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC66
; CURRENT APPLICATION NUMBER: US/10/017,306A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-306A-105
```

```
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
DB 20 CAGGAGCAACAGCAGCAGC 2
```

RESULT 221
US-10-017-867A-105/c
; Sequence 105, Application US/10017867A
; Publication No. US20030180792A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC60
; CURRENT APPLICATION NUMBER: US/10/017.867A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
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; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30

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; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
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Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2
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RESULT 222

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US-10-012-064A-105/c
; Sequence 105, Application US/10012064A
; Publication No. US20030180836A1
; GENERAL INFORMATION:
```

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C19
; CURRENT APPLICATION NUMBER: US/10/012,064A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-064A-105
```

```
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2
```

RESULT 223

```
US-10-013-909A-105/c
; Sequence 105, Application US/10013909A
; Publication No. US20030186318A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C35
; CURRENT APPLICATION NUMBER: US/10/013,909A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-909A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 224
US-10-015-671A-105/c
; Sequence 105, Application US/10015671A
; Publication No. US20030186319A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C47
; CURRENT APPLICATION NUMBER: US/10/015,671A
; CURRENT FILING DATE: 2001-12-11
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-671A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 225
US-10-015-610A-105/c
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; Sequence 105, Application US/10015610A
; Publication No. US2003018631A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C52
; CURRENT APPLICATION NUMBER: US/10/015,610A
; CURRENT FILING DATE: 2001-12-12
; Prior Application Number: 60/098716
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098723
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098749
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098750
; Prior Filing Date: 1998-09-01
; Prior Application Number: 60/098803
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/098821
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/098843
; Prior Filing Date: 1998-09-02
; Prior Application Number: 60/099536
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099596
; Prior Filing Date: 1998-09-09
; Prior Application Number: 60/099598
; Prior Filing Date: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-610A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 226
US-10-012-137A-105/c
; Sequence 105, Application US/10012137A
; Publication No. US20030187189A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
```

```
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C29
; CURRENT APPLICATION NUMBER: US/10/012,137A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-137A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 227
US-10-012-752A-105/c
; Sequence 105, Application US/10012752A
; Publication No. US20030187190A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C24
; CURRENT APPLICATION NUMBER: US/10/012,752A
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-752A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 228
US-10-012-754A-105/c
; Sequence 105, Application US/10012754A
; Publication No. US20030187191A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C18
; CURRENT APPLICATION NUMBER: US/10/012,754A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-754A-105

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 229
US-10-013-910A-105/c
; Sequence 105, Application US/10013910A
; Publication No. US20030187192A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C33
; CURRENT APPLICATION NUMBER: US/10/013,910A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-910A-105

Query Match      0.5%;   Score 17.4;   DB 1;   Length 21;
Best Local Similarity 94.7%;   Pred. No. 1.9e+02;
Matches 18;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      1400 CAGCAGCAACAGCAGCAGC 1418
      ||| ||||| ||||| |||||
Db      20 CAGGAGCAACAGCAGCAGC 2

RESULT 230
US-10-013-911A-105/c
; Sequence 105, Application US/10013911A
; Publication No. US20030187193A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Pong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC39
; CURRENT APPLICATION NUMBER: US/10/013,911A
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29

```

;; PRIOR APPLICATION NUMBER: 60/102307
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102330
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102331
;; PRIOR FILING DATE: 1998-09-29
;; PRIOR APPLICATION NUMBER: 60/102484
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102487
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102570
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102571
;; PRIOR FILING DATE: 1998-09-30
;; PRIOR APPLICATION NUMBER: 60/102684
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102687
;; PRIOR FILING DATE: 1998-10-01
;; PRIOR APPLICATION NUMBER: 60/102965
;; PRIOR FILING DATE: 1998-10-02
;; PRIOR APPLICATION NUMBER: 60/103258
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103314
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103315
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103328
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103395
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103396
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103401
;; PRIOR FILING DATE: 1998-10-07
;; PRIOR APPLICATION NUMBER: 60/103449
;; PRIOR FILING DATE: 1998-10-06
;; PRIOR APPLICATION NUMBER: 60/103633
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103678
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103679
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/103711
;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: 60/104257
;; PRIOR FILING DATE: 1998-10-14
;; PRIOR APPLICATION NUMBER: 60/104987
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105000
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105002
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: 60/105104
;; PRIOR FILING DATE: 1998-10-21
;; PRIOR APPLICATION NUMBER: 60/105169
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105266
;; PRIOR FILING DATE: 1998-10-22
;; PRIOR APPLICATION NUMBER: 60/105693
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105881
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105882
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/106023
;; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2
||| ||||| ||||| |||||
||| ||||| ||||| |||||

RESULT 231
US-10-013-912A-105/c
; Sequence 105, Application US/10013912A
; Publication No. US20030187194A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C32
; CURRENT APPLICATION NUMBER: US/10/013,912A
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-912A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2
||| ||||| ||||| |||||
||| ||||| ||||| |||||

RESULT 232
US-10-015-653A-105/c
; Sequence 105, Application US/10015653A

Publication No. US20030187195A1

GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan I.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2830P1C43
 CURRENT APPLICATION NUMBER: US/10/015,653A
 CURRENT FILING DATE: 2002-06-25
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO 105
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotide probe
 US-10-015-653A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| ||||| |||||
 Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 233

US-10-012-101B-105/c
 Sequence 105, Application US/10012101B
 Publication No. US20030187239A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan I.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2830P1C6
 CURRENT APPLICATION NUMBER: US/10/012,101B
 CURRENT FILING DATE: 2001-12-06
 Prior application removed - See file Wrapper or Palm
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO 105
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotide probe
 US-10-012-101B-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| ||||| |||||
 Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 234

US-10-015-480A-105/c
 Sequence 105, Application US/10015480A
 Publication No. US20030190667A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan I.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2830P1C50
 CURRENT APPLICATION NUMBER: US/10/015,480A
 CURRENT FILING DATE: 2002-06-25
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 477
 SEQ ID NO 105
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotide probe
 US-10-015-480A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| ||||| |||||
 Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 235

US-10-015-715A-105/c
 Sequence 105, Application US/10015715A
 Publication No. US20030190668A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan I.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

```
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC56
; CURRENT APPLICATION NUMBER: US/10/015,715A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-715A-105
```

```
Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2
```

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RESULT 236
US-10-012-237A-105/c
; Sequence 105, Application US/10012237A
; Publication No. US20030191281A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC21
; CURRENT APPLICATION NUMBER: US/10/012,237A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-237A-105
```

```
Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1400 CAGCAGCAACAGCAGCAGC 1418
    ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2
```

```
RESULT 237
US-10-013-906A-105/c
; Sequence 105, Application US/10013906A
; Publication No. US20030191282A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
```

```
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC36
; CURRENT APPLICATION NUMBER: US/10/013,906A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
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; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258

; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGCAGCAACAGCAGCAGC 2

RESULT 238
US-10-015-388A-105/c
; Sequence 105, Application US/10015388A
; Publication No. US20030191299A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

US-10-015-385A-105/c
; Sequence 105, Application US/10015385A
; Publication No. US20030195347A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2830PIC51
; CURRENT APPLICATION NUMBER: US/10/015,385A
; CURRENT FILING DATE: 2002-07-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-015-385A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps

QY 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| |||||
Db 20 CAGGAGCACAGCAGCAGC 2

RESULT 241

US-10-007-236A-105/c
; Sequence 105, Application US/10007236A
; Publication No. US20030198993A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
; FILE REFERENCE: P2830PIC12
; CURRENT APPLICATION NUMBER: US/10/007,236A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-007-236A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 242

US-10-015-389A-105/c
; Sequence 105, Application US/10015389A
; Publication No. US20030199675A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C48
; CURRENT APPLICATION NUMBER: US/10/015.389A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-389A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 243

US-10-015-519A-105/c
; Sequence 105, Application US/10015519A
; Publication No. US20030203401A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C49
; CURRENT APPLICATION NUMBER: US/10/015.519A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-519A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 244

US-10-013-915A-105/c
; Sequence 105, Application US/10013915A
; Publication No. US20030204053A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C37
; CURRENT APPLICATION NUMBER: US/10/013.915A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-915A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 245

US-10-015-394A-105/c
; Sequence 105, Application US/10015394A
; Publication No. US20030204054A1
; GENERAL INFORMATION:

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth L.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C53
; CURRENT APPLICATION NUMBER: US/10/015,390A
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
; US-10-015-390A-105

      Query Match          0.5%;      Score 17.4;  DB 1;  Length 21;
      Best Local Similarity 94.7%;      Pred. No. 1.9e+02;
      Matches 18;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps

QY      1400 CAGCAGCAACAGCAGCAGC 1418
           ||| ||||| ||||| |||||
DB      20 CAGGAGCAACAGCAGCAGC 2

RESULT 247
US-10-006-746A-105/c
; Sequence 105, Application US/10006746A
; Publication NO. US20030220471A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C5
; CURRENT APPLICATION NUMBER: US/10/006,746A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602

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Tue Aug 16 13:15:19 2005

;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105694
;; PRIOR FILING DATE: 1998-10-26
;; PRIOR APPLICATION NUMBER: 60/105807
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105881
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/105882
;; PRIOR FILING DATE: 1998-10-27
;; PRIOR APPLICATION NUMBER: 60/106023
;; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 248
US-10-226-254A-105/c
; Sequence 105, Application US/10226254A
; Publication No. US20030224478A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C68
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-226-254A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 249
US-10-011-795A-105/c
; Sequence 105, Application US/10011795A
; Publication No. US20040005626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C25
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US/10/011,795A
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
||| ||||| ||||| ||||| |||||
DB 20 CAGGAGCAACAGCAGCAGC 2

RESULT 250
US-10-012-231A-105/c
; Sequence 105, Application US/10012231A
; Publication No. US20040014130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830PIC23
 ; CURRENT APPLICATION NUMBER: US/10/012,231A
 ; CURRENT FILING DATE: 2002-06-10
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 105
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide probe
 US-10-012-231A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| ||||| |||||
 Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 251

US-10-015-395A-105/c
 ; Sequence 105, Application US/10015395A
 ; Publication No. US20040073015A1
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830PIC57
 ; CURRENT APPLICATION NUMBER: US/10/015,395A
 ; CURRENT FILING DATE: 2001-12-12
 ; Prior application removed - See file Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 477
 ; SEQ ID NO 105
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide probe
 US-10-015-395A-105

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
 ||| ||||| ||||| ||||| |||||
 Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 252

US-10-751-736-8809/c
 ; Sequence 8809, Application US/10751736
 ; Publication No. US20040265230A1
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Martinez, Robert
 ; APPLICANT: Brown, Eugene
 ; APPLICANT: Liu, Wei
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
 ; TITLE OF INVENTION: CANCERS
 ; FILE REFERENCE: AM100927 (031896-002000)
 ; CURRENT APPLICATION NUMBER: US/10/751,736
 ; CURRENT FILING DATE: 2003-01-06
 ; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
 ; PRIOR FILING DATE: 2003-01-06
 ; NUMBER OF SEQ ID NOS: 54873
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 8809
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-751-736-8809

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1555 ACAACAGCAGCAGCAGCAG 1573
 ||| ||||| ||||| ||||| |||||
 Db 21 AGAACAGCAGCAGCAGCAG 3

RESULT 253

US-10-751-736-39221
 ; Sequence 39221, Application US/10751736
 ; Publication No. US20040265230A1
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth
 ; APPLICANT: Martinez, Robert
 ; APPLICANT: Brown, Eugene
 ; APPLICANT: Liu, Wei
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
 ; FILE OF INVENTION: CANCERS
 ; FILE REFERENCE: AM100927 (031896-002000)
 ; CURRENT APPLICATION NUMBER: US/10/751,736
 ; CURRENT FILING DATE: 2003-01-06
 ; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
 ; PRIOR FILING DATE: 2003-01-06
 ; NUMBER OF SEQ ID NOS: 54873
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 39221
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: RNAi
 US-10-751-736-39221

Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAACAGCAGCAG 1447
 ||| ||||| ||||| ||||| |||||
 Db 1 GCAGCAGCAACAGCAGCAG 19

RESULT 254

US-10-012-149A-105/c
 ; Sequence 105, Application US/10012149A
 ; Publication No. US20050043520A1
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnovers, Luc
 ; APPLICANT: Eaton, Dan I.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey

```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC26
; CURRENT APPLICATION NUMBER: US/10/012.149A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 105
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-149A-105

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
      ||| ||||| ||||| |||||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 255
US-10-730-771-62
; Sequence 62, Application US/10730771
; Publication No. US20050074787A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian-Bing
; APPLICANT: Hirschhorn, Joel N.
; APPLICANT: Huang, Xiaohua
; APPLICANT: Kaplan, Paul S.
; APPLICANT: Lander, Eric S.
; APPLICANT: Lockhart, David J.
; APPLICANT: Ryder, Thomas
; APPLICANT: Sklar, Pamela
; TITLE OF INVENTION: UNIVERSAL ARRAYS
; FILE REFERENCE: 2825.1016-007
; CURRENT APPLICATION NUMBER: US/10/730,771
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US 60/126,473
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 60/140,359
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/536,841
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Template sequence
US-10-730-771-62

Query Match          0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1404 AGCAACAGCAGCAGCAGCAGC 1424
      ||| ||||| ||||| |||||
Db 1 AGGAACAGCAACAGCAGCAGC 21

RESULT 256
```

```
US-10-494-343-167
; Sequence 167, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Pham, Thuymy
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 167
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-167

Query Match          0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGC 1445
      ||| ||||| ||||| |||||
Db 1 GCAGCAGCAGCAACAGC 17

RESULT 257
US-10-494-343-168
; Sequence 168, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Pham, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 168
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-168

Query Match          0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1430 CAGCAGCAGCAACAGCA 1446
      ||| ||||| ||||| |||||
Db 1 CAGCAGCAGCAACAGCA 17

RESULT 258
US-10-494-343-169
; Sequence 169, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
```

; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 169
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-169

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1431 AGCAGCAGCAACAGCAG 1447
Db 1 AGCAGCAGCAACAGCAG 17
|||||

RESULT 259
US-10-494-343-170
; Sequence 170, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 170
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-170

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1432 GCAGCAGCAACAGCAGC 1448
Db 1 GCAGCAGCAACAGCAGC 17
|||||

RESULT 260
US-10-494-343-171
; Sequence 171, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30

; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 171
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-171

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCA 1416
Db 1 CAGCAGCAACAGCAGCA 17
|||||

RESULT 261
US-10-494-343-172
; Sequence 172, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 172
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-172

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1401 AGCAGCAACAGCAGCAG 1417
Db 1 AGCAGCAACAGCAGCAG 17
|||||

RESULT 262
US-09-933-638A-9
; Sequence 9, Application US/09933638A
; Patent No. US20020160952A1
; GENERAL INFORMATION:
; APPLICANT: Kazantsev, Aleksey G.
; APPLICANT: Thompson, Leslie M.
; TITLE OF INVENTION: INHIBITION OF PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: 01997-289001
; CURRENT APPLICATION NUMBER: US/09/933,638A
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/226,502
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Fast-SEQ for Windows Version 4.0

```
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-933-638A-9

Query Match          0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1397 CAACAGCAGCAACAGCA 1413
Db 1 CAACAGCAGCAACAGCA 17

RESULT 263
US-09-933-638A-10/C
; Sequence 10, Application US/09933638A
; Patent No. US20020160952A1
; GENERAL INFORMATION:
; APPLICANT: Kazantsev, Aleksey G.
; APPLICANT: Thompson, Leslie M.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: INHIBITION OF PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: 01997-289001
; CURRENT APPLICATION NUMBER: US/09/933,638A
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/226,502
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-933-638A-10

Query Match          0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 CAGCAGCAACAGCAACA 1467
Db 18 CAGCAGCAACAGCAACA 2

RESULT 264
US-10-194-584-1
; Sequence 1, Application US/10194584
; Publication No. US20030027288A1
; GENERAL INFORMATION:
; APPLICANT: Housman, David E.
; APPLICANT: Preisinger, Elizabeth A.
; APPLICANT: Kazantsev, Aleksey G.
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGENTS WHICH INHIBIT AGGREGATION
; FILE REFERENCE: 01997-261002
; CURRENT APPLICATION NUMBER: US/10/194,584
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/405,048
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
```

```
US-10-194-584-1

Query Match          0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1397 CAACAGCAGCAACAGCA 1413
Db 1 CAACAGCAGCAACAGCA 17

RESULT 265
US-10-194-584-2/C
; Sequence 2, Application US/10194584
; Publication No. US20030027288A1
; GENERAL INFORMATION:
; APPLICANT: Housman, David E.
; APPLICANT: Preisinger, Elizabeth A.
; APPLICANT: Kazantsev, Aleksey G.
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGENTS WHICH INHIBIT AGGREGATION
; FILE REFERENCE: 01997-261002
; CURRENT APPLICATION NUMBER: US/10/194,584
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/405,048
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-10-194-584-2

Query Match          0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1451 CAGCAGCAACAGCAACA 1467
Db 18 CAGCAGCAACAGCAACA 2

RESULT 266
US-10-436-231-1
; Sequence 1, Application US/10436231
; Publication No. US20040175704A1
; GENERAL INFORMATION:
; APPLICANT: StrataGene
; APPLICANT: Sorge, Joseph A.
; APPLICANT: Firmin, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR POLYNUCLEOTIDE SEQUENCE DETECTION
; FILE REFERENCE: 25436/2392
; CURRENT APPLICATION NUMBER: US/10/436,231
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 60/452,481
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Example Allele A comprising tandem repeats
US-10-436-231-1

Query Match          0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1407 AACAGCAGCAGCAGCAG 1423
| | | | | | | | | | | | | | | | | |
Db 2 AACAGCAGCAGCAGCAG 18

RESULT 267

US-10-436-231-2/c
; Sequence 2, Application US/10436231
; Publication No. US20040175704A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; APPLICANT: Sorage, Joseph A
; APPLICANT: Firmin, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR POLYNUCLEOTIDE SEQUENCE DETECTION
; FILE REFERENCE: 25436/2392
; CURRENT APPLICATION NUMBER: US/10/436,231
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 60/452,481
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Example Allele A comprising tandem repeats
US-10-436-231-2

Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1407 AACAGCAGCAGCAGCAG 1423
| | | | | | | | | | | | | | | | | |
Db 17 AACAGCAGCAGCAGCAG 1

RESULT 268

US-09-948-002-35
; Sequence 35, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/09/948,002
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-09-948-002-35

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAGC 1430
| | | | | | | | | | | | | | | | | |
Db 1 GTAGCAGCAGCGGCAGCAGC 20

RESULT 269

US-09-920-033-22
; Sequence 22, Application US/09920033
; Publication No. US20030087853A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
; FILE REFERENCE: ISPH-0592
; CURRENT APPLICATION NUMBER: US/09/920,033
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-09-920-033-22

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1532 GCCCAACAGCAGCAGCAGCA 1551
| | | | | | | | | | | | | | | | | |
Db 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 270

US-10-060-301-43
; Sequence 43, Application US/10060301
; Publication No. US20020182622A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Yusuke et al.
; TITLE OF INVENTION: A METHOD FOR SNP (SINGLE NUCLEOTIDE POLYMORPHISM) TYPING
; FILE REFERENCE: 1254-0195p
; CURRENT APPLICATION NUMBER: US/10/060,301
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: JP 2001-25700
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Forward primer for SNP ID 22
US-10-060-301-43

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1601 CAGCAGCAGCAACCAACCATC 1620
| | | | | | | | | | | | | | | | | |
Db 1 CAGCAGCAACACACACCGTC 20

RESULT 271

US-10-147-196-22
; Sequence 22, Application US/10147196
; Publication No. US20030215943A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
; FILE REFERENCE: ISPH-0664
; CURRENT APPLICATION NUMBER: US/10/147,196
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 124
; SEQ ID NO 22

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-147-196-22

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
Db 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 272
US-10-388-263-554
; Sequence 554, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowseert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 554
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-554

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
Db 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 273
US-10-210-479-79/c
; Sequence 79, Application US/10210479
; Publication No. US20040023380A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSION
; FILE REFERENCE: RTS-0385
; CURRENT APPLICATION NUMBER: US/10/210,479
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-479-79

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1645 AAGCCAGCCTTTGCTAAGCT 1664
Db 20 AAGCCAGCCTTTGCTAAGCT 1

RESULT 274
US-10-633-163-35
; Sequence 35, Application US/10633163
; Publication No. US20040063655A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR BETA EXPRESSION
; FILE REFERENCE: ISPH-0607
; CURRENT APPLICATION NUMBER: US/10/633,163
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/948,002
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 09/661,753
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/154,546
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-633-163-35

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAGC 1430
Db 1 GTAGCAGCAGCGGCAGCAGC 20

RESULT 275
US-10-712-795-22
; Sequence 22, Application US/10712795
; Publication No. US20040214325A1
; GENERAL INFORMATION:
; APPLICANT: Crooke et al.
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
; FILE REFERENCE: 30566/39662
; CURRENT APPLICATION NUMBER: US/10/712,795
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,234
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US03/15493
; PRIOR FILING DATE: 2003-05-13
; NUMBER OF SEQ ID NOS: 892
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-712-795-22

Query Match          0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
```

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACGACGACGACGCA 1551
|||||
Db 1 GCCCGCCGACGACGACGCA 20

RESULT 276

US-10-920-612-22
; Sequence 22, Application US/10920612
; Publication No. US2005009088A1
; GENERAL INFORMATION:
; APPLICANT: Crooke et al.
; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
; FILE REFERENCE: 30566/39634A
; CURRENT APPLICATION NUMBER: US/10/920,612
; CURRENT FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: PCT/US03/15493
; PRIOR FILING DATE: 2003-11-15
; PRIOR APPLICATION NUMBER: US 10/712,795
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,234
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 892
; SEQ ID NO 22
; TYPE: DNA
; LENGTH: 20
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-920-612-22

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACGACGACGACGCA 1551
|||||
Db 1 GCCCGCCGACGACGACGCA 20

RESULT 277

US-10-831-901A-11559
; Sequence 11559, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 892
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11559
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11559

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11559
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11559

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1543 GCAGCAGCAGCAACAACAGC 1562
|||||
Db 1 GTAGCAGCAGCAACAATAGC 20

RESULT 278

US-10-831-901A-11560
; Sequence 11560, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11560
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11560

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1542 AGCAGCAGCAGCAACAACAG 1561
|||||
Db 1 AGTAGCAGCAGCAACAATAG 20

RESULT 279

US-09-906-419-91
; Sequence 91, Application US/09906419

; Publication No. US20030037357A1
; GENERAL INFORMATION:
; APPLICANT: Shockey, Jay
; APPLICANT: Schnurr, Judy
; APPLICANT: Browse, John
; TITLE OF INVENTION: Plant Acyl-CoA Synthetases
; FILE REFERENCE: DOM-04679
; CURRENT APPLICATION NUMBER: US/09/906,419
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/220,474
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-906-419-91

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2902 CAGGGCTTTTCAAGGAACGTG 2921
|||||
Db 2 CAGGGCTTCTCAAGGAATG 21

RESULT 280

US-10-119-136-91
; Sequence 91, Application US/10119136
; Publication No. US20030097676A1
; GENERAL INFORMATION:
; APPLICANT: Shockey, Jay
; APPLICANT: Schnurr, Judy
; APPLICANT: Browse, John
; TITLE OF INVENTION: Plant Acyl-CoA Synthetases
; FILE REFERENCE: DOM-04695
; CURRENT APPLICATION NUMBER: US/10/119,136
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/906,419
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/220,474
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-119-136-91

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2902 CAGGGCTTTTCAAGGAACGTG 2921
|||||
Db 2 CAGGGCTTCTCAAGGAATG 21

RESULT 281

US-10-410-031-91
; Sequence 91, Application US/10410031
; Publication No. US20040010817A1
; GENERAL INFORMATION:
; APPLICANT: Shockey, Jay M.
; APPLICANT: Schnurr, Judy
; APPLICANT: Browse, John A.

; TITLE OF INVENTION: Plant Acyl-CoA Synthetases
; FILE REFERENCE: DOM-07654
; CURRENT APPLICATION NUMBER: US/10/410,031
; CURRENT FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-410-031-91

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2902 CAGGGCTTTTCAAGGAACGTG 2921
|||||
Db 2 CAGGGCTTCTCAAGGAATG 21

RESULT 282

US-10-380-195A-2
; Sequence 2, Application US/10380195A
; Publication No. US20040072776A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Kiyama, Satoshi
; APPLICANT: Nelson, Colleen
; APPLICANT: Rennie, Paul
; TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
; FILE REFERENCE: UBC-P-023
; CURRENT APPLICATION NUMBER: US/10/380,195A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: PCT/US01/28748
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: US 60/232,641
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IGFBP2 antisense
; US-10-380-195A-2

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
|||||
Db 2 GCCCAGTAGCAGCAGCAGCA 21

RESULT 283

US-10-380-195A-46
; Sequence 46, Application US/10380195A
; Publication No. US20040072776A1
; GENERAL INFORMATION:
; APPLICANT: Gleave, Martin
; APPLICANT: Kiyama, Satoshi
; APPLICANT: Nelson, Colleen
; APPLICANT: Rennie, Paul
; TITLE OF INVENTION: Antisense Insulin-Like Growth Factor Binding Protein (IGFBP)-2
; FILE REFERENCE: UBC-P-023
; CURRENT APPLICATION NUMBER: US/10/380,195A


```
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: PCT/US01/28748
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: US 60/232,641
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IGFBP2 antisense
US-10-380-195A-46

Query Match          0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1532 GCCCAACAGCAGCAGCAGCA 1551
    ||||| ||||| ||||| |||||
Db 2 GCCCAGTAGCAGCAGCAGCA 21

RESULT 284
US-10-751-736-10540/c
; Sequence 10540, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10540
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-10540

Query Match          0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCAGC 1430
    ||||| ||||| ||||| |||||
Db 20 GCAGCAGCAGCAGCAGCAGCATC 1

RESULT 285
US-10-751-736-10541/c
; Sequence 10541, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
```

```
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10541
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-751-736-10541

Query Match          0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 974 ATGCAGCAGCAGCAGCAGCA 993
    ||||| ||||| ||||| |||||
Db 20 ATGCAGCAGCAGCAGCAGCA 1

RESULT 286
US-10-751-736-18508/c
; Sequence 18508, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18508
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-18508

Query Match          0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2147 ACTCCCAATTCAGCCTCCT 2166
    ||||| ||||| ||||| |||||
Db 21 AATCTCAATTCAGCCTCCT 2

RESULT 287
US-10-751-736-18509/c
; Sequence 18509, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18509
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI
US-10-751-736-18509
```

```
Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2146 AACTCCCAATTCAGCCTCC 2165
Dbb|||||
Db 20 AAATCTCAATTCAGCCTCC 1

RESULT 288
US-10-751-736-49304/c
; Sequence 49304, Application US/10751736
; Publication No. US2004026230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49304
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-49304

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1967 AAAATTGCTCCACAGATCA 1986
Dbb|||||
Db 21 AAAATTGCAGCACAGATCA 2

RESULT 289
US-10-847-918-3217
; Sequence 3217, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3217
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-3217

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACGACGACGCA 1419
Dbb|||||
Db 1400 CAGCAGCAACGACGACGCA 1419
```

```
Db 1 CAGCATCAACGGCAGCAGCA 20

RESULT 290
US-10-181-603-11
; Sequence 11, Application US/10181603
; Publication No. US20030049662A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD7 EXPRESSION
; FILE REFERENCE: RTSP-0342
; CURRENT APPLICATION NUMBER: US/10/181,603
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US01/01165
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/487,444
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-603-11

Query Match      0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1406 CAACAGCAGCAGCAGCAG 1423
Dbb|||||
Db 1 CGACAGCAGCAGCAGCAG 18

RESULT 291
US-10-730-771-206
; Sequence 206, Application US/10730771
; Publication No. US20050074787A1
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian-Bing
; APPLICANT: Hirschhorn, Joel N.
; APPLICANT: Huang, Xiaohua
; APPLICANT: Kaplan, Paul
; APPLICANT: Lander, Eric S.
; APPLICANT: Lockhart, David J.
; APPLICANT: Ryder, Thomas
; APPLICANT: Sklar, Pamela
; TITLE OF INVENTION: UNIVERSAL ARRAYS
; FILE REFERENCE: 2825.1016-007
; CURRENT APPLICATION NUMBER: US/10/730,771
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US 60/126,473
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 60/140,359
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/536,841
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Template sequence
US-10-730-771-206

Query Match      0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1395 AGCAACAGCAGCAACAGC 1412
| | | | | | | | | | | | | | | |
Db 1 AGCAACAGCAGCAACAGC 18

RESULT 292
US-09-865-866-61
; Sequence 61, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-61

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2556 TGACGCTTCGAGGATCC 2573
| | | | | | | | | | | | | | | |
Db 3 TGACGCTTCGAGGATCC 20

RESULT 293
US-10-186-157-17/c
; Sequence 17, Application US/10186157
; Publication No. US20040002151A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SELENOPHOSPHATE SYNTHETASE 2 EXPRESSION
; FILE REFERENCE: RTS-0193
; CURRENT APPLICATION NUMBER: US/10/186,157
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-186-157-17

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 CGGGCTTGACTCAGGGCC 755
| | | | | | | | | | | | | | | |
Db 18 CGGGCTTGACTCAGGGCC 1

RESULT 294
US-10-380-126-39/c
; Sequence 39, Application US/10380126
; Publication No. US20040029824A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-1 EXPRESSION
; FILE REFERENCE: RTSP-0175
```

```
; CURRENT APPLICATION NUMBER: US/10/380,126
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/657,042
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-380-126-39

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 976 GCAGCAGCAGCAGCA 993
| | | | | | | | | | | | | | | |
Db 19 GCAGCAGCAGCAGCA 2

RESULT 295
US-10-831-901A-11557
; Sequence 11557, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/465,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11557
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11557

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1545 AGCAGCAGCAACACAGC 1562
| | | | | | | | | | | | | | | |
Db 1 AGCAGCAGCAACACATAGC 18
```

```
RESULT 296
US-10-831-901A-11558
; Sequence 11558, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; FILE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL0008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/469,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 3063
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11558
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-11558

Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1545 AGCAGCAGCAACACAGC 1562
Db 2 AGCAGCAGCAACATAGC 19
|||||

RESULT 297
US-10-643-038-61
; Sequence 61, Application US/10643038
; Publication No. US20050143331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-61
```

```
Query Match          0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2556 TGACGCTGTCAGGAGTCC 2573
Db 3 TGACTTCTGCAGGAGTCC 20
|||||

RESULT 298
US-09-792-818-608
; Sequence 608, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insert
; TITLE OF INVENTION: (Grid) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 608
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-608

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.6e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 975 TGCAGCAGCACCAGCA 990
Db 2 UGCAGCAGCACCAGCA 17
|||||

RESULT 299
US-10-494-343-166
; Sequence 166, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 166
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-166

Query Match          0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAG 1444
|||||
```

```
Db      2 GCAGCAGCAGCAACAG 17

RESULT 300
US-10-436-231-5
; Sequence 5, Application US/10436231
; Publication No. US20040175704A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; APPLICANT: Firmin, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR POLYNUCLEOTIDE SEQUENCE DETECTION
; FILE REFERENCE: 25436/2392
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/436,231
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Example Allele A comprising tandem repeats
US-10-436-231-5

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1402 GCAGCAGCAGCAGCAG 1417
      |||||
Db      1 GCAGCAACAGCAGCAG 16

RESULT 301
US-10-436-231-5
; Sequence 5, Application US/10436231
; Publication No. US20040175704A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; APPLICANT: Firmin, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR POLYNUCLEOTIDE SEQUENCE DETECTION
; FILE REFERENCE: 25436/2392
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/436,231
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Example Allele A comprising tandem repeats
US-10-436-231-5

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1409 CAGCAGCAGCAGCAGC 1424
      |||||
Db      1 CAGCAGCAGCAGCAGC 16

RESULT 302
US-10-436-231-6/c
; Sequence 6, Application US/10436231
; Publication No. US20040175704A1
; GENERAL INFORMATION:
; APPLICANT: Stratagene
; APPLICANT: Firmin, Andrew
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR POLYNUCLEOTIDE SEQUENCE DETECTION
; FILE REFERENCE: 25436/2392
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US/10/436,231
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Example Allele A comprising tandem repeats
US-10-436-231-6

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1409 CAGCAGCAGCAGCAGC 1424
      |||||
Db      18 CAGCAGCAGCAGCAGC 3

RESULT 303
US-10-148-835-86/c
; Sequence 86, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed
; OTHER INFORMATION: oligonucleotide primer for PCR
US-10-148-835-86

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      986 CAGCAGCAGCAGCAGC 1001
      |||||
Db      18 CAGCAGCAGCAGCAGC 3

RESULT 304
US-10-704-263-201/c
; Sequence 201, Application US/10704263
; Publication No. US20050101013A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: James Karras
; TITLE OF INVENTION: MODULATION OF STATS EXPRESSION
; FILE REFERENCE: RTS-0569
; CURRENT APPLICATION NUMBER: US/10/704,263
; CURRENT FILING DATE: 2003-11-06
; NUMBER OF SEQ ID NOS: 213
; SEQ ID NO 201
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Compound
US-10-704-263-201
    Query Match          0.4%; Score 16; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1553 CAACAACAGCAGCAGC 1568
    |||||
Db 20 CAACAACAGCAGCAGC 5

RESULT 305
US-10-923-329-8/c
; Sequence 8, Application US/10923329
; Publication No. US20050164968A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Richards, Ivan
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of ADAM33 Gene Expression
; FILE REFERENCE: 400/225 (MBH04-672)
; CURRENT APPLICATION NUMBER: US/10/923,329
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/543,480
; PRIOR FILING DATE: 2004-02-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 514
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 204
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-923-329-204

Query Match          0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGC 1427
    |||||
Db 1 CAGCAGTAGTAGCAGCAGC 19

RESULT 307
US-10-215-432-43/c
; Sequence 43, Application US/10215432
; Publication No. US20030109476A1
; GENERAL INFORMATION:
; APPLICANT: Eric B. Kmiec
; APPLICANT: Hetal Parekh-Olmedo
; TITLE OF INVENTION: Composition and methods for the
; FILE REFERENCE: NApPro-10
; CURRENT APPLICATION NUMBER: US/10/215,432
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Converted HD sequence
US-10-215-432-43

Query Match          0.4%; Score 15.6; DB 1; Length 30;
Best Local Similarity 70.0%; Pred. No. 4.9e+02;
```

```
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
RESULT 308
US-09-848-754A-175
; Sequence 175, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 175
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-175
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.9e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3633 GAGAACCTAGAAAACAT 3649
Db 1 GAGAACCUAGAAAUCAU 17
RESULT 309
US-09-792-818-360
; Sequence 360, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 360
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-360
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 985 CCAGCAGCAGCAGCAGC 1001
Db 1 CCUGCAGCAGCAGCAGC 17
RESULT 310
US-09-792-818-361
; Sequence 361, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
```

```
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 361
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-361
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 976 GCAGCAGCAGCAGCAGC 992
Db 1 GCAGCAGCAGCAGCAGC 17
```

```
RESULT 311
US-09-792-818-362
; Sequence 362, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBH00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 362
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-362
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 978 AGCAGCAGCAGCAGCAGC 994
Db 1 AGCAGCAGCAGCAGCAGC 17
```

```
RESULT 312
US-09-792-818-363
; Sequence 363, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
```

```
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 363
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-363
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 979 GCAGCACCAGCAGCAGC 995
Db 1 GCAGCACCAGCACCAGC 17
```

RESULT 313

```
US-09-792-818-609
; Sequence 609, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 609
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-609
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 986 CAGCAGCAGCAGCAGCC 1002
Db 1 CAGCACCAGCACCAGCC 17
```

RESULT 314

```
US-10-138-674-2491/c
; Sequence 2491, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2491
; LENGTH: 17
```

```
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-2491
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 326 TTGCCTATGAGCCCAAGC 342
Db 17 TTGCCTGTGAGCCAAGC 1
```

RESULT 315

```
US-10-287-949A-2491/c
; Sequence 2491, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2491
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-2491
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 326 TTGCCTATGAGCCCAAGC 342
Db 17 TTGCCTGTGAGCCAAGC 1
```

RESULT 316

```
US-10-494-343-174
; Sequence 174, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: P50184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 174
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-174
```

```
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```


Qy 1505 CAGCAACAGCAGCAGAG 1521
|||
Db 1 CAGCAACAGCAGCAGGG 17

RESULT 317
US-09-968-122-9
; Sequence 9, Application US/09968122
; Publication No. US20030158397A1
; GENERAL INFORMATION:
; APPLICANT: Ramos, Juan Luis
; APPLICANT: Ben-Bassat, Arle
; APPLICANT: Godoy, Patricia
; APPLICANT: Ramos-Gonzalez, Maria Isabel
; APPLICANT: Duque, Estrella
; TITLE OF INVENTION: Methods for Production of p-Hydroxybenzoate in Bacteria
; FILE REFERENCE: BC1030 US NA
; CURRENT APPLICATION NUMBER: US/09/968,122
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/236,879
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: artificial sequence, primer
; FEATURE:
; OTHER INFORMATION: :
US-09-968-122-9

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 977 CAGCAGCACCAGCAGCA 993
|||
Db 1 CAGCAGCACCAGCATCA 17

RESULT 318
US-10-432-422-27/c
; Sequence 27, Application US/10432422
; Publication No. US20040076981A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Yoder, Olen
; APPLICANT: Turgeon, Barbara G.
; APPLICANT: Lu, Shen-wen
; TITLE OF INVENTION: Fungal Iron Reductase Gene
; FILE REFERENCE: 1360.017W01
; CURRENT APPLICATION NUMBER: US/10/432,422
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/252,732
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/252,649
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-432-422-27

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 978 AGCAGCACCAGCAGCAG 994
|||
Db 18 AGAAGCACCAGCAGCAG 2

RESULT 319
US-10-444-925-183
; Sequence 183, Application US/10444925
; Publication No. US20040009946A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Stephen Patrick
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Wilson, Linda K.
; TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION
; TITLE OF INVENTION: BY RNA INTERFERENCE
; FILE REFERENCE: 200125.441
; CURRENT APPLICATION NUMBER: US/10/444,925
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-925-183

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 2.4e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3674 CCATATTCACTCTCTCAC 3690
|||
Db 2 CCAUUAUCACACCCUCAC 18

RESULT 320
US-10-883-218-297
; Sequence 297, Application US/10883218
; Publication No. US20050124567A1
; GENERAL INFORMATION:
; APPLICANT: Haeberli, Peter
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of TRPM7 Gene Expression
; TITLE OF INVENTION: Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/195 (MBHB04-535)
; CURRENT APPLICATION NUMBER: US/10/883,218
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2003-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/427,160
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 930
; SOFTWARE: PatentIn version 3.3

```
; SEQ ID NO 297
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-883-218-297

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 2.4e+02;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 143 CTCACGGGTTCTTGAA 159
      ||||| ||||| ||||| |||||
Db 1 CUCCAGGUUCUUGAA 17

RESULT 321
US-10-883-218-699/c
; Sequence 699, Application US/10883218
; Publication No. US20050124567A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Haeblerli, Peter
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of TRPM7 Gene Expression
; FILE REFERENCE: 400/195 (MBH04-535)
; CURRENT APPLICATION NUMBER: US/10/883,218
; PRIOR FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2003-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 930
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 699
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-883-218-699

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 143 CTCACGGGTTCTTGAA 159
      ||||| ||||| ||||| |||||
Db 19 CTCACAGGTTCTTGAA 3

RESULT 322
US-10-893-010-39/c
; Sequence 39, Application US/10893010
```

```
; Publication No. US20050164224A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression
; FILE REFERENCE: 400/170 (MBH02-1005-C)
; CURRENT APPLICATION NUMBER: US/10/893,010
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: PCT/US 03/03662
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 526
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-893-010-39

Query Match          0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 549 AGGAACGTGTTCAATGAA 565
      ||||| ||||| ||||| |||||
Db 17 AGGAAGTGTTCATGAA 1

RESULT 323
US-10-893-010-278
; Sequence 278, Application US/10893010
; Publication No. US20050164224A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Thompson, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Cyclin D1 Gene Expression
; FILE REFERENCE: 400/170 (MBH02-1005-C)
; CURRENT APPLICATION NUMBER: US/10/893,010
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: PCT/US 03/03662
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: US 60/411,275
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
```

```
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 10/720,448
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US03/05346
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: PCT/US03/05028
; PRIOR FILING DATE: 2003-02-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 526
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: s1NA antisense region
US-10-893-010-278

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 2.4e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      549 AGGAAGUGUCAAUGAA 565
Db      3 AGGAAGUGUCAAUGAA 19

RESULT 324
US-09-880-313A-228
; Sequence 228, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 228
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-880-313A-228

Query Match      0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2586 GTACACCTGCAGCCT 2600
Db      1 GTACACCTGCAGCCT 15

RESULT 325
US-10-494-343-165
; Sequence 165, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shanon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
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; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 165
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-494-343-165

Query Match      0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1429 GCAGCAGCAGCAACA 1443
Db      3 GCAGCAGCAGCAACA 17

RESULT 326
US-10-498-848-6
; Sequence 6, Application US/10498848
; Publication No. US20050153289A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Method of Analyzing Gene Expression
; FILE REFERENCE: P02-0155PCT
; CURRENT APPLICATION NUMBER: US/10/498,848
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: JP 2001-382053
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: JP 2002-45104
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: JP 2002-140111
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: JP 2002-333769
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-498-848-6

Query Match      0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3447 AAACCCCATGTCATG 3461
Db      4 AAACCCCATGTCATG 18

RESULT 327
US-09-280-030-28/c
; Sequence 28, Application US/09280030A
; Patent No. US20010021515A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Seiji
; APPLICANT: Higashikuni, Naohiko
; APPLICANT: Kudo, Toshiyuki
; APPLICANT: Kondo, Masaaki
; TITLE OF INVENTION: DNAs ENCODING NEW FUSION PROTEINS AND PROCESSES FOR
; TITLE OF INVENTION: PREPARING USEFUL POLYPEPTIDES THROUGH EXPRESSION OF THE
; TITLE OF INVENTION: DNAs
; FILE REFERENCE: 382.1026
; CURRENT APPLICATION NUMBER: US/09/280,030A
; CURRENT FILING DATE: 1999-03-26
```

```
; EARLIER APPLICATION NUMBER: JP10-87339/1998
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designated is
; OTHER INFORMATION: a reverse primer for PCR amplification of
; OTHER INFORMATION: MWPsp-MWPmp5 DNA
US-09-280-030-28

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCA 1428
Db 18 GCAGCAGAGAGCAGCA 1

RESULT 328
US-09-426-548-43
; Sequence 43, Application US/09426548
; Patent No. US20010044936A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, David
; APPLICANT: Lin-Goerke, Julli L.
; APPLICANT: Ling, Jessica
; TITLE OF INVENTION: No. US20010044936A1el Mutations in Human MLH1 and MSH2 Genes Used
; TITLE OF INVENTION: Diagnosing Colorectal Cancer
; FILE REFERENCE: DEX-0054
; CURRENT APPLICATION NUMBER: US/09/426,548
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-426-548-43

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1223 CAAAAGCCTCAGATCTC 1240
Db 1 CAAAAGCTTCAGATCTC 18

RESULT 329
US-09-861-893-11
; Sequence 11, Application US/09861893
; Patent No. US2002004527A1
; GENERAL INFORMATION:
; APPLICANT: Feinberg, Andrew
; APPLICANT: Strichman-Almashanu, Liora
; APPLICANT: Jiang, Shan
; TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING AND
; TITLE OF INVENTION: METHYLATED CpG ISLANDS
; FILE REFERENCE: 01107.00128
; CURRENT APPLICATION NUMBER: US/09/861,893
; CURRENT FILING DATE: 2001-05-22
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
```

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-861-893-11

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1024 CTCCTCTGCTGGACCATC 1041
Db 1 CTCCTCTGCGGGCCATC 18

RESULT 330
US-10-272-865-14
; Sequence 14, Application US/10272865
; Publication No. US20030171335A1
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for
; TITLE OF INVENTION: Treating ssRNA Viral Infection
; FILE REFERENCE: 50450-8046 US00
; CURRENT APPLICATION NUMBER: US/10/272,865
; CURRENT FILING DATE: 2002-10-16
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-272-865-14

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1271 GCCATGGAGCCCGCTCAG 1288
Db 1 GCCATGGAGGCCCATCAG 18

RESULT 331
US-10-272-865-34/c
; Sequence 34, Application US/10272865
; Publication No. US20030171335A1
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for
; TITLE OF INVENTION: Treating ssRNA Viral Infection
; FILE REFERENCE: 50450-8046 US00
; CURRENT APPLICATION NUMBER: US/10/272,865
; CURRENT FILING DATE: 2002-10-16
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antisense oligomer
US-10-272-865-34
```

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1271 GCCATGGAGCCCGTCAG 1288
|||||
Db 18 GCCATGGAGGCCCATCAG 1

RESULT 332

US-10-422-671-14
; Sequence 14, Application US/10422671
; Publication No. US20030224353A1
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for
; FILE REFERENCE: 50450-8046.US01
; CURRENT APPLICATION NUMBER: US/10/422,671
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/272,865
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/329,815
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-422-671-14

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1271 GCCATGGAGCCCGTCAG 1288
|||||
Db 1 GCCATGGAGGCCCATCAG 18

RESULT 333

US-10-422-671-34/c
; Sequence 34, Application US/10422671
; Publication No. US20030224353A1
; GENERAL INFORMATION:
; APPLICANT: Stein, David A.
; APPLICANT: Skilling, Douglas E.
; APPLICANT: Iversen, Patrick L.
; APPLICANT: Smith, Alvin W.
; TITLE OF INVENTION: Antisense Antiviral Agent and Method for
; FILE REFERENCE: 50450-8046.US01
; CURRENT APPLICATION NUMBER: US/10/422,671
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/272,865
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/329,815
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antisense oligomer
US-10-422-671-34

Query Match 0.4%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1271 GCCATGGAGCCCGTCAG 1288
|||||
Db 18 GCCATGGAGGCCCATCAG 1

RESULT 334

US-10-349-607-60
; Sequence 60, Application US/10349607
; Publication No. US20030224463A1
; GENERAL INFORMATION:
; APPLICANT: Liskay, Robert M.
; APPLICANT: Bronner, Eric C.
; APPLICANT: Baker, Sean M.
; APPLICANT: Bollag, Roni J.
; APPLICANT: Kolodner, Richard D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO DNA MISMATCH REPAIR GENES
; FILE REFERENCE: OHSU 3066
; CURRENT APPLICATION NUMBER: US/10/349,607
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 09/265,503
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 08/352,902
; PRIOR FILING DATE: 1994-12-04
; PRIOR APPLICATION NUMBER: 08/209,521
; PRIOR FILING DATE: 1994-03-08
; PRIOR APPLICATION NUMBER: 08/168,877
; PRIOR FILING DATE: 1993-12-17
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-349-607-60

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1223 CAAAAGCCTCAGATCTC 1240
|||||
Db 1 CAAAAGCTTCAGATCTC 18

RESULT 335

US-10-317-444-447/c
; Sequence 447, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; APPLICANT: Keys, Christine
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7 Sakai
US-10-317-444-447

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1579 ACAACAGCACACACAGCA 1596

```

; ||||| |||||
Db 18 AAACAGCAAAACAGCA 1

RESULT 336
US-10-317-444-448
; Sequence 448, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; APPLICANT: Keys, Christine
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7 Sakai
US-10-317-444-448

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1579 ACAACAGCAACAACAGCA 1596
Db 1 AAACAGCAAAACAGCA 18

RESULT 337
US-10-317-444-449/c
; Sequence 449, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; APPLICANT: Keys, Christine
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 449
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7 EDL933
US-10-317-444-449

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1579 ACAACAGCAACAACAGCA 1596
Db 18 AAACAGCAAAACAGCA 1

RESULT 338
US-10-317-444-450
; Sequence 450, Application US/10317444
; Publication No. US20030235837A1
; GENERAL INFORMATION:
; APPLICANT: Keim, Paul
; APPLICANT: Keys, Christine
; TITLE OF INVENTION: High resolution typing system for pathogenic E. coli
; FILE REFERENCE: NAU2020US
```

```

; CURRENT APPLICATION NUMBER: US/10/317,444
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/339,687
; PRIOR FILING DATE: 2001-12-11
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 450
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7 EDL933
US-10-317-444-450

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1579 ACAACAGCAACAACAGCA 1596
Db 1 AAACAGCAAAACAGCA 18

RESULT 339
US-10-138-674-2184
; Sequence 2184, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2184
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-2184

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1094 ACATTGAGCCACAGAGC 1111
Db 1 ACAUGCAGCCACAGAGC 18

RESULT 340
US-10-287-949A-2184
; Sequence 2184, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2184
; LENGTH: 18
; TYPE: RNA
```

```
; ORGANISM: Homo sapiens
US-10-287-949A-2184

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1094 ACATTGAGCCGACGAGC 1111
    |||: ||||| |||||
Db 1 ACAUGCAGCCCACTUGAGC 18

RESULT 341
US-10-702-817-24
; Sequence 24, Application US/10702817
; Publication No. US2004014741A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFRI EXPRESSION
; FILE REFERENCE: ISPH-0797
; CURRENT APPLICATION NUMBER: US/10702,817
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 09/106,038
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: PCT/US99/13763
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 09/695,451
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-702-817-24

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1406 CAACGAGCAGCAGCAGCAG 1423
    ||| ||||| |||||
Db 1 CACGAGCGGCGCAGCAGCAG 18

RESULT 342
US-10-702-817-25
; Sequence 25, Application US/10702817
; Publication No. US2004014741A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFRI EXPRESSION
; FILE REFERENCE: ISPH-0797
; CURRENT APPLICATION NUMBER: US/10702,817
; CURRENT FILING DATE: 2003-11-06
; PRIOR APPLICATION NUMBER: US 09/106,038
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: PCT/US99/13763
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 09/695,451
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-702-817-25
```

```
Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 977 CAGCAGCAGCAGCAGCAGCAG 994
    ||| ||||| ||||| |||||
Db 1 CAGGAGCAGCAGCAGCGCAG 18

RESULT 343
US-10-296-263-11
; Sequence 11, Application US/10296263
; Publication No. US2005015340A1
; GENERAL INFORMATION:
; APPLICANT: Feinberg, Andrew
; APPLICANT: Strichman-Almashanu, Liora
; APPLICANT: Jiang, Shan
; TITLE OF INVENTION: METHODS FOR ASSAYING GENE IMPRINTING AND
; TITLE OF INVENTION: METHYLATED CPG ISLANDS
; FILE REFERENCE: 01107.00128
; CURRENT APPLICATION NUMBER: US/10/296,263
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/206,158
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/206,161
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-263-11

Query Match          0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1024 CTCCTCTGCTGGACCATC 1041
    ||||| ||||| |||||
Db 1 CTCCTCTGCGGGGCATC 18

RESULT 344
US-09-866-108-7201
; Sequence 7201, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
```

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7201
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7201

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 322 GACCTTGCTATGAGC 337
|||||
Db 2 GACCTTGCCGATGAGC 17

RESULT 345

US-09-866-108-7202
; Sequence 7202, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7202
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7202

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 322 GACCTTGCTATGAGC 337
|||||
Db 1 GACCTTGCCGATGAGC 16

RESULT 346

US-09-866-108-8467
; Sequence 8467, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8467
; LENGTH: 17


```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-8467

```

```
Query Match          0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. NO. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 602 GAACTGGAGAACATGA 617
||| ||||| ||||| |||||
Db 2 GAGCTGGAGAACATGA 17

RESULT 347
US-09-866-108-8468
; Sequence 8468, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

```
Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 602 GAAC TGGAGAACATGA 617

Db**** 1 GAGCTGGAGAACATGA 16

```

RESULT 348
US-09-780-533A-234
; Sequence 234, Application US/09780533A
; Publication No. US2003060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowwira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NCO Gene
; FILE REFERENCE: MEHB00.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 234
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-234

```

```

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. NO. 2.5e+02;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1689 TCCTACTTCAGCAAT 1704
      :|||:|||||:
Db 2 UCCUACUUCAGAAAAU 17

```

```

RESULT 349
US-09-780-533A-235
; Sequence 235, Application US/09780533A
; Publication No. US2003060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerl, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCES: MBH900.878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-235

```

```

Query Match      0.4%;   Score 14.4;  DB 1;   Length 17;
Best Local Similarity 62.5%;   Pred. NO. 2.5e+02;
Matches 10;  Conservative 5;  Mismatches 1;  Indels 0;  Gaps 0;

QY  1689  TCCTACTTCAGCAAT 1704
      |||:|:|:|:|:|
Db    1  UCCUACUUCAGAAAAU 16

```

RESULT 350
US-09-848-754A-1158
; Sequence 1158, Application US/09848754A
; Publication No. US20030073207A1

```
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; NUMBER OF SEQ ID NOS: 2001-05-03
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1158
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-1158

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.5e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3633 GAGAACCTAGAAACA 3648
Db      |||||:|||||
        2 GAGAACCUAGAAUCA 17

RESULT 351
US-09-848-754A-3275
; Sequence 3275, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; NUMBER OF SEQ ID NOS: 2001-05-03
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3275
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-3275

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 2.5e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3634 AGAACCTAGAAACAAT 3649
Db      |||||:|||||
        1 AGAACCUAGAAAUCAU 16

RESULT 352
US-09-827-395A-505/c
; Sequence 505, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor Gene Expression
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 505
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-505/c

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2649 CCAGAGCGGCGAGTGGC 2664
Db      |||||:|||||
        16 CCAGAGCGGCGAGTGGC 1

RESULT 353
US-09-827-395A-765/c
; Sequence 765, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor Gene Expression
; FILE REFERENCE: MBH00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 765
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-765

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2650 CCAGAGCGGCGAGTGGCT 2665
Db      |||||:|||||
        17 CCAGAGCGGCGAGTGGCT 2

RESULT 354
US-09-740-332-2661/c
; Sequence 2661, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2661
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2661

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1660 AAGTCCACCTTTGCCA 1675
| | | | | | | | | | | | | | | | | |
Db 16 AAGTCCACCTTTGACA 1

RESULT 355
US-09-792-818-383
; Sequence 383, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 383
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-383

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCUGCAGCAGC 1424
| | | | | | | | | | | | | | | | | |
Db 2 CAGCAGCUGCAGCAGC 17

RESULT 356
US-09-792-818-524
; Sequence 524, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; TITLE OF INVENTION: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 524
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-524

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCUGCAGCAGC 1424
| | | | | | | | | | | | | | | | | |
Db 1 CAGCAGCUGCAGCAGC 16

RESULT 357

US-09-817-879-2661/c
; Sequence 2661, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2661
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2661

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1660 AAGTCCACCTTTGCCA 1675
| | | | | | | | | | | | | | | | | |
Db 16 AAGTCCACCTTTGACA 1

RESULT 358
US-10-061-201-574
; Sequence 574, Application US/10061201
; Publication No. US2003016229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 574
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-574

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2553 CCCTGACGCTCTGCAGG 2568
||| |||||||||
Db 2 CCCAGACGCTCTGCAGG 17

RESULT 359
US-10-061-201-575
; Sequence 575, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT FILING DATE: 2002-01-30
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006659
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 575
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-575

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2553 CCCTGACGCTCTGCAGG 2568
||| |||||||||
Db 1 CCCAGACGCTCTGCAGG 16

RESULT 360
US-10-430-882-505/c
; Sequence 505, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 575
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-505

; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 505
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-505

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2649 CCCAGAGGGCAGTGGC 2664
||||| |||||||
Db 16 CCCAGACGGCAGTGGC 1

RESULT 361
US-10-430-882-765/c
; Sequence 765, Application US/10430882
; Publication No. US20030203870A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowrira
; APPLICANT: Peter Haerberli
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-H (400/112)
; CURRENT FILING DATE: 2003-05-06
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 09/827,395
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04273
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/10512
; PRIOR FILING DATE: 2002-04-03
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 765
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-430-882-765

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2650 CCAGAGGGCAGTGGCT<2665
||||| |||||||
Db 17 CCAGACGGCAGTGGCT 2

RESULT 362
US-10-138-674-1755
; Sequence 1755, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1755
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1755

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3494 AATTGCTCTAATAGA 3509
|||:|:|:|:|:|:|
Db 1 AAUUGCUCUAAUUGA 16

RESULT 363

US-10-138-674-6407
; Sequence 6407, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6407
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6407

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3494 AATTGCTCTAATAGA 3509
|||:|:|:|:|:|:|
Db 2 AAUUGCUCUAAUUGA 17

RESULT 364

US-10-138-674-8510
; Sequence 8510, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8510
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens

US-10-138-674-8510

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3343 AAACAGAACTGTGCTG 3358
|||||:|:|:|:|:|
Db 2 AAACAAAACUGUGUG 17

RESULT 365

US-10-287-949A-1755
; Sequence 1755, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1755
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1755

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3494 AATTGCTCTAATAGA 3509
|||:|:|:|:|:|:|
Db 1 AAUUGCUCUAAUUGA 16

RESULT 366

US-10-287-949A-6407
; Sequence 6407, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6407
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-6407

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3494 AATTGCTCTAATAGA 3509
|||:|:~|:|:|:|:|
Db 2 AAUUGCUCUAAUUGA 17

```
RESULT 367
US-10-287-949A-8510
; Sequence 8510, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8510
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8510

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3343 AAACAGAACTGTGGTG 3358
||||| ||||| ||||| |||||
Db 2 AAACAAAACUGUGGUG 17

RESULT 368
US-10-712-672-2609/c
; Sequence 2609, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2609
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-2609

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2851 CCAGCCACCATCCCTG 2866
||||| ||||| ||||| |||||
Db 17 CCAGCGACCATCCCTG 2

RESULT 369
US-10-669-841-5254/c
; Sequence 5254, Application US/10669841
```

```
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPAT
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5254
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-5254

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1660 AAGGTCACCTTTGCCA 1675
||||| ||||| ||||| |||||
Db 16 AAGGTCACCTTTGACA 1

RESULT 370
US-10-723-361-7201
; Sequence 7201, Application US/10723361
; Publication No. US20040137599A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: Ji, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
```

FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7201
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7201

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 322 GACCTTGCCTATGAGC 337
||| ||||| |||||
Db 2 GACCTTGCCTATGAGC 17

RESULT 371
US-10-723-361-7202
; Sequence 7202, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7202
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7202

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 322 GACCTTGCCTATGAGC 337
||| ||||| |||||
Db 1 GACCTTGCCTATGAGC 16

RESULT 372
US-10-723-361-8467
; Sequence 8467, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 8467
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8467

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 602 GAACGTGGAGCAATGA 617
||| ||||| |||||

```
Dbb 2 GAGCTGGAGAACATGA 17

RESULT 373
US-10-723-361-8468
; Sequence 8468, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723.361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 8468
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-8468

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 602 GAAGCTGGAGAACATGA 617
Db 1 GAGCTGGAGAACATGA 16

RESULT 374
US-10-712-633-3573
; Sequence 3573, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; FILE REFERENCE: MHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712.633
; CURRENT FILING DATE: 2003-11-13
```

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; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3573
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-3573

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3343 AAACAGNACTGTGTG 3358
Db 2 AAACAAACUGUGUG 17

RESULT 375
US-10-494-343-175
; Sequence 175, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 175
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-175

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1506 AGCAACAGCAGCAGAG 1521
Db 1 AGCAACAGCAGCAGGG 16

RESULT 376
US-10-388-263-343/c
; Sequence 343, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
```



```
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-343

Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 73 GAAGCAGGAGGAGGAG 88
Db 18 GAAGCAGGAGGAGGAG 3

RESULT 377
US-10-468-655-42/c
; Sequence 42, Application US/10468655
; Publication No. US20040197784A1
; GENERAL INFORMATION:
; APPLICANT: Miano, Joseph W.
; APPLICANT: Streb, Jeffrey W.
; APPLICANT: Chen, Jiyan
; TITLE OF INVENTION: RETINOID INDUCIBLE PROTEINS OF VASCULAR SMOOTH MUSCLE
; TITLE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: 176/61022
; CURRENT APPLICATION NUMBER: US/10/468,655
; CURRENT FILING DATE: 2003-08-20
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/271,183
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-468-655-42

Query Match          0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAG 1444
Db 17 GCAGCAGCAGCAACAG 2

RESULT 378
US-10-467-019-7
; Sequence 7, Application US/10467019
; Publication No. US20040048314A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: No. US20040048314A1el Physiological Active Peptide and Its Use
; FILE REFERENCE: P01-0295PCT
; CURRENT APPLICATION NUMBER: US/10/467,019
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: JP2001-026820
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA primer, hBv8-F1 primer
US-10-467-019-7

Query Match          0.4%; Score 14.4; DB 1; Length 26;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1931 CTTCTTCTCCAGCAGCAGATGCTG 1954
Db 1 CTACTTCTGCTGCTGCCGCTGCTG 24

RESULT 379
US-10-376-770-220/c
; Sequence 220, Application US/10376770
; Publication No. US20040106102A1
; GENERAL INFORMATION:
; APPLICANT: Dhallan, Ravinder S.
; TITLE OF INVENTION: RAPID ANALYSIS OF VARIATIONS IN A GENOME
; FILE REFERENCE: 543312000320
; CURRENT APPLICATION NUMBER: US/10/376,770
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 10/093,618
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/360,232
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/378,354
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 262
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 6, 7
; OTHER INFORMATION: These nucleotides may be absent
US-10-376-770-220

Query Match          0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3174 TGTTCAGGTGGACT 3187
Db 14 TGTTCAGGTGGACT 1

RESULT 380
US-10-661-165-220/c
; Sequence 220, Application US/10661165
; Publication No. US20040137470A1
; GENERAL INFORMATION:
; APPLICANT: Dhallan, Ravinder S.
; TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: 543312000420
; CURRENT APPLICATION NUMBER: US/10/661,165
; CURRENT FILING DATE: 2003-09-11
```

```
; PRIOR APPLICATION NUMBER: PCT/US03/06198
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/378,354
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 10/093,618
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/360,232
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: PCT/US03/27308
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 10/376,770
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 628
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; LOCATION: (6)...(7)
; OTHER INFORMATION: These nucleotides may be absent
US-10-661-165-220

Query Match          0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3174 TGTTCAGGTGGACT 3187
Db      14 TGTTCAGGTGGACT 1

RESULT 381
US-10-494-343-164
; Sequence 164, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: P80184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 164
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-164

Query Match          0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAAC 1442
Db      4 GCAGCAGCAGCAAC 17

RESULT 382
US-10-011-993-35/c
; Sequence 35, Application US/10011993
; Publication No. US20030119004A1
; GENERAL INFORMATION:
; APPLICANT: WENZ, H. MICHAEL
```

```
; APPLICANT: SCHROTH, GARY P.
; APPLICANT: CHEN, CAIFU
; TITLE OF INVENTION: METHODS FOR QUANTITATING NUCLEIC ACIDS USING COUPLED
; TITLE OF INVENTION: LIGATION AND AMPLIFICATION
; FILE REFERENCE: 07414.0030-00000
; CURRENT APPLICATION NUMBER: US/10/011,993
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: PCT/US01/17329
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 09/724,755
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/584,905
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: oligonucleotide
; FEATURE:
; OTHER INFORMATION: This sequence may encompass 1-10 cag repeats
US-10-011-993-35

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTCTCCAGCAGCAGATGCTG 1954
Db      30 CTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 383
US-10-357-322-4/c
; Sequence 4, Application US/10357322
; Publication No. US20030180768A1
; GENERAL INFORMATION:
; APPLICANT: Ranum et al.
; TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
; FILE REFERENCE: Regents of the University of Minnesota
; CURRENT APPLICATION NUMBER: US/10/357,322
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/684,843
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/056,170
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 09/135,994
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-322-4

Query Match          0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTCTCCAGCAGCAGATGCTG 1954
Db      30 CTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 384
US-09-179-536B-90
; Sequence 90, Application US/09179536B
; Patent No. US20020042112A1
; GENERAL INFORMATION:
```

APPLICANT: Hubert K ster
David M. Lough
Guobing Xiang
TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
NUMBER OF SEQUENCES: 320
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/179,536B
FILING DATE: 26-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/20444
FILING DATE: 06-Nov-1997
APPLICATION NUMBER: 08/947,801
FILING DATE: 08-Oct-97
APPLICATION NUMBER: 08/933,792
FILING DATE: 19-Sep-97
APPLICATION NUMBER: 08/787,639
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/786,988
FILING DATE: 23-Jan-97
APPLICATION NUMBER: 08/746,055
FILING DATE: 06-No. US20020042112A1-96
APPLICATION NUMBER: 08/746,036
FILING DATE: 06-No. US20020042112A1-96
APPLICATION NUMBER: 08/744,590
FILING DATE: 06-No. US20020042112A1-96
APPLICATION NUMBER: 08/744,481
FILING DATE: 06-No. US20020042112A1-96
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2004B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-450-8400
TELEFAX: 858-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 90:
US-09-179-536B-90

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1399 ACAGCAGCAACAGCAGC 1415
Db 1 ACAGCAGCAACAGCATC 17
RESULT 385
US-09-866-108-664

Sequence 664, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aemica Sequence Listing Engine
SEQ ID NO 664
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-664
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 664 TCAGCAAGCCAGAGGA 680
Db 1 TCAGCAAGCCAGAGAA 17
RESULT 386
US-09-866-108-665
Sequence 665, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 665
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-665

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 665 CAGCAAGCCAGAGAG 681
|||||
Db 1 CAGCAAGCCAGAGAG 17

RESULT 387

US-09-866-108-1872
; Sequence 1872, Application US/09/866,108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1872
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-1872

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1022 CCCTCTCTGCTGACC 1038
|||||
Db 1 CCCTCTGAGCTGACC 17

RESULT 388

US-09-866-108-1873
; Sequence 1873, Application US/09/866,108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30


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; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 244
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-244

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2674 CCAGTTAACACCCAGCAG 2690
Db      1 CCAGTTAAGACCATCAG 17

RESULT 397
US-09-872-462-245
; Sequence 245, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 246
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-246

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2674 CCAGTTAACACCCAGCAGT 2691
Db      1 CAGTTAAGACCATCAGT 17

RESULT 398
US-09-872-462-246
; Sequence 246, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 246
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-246

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2676 AGTTAACACCCAGCAGTG 2692
Db      1 AGTTAAGACCATCAGTG 17

RESULT 399
US-09-872-462-247
; Sequence 247, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
```

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; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 245
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-245

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2675 CAGTTAACACCCAGCAGT 2691
Db      1 CAGTTAAGACCATCAGT 17

RESULT 398
US-09-872-462-246
; Sequence 246, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEOMICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 246
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-246

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2676 AGTTAACACCCAGCAGTG 2692
Db      1 AGTTAAGACCATCAGTG 17

RESULT 399
US-09-872-462-247
; Sequence 247, Application US/09872462
; Patent No. US20020169295A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
```


APPLICANT: Corrigan, Amy
; TITLE OF INVENTION: HUMAN NEDD1
; FILE REFERENCE: AEWICA-9
; CURRENT APPLICATION NUMBER: US/09/872,462
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 247
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-872-462-247

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2677 GTTAACACCCAGCAGTGC 2693
Db 1 GTTAAGACCATCAGTGC 17

RESULT 400
US-09-864-785-140
; Sequence 140, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 140
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-140

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1176 AGCGCGGCCCTCAGCC 1192

Db 1 AGGCAGGCCCCUCCGCC 17
RESULT 401
US-09-864-785-366
; Sequence 366, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 366
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-366

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1792 CCCAGTCCAGTCCTA 1808
Db 1 CCCGUGCCAGUCCUA 17

RESULT 402
US-09-864-785-375
; Sequence 375, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 375
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-375

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.9e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 756 CCTCAGGCTCTCCTCAG 772
Db 1 CCCGAGGCCUCCUCCAG 17

RESULT 403
US-09-864-785-1591/c
; Sequence 1591, Application US/09864785

```
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-kappa B
; FILE REFERENCE: 400/022 (MBHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1591
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1591

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1407 AACGACGACGACGACG 1423
DB 17 AACTGCAGCTGCAGCAG 1

RESULT 404
US-09-780-533A-766
; Sequence 766, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 766
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-766

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGC 1427
DB 1 GCGGCAGCAGCTGCAGCAG 17

RESULT 405
US-09-780-533A-767
; Sequence 767, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
```

```
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 767
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-767

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGC 1427
DB 1 GCAGCAGCTGCAGCAGC 17

RESULT 406
US-09-780-533A-1103
; Sequence 1103, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1103
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1103

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1687 GCTCCTACTTTCAGCAAA 1703
DB 1 GAUCCUACUUCAGAAAA 17

RESULT 407
US-09-780-533A-1549
; Sequence 1549, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1549
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1549

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCA 1425
Db 1 CAGCAGCAGCAGCAUCA 17

RESULT 408
US-09-780-533A-1792
; Sequence 1792, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowirra, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1792
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1792

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCA 1425
Db 1 CGGCAGCAGCAGCAGCA 17

RESULT 409
US-09-780-533A-2456
; Sequence 2456, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowirra, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2456
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2456

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1700 CAAATGCAGAAATCAGCC 1716
Db 1 CAAAAGCAGAAUCUGCC 17

RESULT 410
US-09-927-046-332
; Sequence 332, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-332

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1648 CCAGCCTTTGCTAAGGT 1664
Db 1 CCAGGCAUUGCUAAGGU 17

RESULT 411
US-09-927-046-811/c
; Sequence 811, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 811
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-811

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 269 GCAGGACAAAGGTGGCCT 285

Db 17 GCAGGAAAAGCTGCCT 1

RESULT 412

US-09-877-478-618/c
; Sequence 618, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 618
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-618

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1154 GTAATGGCTAACTACAT 1170
Db 17 GTAATGATTAACTACAT 1

RESULT 413

US-09-877-478-2137/c
; Sequence 2137, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2137
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-09-877-478-2137

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1153 AGTAATGGCTAACTACA 1169
Db 17 AGTAATGATTAACTACA 1

RESULT 414

US-09-776-474-125/c
; Sequence 125, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK-1)
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 125
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-125

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 666 AGCAAGCCAGAGGAGC 682
Db 17 AGCAGCTAGAGGAGC 1

RESULT 415

US-09-776-474-478/c
; Sequence 478, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Boher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim

```
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 478
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-478

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      667  GCAAAGCCAGGAGGAGCA 683
Db      17  GCAGAGCTAGAGGAGCA 1

RESULT 416
US-09-776-474-833/c
; Sequence 833, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Bocher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK)
; FILE REFERENCE: MBHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 833
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-833

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      665  CAGCAAGCCAGGAGGAG 681
Db      17  CAGCAGAGCTAGAGGAG 1

RESULT 417
US-09-780-164-191/c
; Sequence 191, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 191
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-780-164-191
```

```
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 191
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-191

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3416  TAAAAAGGTAATAGAA 3432
Db      17  TAAAAAGGAAACAGAA 1

RESULT 418
US-09-780-164-194/c
; Sequence 194, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 194
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-164-194

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3201  ATGCTTAAAAATCGAAA 3217
Db      17  ATGTTTAAAAAAGGAAA 1

RESULT 419
US-09-827-395A-504/c
; Sequence 504, Application US/09827395A
; Publication No. US20030113891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Lawrence Blatt
; APPLICANT: James McSwiggen
; APPLICANT: Bharat Chowira
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO and NOGO Receptor G
; FILE REFERENCE: MBHB00-878-C (400/017)
; CURRENT APPLICATION NUMBER: US/09/827,395A
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/780,533
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2617
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 504
; LENGTH: 17
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-827-395A-504

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2651 CAGAGGGCAGTGGCTCC 2667
    ||||| ||||| |||||
Db 17 CAGACGGCAGTGGCTGC 1

RESULT 420
US-09-740-332-2156/c
; Sequence 2156, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2156
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-2156

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 693 CTTCTTACCCATGGAG 709
    ||||| ||||| |||||
Db 17 CATCTTACCCATAG 1

RESULT 421
US-09-297-576A-90
; Sequence 90, Application US/09297576A
; Publication No. US20030129589A1
; GENERAL INFORMATION:
; APPLICANT: KOSTER, Hubert
; APPLICANT: LITTLE, Daniel P.
; APPLICANT: BRAUN, Andreas
; APPLICANT: LOUGH, David M.
; APPLICANT: XIANG, Guobing
; APPLICANT: VAN DEN BOOM, Dirk
; APPLICANT: JURINKE, Christian
; APPLICANT: RUPPERT, Andreas
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/09/297,576A
; FILING DATE: 07-Jun-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-No. US20030129589A1-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-450-8499
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
US-09-297-576A-90

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1399 ACAGCAGCAACAGCAGC 1415
    ||||| ||||| |||||
Db 1 ACAGCAGCAACAGCATC 17

RESULT 422
US-09-792-818-458
; Sequence 458, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Insert
; FILE REFERENCE: (GRID) Gene
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 458
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-458
```

```
Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2508 CACCAACTGGCCCTCT 2524
Db 1 CAACAAGCGGCCCCUCU 17

RESULT 423
US-09-792-818-607
; Sequence 607, Application US/09792818
; Publication No. US20030134806A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Von Carlowitz, Ira
; APPLICANT: McSwiggen, Jim
; APPLICANT: Hamblin, Paul
; APPLICANT: Ellis, Jonathan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse
; FILE REFERENCE: MBHB00-901-A (400/013)
; CURRENT APPLICATION NUMBER: US/09/792,818
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 2304
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 607
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-792-818-607

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 983 CACCAGCAGCAGCACCA 999
Db 1 CCCCUGCAGCAGCACCA 17

RESULT 424
US-09-817-879-2156/c
; Sequence 2156, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: Hepatitis C Virus Infection
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2156
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-2156

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 693 CCTCCTTACCATTGAG 709
Db 17 CATCCTTACCATTAG 1
```

```
RESULT 425
US-10-060-830-706
; Sequence 706, Application US/10060830
; Publication No. US20030032154A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN LCCL DOMAN CONTAINING PROTEIN
; FILE REFERENCE: PB0169
; CURRENT APPLICATION NUMBER: US/10/060,830
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/325,062
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 1123
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 706
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-830-706

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1180 CGGCCCTCAGCCAGG 1196
Db 1 CTGCTCCTCAGCCAGG 17

RESULT 426
US-10-060-830-709
; Sequence 709, Application US/10060830
; Publication No. US20030032154A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN LCCL DOMAN CONTAINING PROTEIN
; FILE REFERENCE: PB0169
; CURRENT APPLICATION NUMBER: US/10/060,830
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/325,062
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 1123
```

; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 709
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-830-709

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 765 CTCCTCAGCTGAGGCC 781
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CTCCTCAGCCAGGCC 17

RESULT 427
US-10-156-306-1337/c
; Sequence 1337, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156.306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1337
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-1337

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 672 GCCAGAGGACACACT 688
| | | | | | | | | | | | | | | | | | | | | |
Db 17 GCCAGAGGACAACT 1

RESULT 428
US-10-156-306-7003/c
; Sequence 7003, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156.306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7003
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-7003

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2230 TGGAAATCGCTTGTGA 2246
| | | | | | | | | | | | | | | | | | | | | |
Db 17 TGGAAATCGCTTGTGA 1

RESULT 429
US-10-238-700-3082/c
; Sequence 3082, Application US/10238700
; Publication No. US2003015321A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels of IKK-Gamma and PKR
; FILE REFERENCE: 400/057 (MBH01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238.700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3082
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3082

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 237 TCAAAAGAAATTCGTGT 253
| | | | | | | | | | | | | | | | | | | | | |
Db 17 TCAAAAGACTTGGTGT 1

RESULT 430
US-10-061-201-572
; Sequence 572, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061.201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 572
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-572

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;


```

RESULT 434
US-10-340-192-17
; Sequence 17, Application US/10340192
; Publication No. US20030170700A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: Shang, Jin
; APPLICANT: Bowen, Benjamin A
; TITLE OF INVENTION: SECRETED AND CELL SURFACE POLYPEPTIDES AFFECTED BY CHOLESTEROL AN
; FILE REFERENCE: 37-000610US
; CURRENT APPLICATION NUMBER: US/10/340,192
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-340-192-17

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3348 GAATGTGGTGTCAATG 3364
Db 1 GATCTGTGGTGCATG 17

RESULT 435
US-10-148-687-56
; Sequence 56, Application US/10148687
; Publication No. US20030185836A1
; GENERAL INFORMATION:
; APPLICANT: WINTER, Gerhard
; APPLICANT: SLADE, Martin Basil
; APPLICANT: WILLIAMS, Keith Leslie
; APPLICANT: GOOLEY, Andrew Arthur
; APPLICANT: Macquarie Research Ltd
; TITLE OF INVENTION: Cryptosporidium sporozoite antigens
; FILE REFERENCE: 047763-5019-US
; CURRENT APPLICATION NUMBER: US/10/148,687
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: PCT/AU00/01492
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: AU PQ4400
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primers
US-10-148-687-56

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2394 TTGGAGCTGGATCTGTT 2410
Db 1 TTGGTGGGGATCTGTT 17

RESULT 436
US-10-230-006-1406/c
; Sequence 1406, Application US/10230006
```

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; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1406
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-1406

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 977 CAGCAGCACCCAGCAGCA 993
Db 17 CATCAGCGCCAGCAGCA 1

RESULT 437
US-10-230-006-2208/c
; Sequence 2208, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2208
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-2208

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 978 AGCAGCACCCAGCAGCAG 994
Db 17 ATCAGCGCCAGCAGCAG 1

RESULT 438
US-10-357-488-9
; Sequence 9, Application US/10357488
; Publication No. US20030194730A1
; GENERAL INFORMATION:
; APPLICANT: Centre For DNA Fingerprinting and Diagnostics
; TITLE OF INVENTION: No. US20030194730A1el FISSR-PCR primers and markers and a method c
; TITLE OF INVENTION: primers and markers for identifying genetic constitution and bre
; TITLE OF INVENTION: varieties.
; FILE REFERENCE: 782-Indian
; CURRENT APPLICATION NUMBER: US/10/357,488
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 260/MAS/2002
; PRIOR FILING DATE: 2002-04-08
```

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; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1147
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Cucumis sativus
US-10-307-005-1147

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      928 CCAGCAGCTCAAAACAGA 944
        ||||| ||||| ||||| ||
DB      17 CCAGCTGCTCAAAACCGA 1

RESULT 441
US-10-307-005-1148
; Sequence 1148, Application US/10307005.
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Camper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; TITLE OF INVENTION: Using Modified Single Stranded Oligonucleotides
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1148
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Cucumis sativus
US-10-307-005-1148

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      928 CCAGCAGCTCAAAACAGA 944
        ||||| ||||| ||||| ||
DB      1 CCAGCTGCTCAAAACCGA 17

RESULT 442
US-10-307-005-1167/c
; Sequence 1167, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware

```

```
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1167
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Cucurbita sp.
US-10-307-005-1167

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 928 CCAGCAGCTCAAAACAGA 944
      ||||| ||||| ||||| |||||
DB 17 CCAGCTGCTCAAAACCGA 1
```

```
RESULT 443
; Sequence 1168, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 1168
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Cucurbita sp.
US-10-307-005-1168

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 928 CCAGCAGCTCAAAACAGA 944
      ||||| ||||| ||||| |||||
DB 1 CCAGCTGCTCAAAACCGA 17
```

```
RESULT 444
US-10-307-005-2559/c
; Sequence 2559, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2559
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Brassica napus
US-10-307-005-2559

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 930 AGCAGCTCAAAACAGATA 946
      ||||| ||||| ||||| |||||
DB 17 AGCAGCTCAAGCAGCTA 1
```

```
RESULT 445
US-10-307-005-2560
; Sequence 2560, Application US/10307005
; Publication No. US20030236208A1
; GENERAL INFORMATION:
; APPLICANT: University of Delaware
; APPLICANT: Eric B. Kmiec
; APPLICANT: Howard B. Gamper
; APPLICANT: Michael C. Rice
; APPLICANT: Jungsup Kim
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations in Plants
; FILE REFERENCE: Napro/009 PCT
; CURRENT APPLICATION NUMBER: US/10/307,005
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: PCT/US01/17672
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/818,875
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2717
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 2560
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Brassica napus
US-10-307-005-2560

Query Match          0.4%; Score 13.8; DB 1; Length 17;
```

```
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 AGCAGCTCAACAGATA 946
DB 1 AGCAGCTCAACAGCTA 17

RESULT 446
US-10-342-902-618/c
; Sequence 618, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MEHB00-845-I)
; CURRENT APPLICATION NUMBER: US/10/342,902
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 618
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B virus
US-10-342-902-618
```

```
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1153 AGTAATGGCTAACTACA 1169
DB 17 AGTAATGATTAACACTACA 1

RESULT 448
US-10-675-685-524
; Sequence 524, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: PB0114
; CURRENT APPLICATION NUMBER: US/10/675,685
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 524
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-675-685-524

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 473 CAATGACCAAGAGAA 489
DB 1 CAATGACCAAGAGAA 17

RESULT 449
US-10-138-674-25
; Sequence 25, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-25

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.9e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TGCTACTTCTCACGGG 2182
Db 1 UGUCGUCUUCACAGG 17

RESULT 450

US-10-138-674-26
; Sequence 26, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-26

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.9e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2167 GCTACTTCTCACGGGA 2183
Db 1 GUCUGUCUUCACAGGA 17

RESULT 451

US-10-138-674-414/c
; Sequence 414, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 414
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-414

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 430 GGAGCCAGGAGAGACTC 446
Db 17 GGAGCCAGAGAGAGATC 1

RESULT 452

US-10-138-674-415/c
; Sequence 415, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 415
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-415

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 429 AGGAGCCAGGAGAGACT 445
Db 17 AGGAGCCAGAGAGAGT 1

RESULT 453

US-10-138-674-1095
; Sequence 1095, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1095
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1095

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.9e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 224 TCATTCTTGATATCAA 240
Db 1 UCAUGUCUGAUUUCAA 17

RESULT 454

US-10-138-674-2132/c

```
; Sequence 2132, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-2132

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1509 AACAGCAGCAGAGCTCA 1525
Db 17 AACAGGAGGAGAGCTCA 1

RESULT 455
US-10-138-674-3256
; Sequence 3256, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3256
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674-3256

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2757 GTCGTGAATCTCAGACCC 2773
Db 1 GGCUGACUCUCACAGCCC 17

RESULT 456
US-10-138-674-4212
; Sequence 4212, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
```

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; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4212
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4212

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.9e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2165 CTGTCTACTTCTCAGG 2181
Db 1 CUGUCUGCUCUCACAG 17

RESULT 457
US-10-138-674-6437
; Sequence 6437, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6437
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6437

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1095 CATTGAGCCACAGAGC 1111
Db 1 CAUGCAGCCACAGAGC 17

RESULT 458
US-10-138-674-7508/c
; Sequence 7508, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7508
; LENGTH: 17
; TYPE: RNA
```



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; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 415
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-415

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      429 AGGAGCCAGAGAGACT 445
Db      17 AGGAGCCAGAGAGAGT 1

RESULT 464
US-10-287-949A-1095
; Sequence 1095, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1095
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1095

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.9e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy      224 TCATTCTTGATATCAA 240
Db      1 UCAUGUCUUGAUUCAA 17

RESULT 465
US-10-287-949A-2132/c
; Sequence 2132, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
```

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; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2132
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-2132

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1509 AACAGCAGCAGAGCTCA 1525
Db      17 AACAGGAGGAGAGCTCA 1

RESULT 466
US-10-287-949A-3256
; Sequence 3256, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3256
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3256

Query Match          0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2757 GTCTGAATCTCAGACCC 2773
Db      1 GCGUGACUCUCAGACCC 17

RESULT 467
US-10-287-949A-4212
; Sequence 4212, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4212
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4212

Query Match          0.4%; Score 13.8; DB 1; Length 17;
```

Best Local Similarity 52.9%; Pred. No. 2.9e+02;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2165 CTGCTACTTCTCAGG 2181
|:|:|: |:|:|:|
Db 1 CUGUCUGCUUCACAG 17

RESULT 468
US-10-287-949A-6437
; Sequence 6437, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6437
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-6437

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1095 CATTGAGCCACAGC 1111
|:|:|:|:|:|:|:|:|
Db 1 CAUGCAGCCACUGAGC 17

RESULT 469
US-10-287-949A-7508/c
; Sequence 7508, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7508
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7508

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3552 TTCCTGAAGCTTCAGG 3568
|:|:|:|:|:|:|:|:|
Db 17 TGCCTGAATTCGAGG 1

RESULT 470

US-10-287-949A-8718
; Sequence 8718, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8718
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8718

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1093 GACATTGAGCCACAGA 1109
|:|:|:|:|:|:|:|:|
Db 1 GACAUGCAGCCACUGA 17

RESULT 471
US-10-712-672-765
; Sequence 765, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 765
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-765

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 91 GCGCGCCTTCGAGGAGG 107
|:|:|:|:|:|:|:|:|
Db 1 GCGCGCCTTCGAGGAGG 17

RESULT 472
US-10-712-672-1142
; Sequence 1142, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Chowrira, Bharat
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
 ; FILE REFERENCE: MBH00-882-C (400/019)
 ; CURRENT APPLICATION NUMBER: US/10/712,672
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIOR APPLICATION NUMBER: US/09/653,225
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: 60/197,769
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/150,713
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 5586
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1142
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-10-712-672-1142

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 2.9e+02;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 853 TCAGAGCCAGGCTCAGC 869
 :|||||||:|
 Db 1 UCAGAGCCAGUCUACC 17

RESULT 473
 US-10-712-672-1409
 ; Sequence 1409, Application US/10712672
 ; Publication No. US20040102413A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
 ; FILE REFERENCE: MBH00-882-C (400/019)
 ; CURRENT APPLICATION NUMBER: US/10/712,672
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIOR APPLICATION NUMBER: US/09/653,225
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: 60/197,769
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/150,713
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 5586
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1409
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-10-712-672-1409

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 2.9e+02;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1016 GCCTTGCCCTCCTCTGC 1032
 |||:|||||:
 Db 1 GCCCGCCCUCCUUGC 17

RESULT 474
 US-10-712-672-2180
 ; Sequence 2180, Application US/10712672
 ; Publication No. US20040102413A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Chowrira, Bharat

; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
 ; FILE REFERENCE: MBH00-882-C (400/019)
 ; CURRENT APPLICATION NUMBER: US/10/712,672
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIOR APPLICATION NUMBER: US/09/653,225
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: 60/197,769
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/150,713
 ; PRIOR FILING DATE: 1999-08-31
 ; NUMBER OF SEQ ID NOS: 5586
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2180
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-10-712-672-2180

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1390 CCAACAGCAACAGCAGC 1406
 |||||||||
 Db 1 CGCCAGCAACAGCAGC 17

RESULT 475
 US-10-380-236A-18
 ; Sequence 18, Application US/10380236A
 ; Publication No. US20040126860A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
 ; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
 ; APPLICANT: HUMAN SERVICES
 ; APPLICANT: Epstein, Neal
 ; APPLICANT: Hassanzadeh, Shahin
 ; APPLICANT: Davis, Julien S.
 ; APPLICANT: Whitsky, Steven S.
 ; TITLE OF INVENTION: Optimize Cardiac Contraction Through Differential Phosphorylation
 ; FILE REFERENCE: 4239-64779
 ; CURRENT APPLICATION NUMBER: US/10/380,236A
 ; CURRENT FILING DATE: 2003-09-25
 ; PRIOR APPLICATION NUMBER: US 60/232,246
 ; PRIOR FILING DATE: 2000-09-12
 ; PRIOR APPLICATION NUMBER: US 60/232,456
 ; PRIOR FILING DATE: 2000-09-13
 ; PRIOR APPLICATION NUMBER: PCT/US01/28639
 ; PRIOR FILING DATE: 2001-09-12
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-380-236A-18

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 845 TCAGTCCCTCAGAGCCA 861
 |||||
 Db 1 TCAGAGCCCGCAGAGCCA 17

RESULT 476
 US-10-669-841-618/c
 ; Sequence 618, Application US/10669841
 ; Publication No. US20040127446A1

GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; FILE REFERENCE: 400/042US (WBH02-249-E)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 618
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-618

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1154 GTAATGGCTAACTACAT 1170
||||| |||||||
Db 17 GTAATGATTAACTACAT 1

RESULT 477
US-10-669-841-1973/c
; Sequence 1973, Application US/10669841
; Publication No. US20040127446A1
GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; FILE REFERENCE: 400/042US (WBH02-249-E)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2002-03-26

; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1973
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Hepatitis B Virus
US-10-669-841-1973
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1153 AGTAATGGCTAACTACA 1169
||||| |||||||
Db 17 AGTAATGATTAACTACA 1
RESULT 478
US-10-669-841-4749/c
; Sequence 4749, Application US/10669841
; Publication No. US20040127446A1
GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPATITIS B VIRUS REPLICATION
; FILE REFERENCE: 400/042US (WBH02-249-E)
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931

;
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4749
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-4749

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 693 CCTCCTTACCCATGAG 709
Db 17 CATCCTTACCCATAG 1

RESULT 479

US-10-723-361-664
; Sequence 664, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 664
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-664

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 664 TCAGCAAGCCAGGAG 680
Db 1 TCAGCAAGCCAGGAG 17

RESULT 480

US-10-723-361-665
; Sequence 665, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 665
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-665
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 665 CAGCAAGCCAGGAG 681
Db 1 CAGCAAGCCAGGAG 17

RESULT 481

US-10-723-361-1872
; Sequence 1872, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1872
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-1872

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1022 CCTCTCTCTGCTGGACC 1038
||||| |||||
DB 1 CCCTCTGAGCTGGACC 17

RESULT 482
US-10-723-361-1873
; Sequence 1873, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2733
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2733

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1873
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-1873

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1023 CCTCTCTCTGCTGGACCA 1039
||||| |||||
DB 1 CCCTCTGAGCTGGACCA 17

RESULT 483
US-10-723-361-2733
; Sequence 2733, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 2733
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2733

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 765 CTCCTCAGCTGAGGCC 781
Db 1 CTACGACGCTGAGGCC 17

RESULT 484

US-10-723-361-7802
; Sequence 7802, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7802
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7802

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCTGAGCA 1425
Db 1 CAGCAGCAGCTGAGCA 17

RESULT 485

US-10-723-361-7803
; Sequence 7803, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 7803
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7803

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCTGAGCAA 1441
Db 1 AGCAGCAGCTGAGCAA 17

RESULT 486

US-10-723-361-10247
; Sequence 10247, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10247
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10247

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1187 TCAGCCAGGCTGGCA 1203
|||||
Db 1 TCAGCCAAAGTGGCA 17

RESULT 487

US-10-723-361-10747
; Sequence 10747, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723.361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10747
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10747

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1771 TGTGTCAGCCAGAAC 1787
|||||
Db 1 TGTGTTGCCTGAACA 17

RESULT 488

US-10-712-633-505/c
; Sequence 505, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan

; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTO
; TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND (

; FILE REFERENCE: MBHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712.633

; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08

; PRIOR APPLICATION NUMBER: US 09/371,772

; PRIOR FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 09/708,690

; PRIOR FILING DATE: 2000-11-07

; PRIOR APPLICATION NUMBER: US 09/870,161

; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: US 60/334,461

; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: US 10/138,674

; PRIOR FILING DATE: 2002-05-03

; NUMBER OF SEQ ID NOS: 5989

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 505

; LENGTH: 17

; TYPE: RNA

; ORGANISM: Homo Sapiens

US-10-712-633-505

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3552 TTCTGTAAGCTTCAGG 3568
|||||
Db 17 TGCTGAATCTTCAGG 1

RESULT 489

US-10-712-633-3854
; Sequence 3854, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan

; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTO
; TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND (

; FILE REFERENCE: MBHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712.633

; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08

; PRIOR APPLICATION NUMBER: US 09/371,772

; PRIOR FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 09/708,690

; PRIOR FILING DATE: 2000-11-07


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; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3854
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-3854

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.2%; Pred. No. 2.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1093 GACATTTCAGCCACAGA 1109
Db 1 GACAUGCAGCCACUGA 17

RESULT 490
US-10-494-343-809
; Sequence 809, Application US/10494343
; Publication No. US20040248138A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Phan, Thuymy
; TITLE OF INVENTION: HUMAN AGIOMOTIN-LIKE PROTEIN 1
; FILE REFERENCE: PB0184
; CURRENT APPLICATION NUMBER: US/10/494,343
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US to be assigned
; PRIOR FILING DATE: to be assigned
; PRIOR APPLICATION NUMBER: PCT/US2002/035129
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/334,773
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 870
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 809
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-494-343-809

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 150 GTTCTTGAAGAGAAA 166
Db 1 GTTCTTGAAGAGAAA 17

RESULT 491
US-10-498-462-1977/c
; Sequence 1977, Application US/10498462
; Publication No. US20040259175A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Jinjiao
; TITLE OF INVENTION: HUMAN PROSTATE CANCER CANDIDATE PROTEIN 1
; FILE REFERENCE: PB01102
; CURRENT APPLICATION NUMBER: US/10/498,462
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: US 60/339,764
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/US02/37506
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 3320
; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 1977
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-498-462-1977

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1772 GTGGTAGCCAGACAC 1788
Db 17 GTGGTGGCCAGAGAC 1

RESULT 492
US-10-730-771-197
; Sequence 197, Application US/10730771
; Publication No. US20050074787A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Jian-Bing
; APPLICANT: Hirschhorn, Joel N.
; APPLICANT: Huang, Xiaohua
; APPLICANT: Kaplan, Paul
; APPLICANT: Lander, Eric S.
; APPLICANT: Lockhart, David J.
; APPLICANT: Ryder, Thomas
; APPLICANT: Sklar, Pamela
; TITLE OF INVENTION: UNIVERSAL ARRAYS
; FILE REFERENCE: 2825.1016-007
; CURRENT APPLICATION NUMBER: US/10/730,771
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US 60/126,473
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 60/140,359
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/536,841
; PRIOR FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Template sequence
US-10-730-771-197

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 815 TCTGCCCTCTCCACTTC 831
Db 1 TCTGCCCTCTGCACCTC 17

RESULT 493
US-10-497-091-296/c
; Sequence 296, Application US/10497091
; Publication No. US20050074863A1
; GENERAL INFORMATION:
; APPLICANT: HELLEDOORN, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: WILLIAMS, Steven
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2
; FILE REFERENCE: MER-130
; CURRENT APPLICATION NUMBER: US/10/497,091
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/BP02/13351
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP02020634.8
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; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: EP02001779.6
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP01128519.4
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-497-091-296

```

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3590 TTGTTTGGAGTAACCA 3606
|||
Db 17 TTCCTTGGAGTAAGCAA 1

```

RESULT 494
US-10-497-091-312
; Sequence 312, Application US/10497091
; Publication No. US20050074863A1
; GENERAL INFORMATION:
; APPLICANT: HELLENDORRN, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: WILLIAMS, Steven
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2
; FILE REFERENCE: MER-130
; CURRENT APPLICATION NUMBER: US/10/497,091
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/EP02/13351
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP02020634.8
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: EP02001778.6
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP01128519.4
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-497-091-312

```

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3590 TTGTTTGGAGTAACCA 36
Db 1 TTCTTTGGAGTAAGCA 17

RESULT 495
US-10-724-270-1761/C
; Sequence 1761, Application US/10724270
; Publication No. US20050080031A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases and Conditions Related to Level
; TITLE OF INVENTION: RAS, HER2 and HIV

```

, FILE REFERENCE: 400/046-US (MH802-326-A)
, CURRENT APPLICATION NUMBER: US/10/724,270
, CURRENT FILING DATE: 2003-11-26
, PRIOR APPLICATION NUMBER: PCT/US02/16840
, PRIOR FILING DATE: 2002-05-29
, PRIOR APPLICATION NUMBER: US 60/318,471
, PRIOR FILING DATE: 2001-09-10
, PRIOR APPLICATION NUMBER: US 60/296,249
, PRIOR FILING DATE: 2001-06-06
, PRIOR APPLICATION NUMBER: US 60/294,140
, PRIOR FILING DATE: 2001-05-29
, PRIOR APPLICATION NUMBER: US 10/238,700
, PRIOR FILING DATE: 2002-09-10
, PRIOR APPLICATION NUMBER: US 10/163,552
, PRIOR FILING DATE: 2002-06-06
, PRIOR APPLICATION NUMBER: US 10/157,580
, PRIOR FILING DATE: 2002-05-29
, PRIOR APPLICATION NUMBER: US 10/693,059
, PRIOR FILING DATE: 2002-10-23
, PRIOR APPLICATION NUMBER: US 10/444,853
, PRIOR FILING DATE: 2003-05-23
, PRIOR APPLICATION NUMBER: US 10/417,012
, PRIOR FILING DATE: 2003-04-16
, Remaining prior Application data removed -
, NUMBER OF SEQ ID NOS: 6910
, SOFTWARE: PatentIn version 3.0
, SEQ ID NO 1761
, LENGTH: 17
, TYPE: RNA
, ORGANISM: Homo sapiens
US-10-724-270-1761

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Query Match	0.4%	Score 13.8;	DB 1;	Length 17;
Best Local Similarity	88.2%	Pred. No. 2.9e+02;		
Matches 15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 237 TCAAAGAATTCGTGT 253
|||||
Db 17 TCAAAGACTTGTGT 1

```

RESULT 496
US-10-911-171-37/c
; Sequence 37, Application US/10911171
; Publication No. US20050136432A1
; GENERAL INFORMATION:
; APPLICANT: We Gene Technologies, Inc
; TITLE OF INVENTION: MYCOBACTERIAL DISEASE DETECTION CHIP AND FABRICATION METHOD
; TITLE OF INVENTION: THEREOF AND METHOD OF DETECTING MYCOBACTERIAL DISEASE AND PRIMER
; TITLE OF INVENTION: SET FOR MYCOBACTERIAL DISEASE AND DRUG RESISTANCE DETECTION
; FILE REFERENCE: 12422-US-PA
; CURRENT APPLICATION NUMBER: US/10/911,171
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: TW 92136102
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
; LENGTH: 17
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; - OTHER INFORMATION: Probe
US-10-911-171-37

```

Query Match	0.4%	Score 13.8	DB 1	Length 17
Best Local Similarity	88.2%	Pred. No. 2.9e+02		
Matches 15: Conservative	0	Mismatches 2	Indels 0	Gaps 0

Qy 1286 CAGGGCAACACCAAGCC 1302
|||
Db 17 CAGGGCAACCAACGCG 1

Search completed: August 16, 2005, 13:15:12
Job time : 24 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2005, 12:53:56 ; Search time 23 Seconds
(without alignments)

3.347 Million cell updates/sec

Title: US-10-698-070-1

Perfect score: 3763

Sequence: 1 aggtgctggcgaagatgg.....taacacaaatatagagctg 3763

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 544 seqs, 10230 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 17

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 553 summaries

Database : fetchlmg.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30.4	0.8	33	1	ABX79926
2	30	0.8	30	1	AZ44310
3	30	0.8	30	1	AAS13781
4	30	0.8	30	1	ADN97224
5	30	0.8	31	1	AAQ98457
6	30	0.8	31	1	AAZ24996
7	29.4	0.8	31	1	AA131042
8	28.4	0.8	30	1	ABZ81777
9	28	0.7	28	1	ABA00946
10	25.4	0.7	29	1	AAA03952
11	25	0.7	25	1	ABZ81767
12	25	0.7	25	1	ABZ81768
13	24	0.6	24	1	ABN87602
14	24	0.6	24	1	ADN97255
15	24	0.6	24	1	ADN97164
16	24	0.6	24	1	ADR68635
17	23.4	0.6	29	1	ADM48412
18	23	0.6	23	1	ABA00945
19	23	0.6	23	1	ADCS9319
20	22.4	0.6	27	1	ADQ43735
21	22	0.6	22	1	ADCS9320
22	22	0.6	25	1	ADC38187
23	22	0.6	25	1	ADC38189
24	22	0.6	25	1	ADC38186
25	22	0.6	25	1	ADC38188
26	21.2	0.6	26	1	ABZ71093
27	21.2	0.6	26	1	ABZ30010
28	21.2	0.6	26	1	ADG69029
29	21	0.6	21	1	AAF99580
30	21	0.6	21	1	ABZ78296
31	21	0.6	21	1	ABL38849
32	21	0.6	21	1	ABK10202
33	21	0.6	21	1	ACH03118

c	34	21	0.6	21	1	ADB37082	Immunostimulatory
	35	21	0.6	25	1	ADC38190	Human AMLP1a scann
	36	21	0.6	25	1	ADC38185	Human AMLP1a scann
	37	20.8	0.6	24	1	ABL61611	Porcine GPR8-relat
	38	20.8	0.6	24	1	ABK94601	G-protein-coupled
	39	20.8	0.6	24	1	ABX92931	Screening method r
	40	20.8	0.6	24	1	ABZ58841	Histidine tag enco
	41	20.8	0.6	24	1	ADC51835	GRB PCR primer, S
c	42	20.4	0.5	22	1	ABK88725	Human MEK4 antise
	43	20	0.5	22	1	AAZ37201	Human Pur alpha an
	44	20	0.5	20	1	ABZ30516	Candida albicans G
c	45	20	0.5	20	1	ABZ31489	Candida albicans G
	46	20	0.5	21	1	AAQ14196	Oligonucleotide pr
	47	20	0.5	25	1	ADC38191	Human AMLP1a scann
	48	20	0.5	25	1	ADC38184	Human AMLP1a scann
	49	19.8	0.5	24	1	ADN97247	Primer of the inve
	50	19.4	0.5	21	1	ABZ81769	Huntington's disea
	51	19.4	0.5	22	1	AAF76808	Codon-Optimised HP
c	52	19.4	0.5	24	1	ABX03797	DNA encoding secre
	53	19.2	0.5	24	1	ADN06499	Human FLAP related
	54	19.2	0.5	24	1	ADS94518	Human 5-lipoxygena
c	55	19	0.5	20	1	AAZ97150	PCR primer used to
	56	19	0.5	23	1	AAF76807	Codon-Optimised HP
c	57	18.8	0.5	22	1	AAZ54149	Antisense oligonuc
	58	18.8	0.5	23	1	AAC85525	Primer ZC21.076.
c	59	18.8	0.5	23	1	ABV72153	PCR primer ZC21.076
	60	18.8	0.5	23	1	ADH62525	Human MAPP DNA spe
c	61	18.4	0.5	20	1	AAV52748	Angiotensin-conver
	62	18.4	0.5	20	1	AAZ55806	Human histone deac
c	63	18.4	0.5	20	1	AAH43116	Antisense oligo, t
	64	18.4	0.5	20	1	AAC89545	Human HDAC-2 antis
c	65	18.4	0.5	20	1	AAC89536	Human HDAC-2 PCR p
	66	18.4	0.5	20	1	AAS20967	PCR primer Snrpn-U
c	67	18.4	0.5	20	1	ABZ86076	Human oligonucleot
	68	18.4	0.5	20	1	ABD22306	Human stanniocalci
c	69	18.4	0.5	20	1	ADP20499	Transcription fact
	70	18	0.5	18	1	AAE63144	Antisense oligonuc
c	71	18	0.5	18	1	AAS13717	Simple sequence re
	72	18	0.5	18	1	ADN97239	Primer of the inve
c	73	18	0.5	18	1	ADO26674	Synthetic leader s
	74	18	0.5	18	1	ADO26644	Synthetic leader s
c	75	18	0.5	18	1	ADO26638	Synthetic leader s
	76	18	0.5	18	1	ADO26610	Synthetic leader s
	77	18	0.5	18	1	ADO26696	Synthetic leader s
c	78	18	0.5	18	1	ADO26614	Synthetic leader s
	79	18	0.5	18	1	ADRO6261	Short tandem (micr
c	80	18	0.5	20	1	AAV68372	Adapter primer oli
	81	18	0.5	20	1	AAV68373	Adapter primer oli
c	82	18	0.5	20	1	ADC65856	Mouse TGF-beta rec
	83	18	0.5	20	1	ADD69519	ISSR-related PCR p
c	84	18	0.5	21	1	ABZ75647	Template (CTGA)6-A
	85	17.8	0.5	21	1	ABK70337	Synthetic antigens
	86	17.8	0.5	22	1	ABX94818	Human cyteine-ric
	87	17.4	0.5	19	1	AAT39475	Steroidogenesis ac
c	88	17.4	0.5	19	1	ADH70599	Human vbeta gene r
	89	17.4	0.5	20	1	AAT86505	S-adenosylmethioni
c	90	17.4	0.5	20	1	AAZ55807	Human histone deac
	91	17.4	0.5	20	1	AAZ35086	Herpesvirus entry
c	92	17.4	0.5	20	1	AAH43117	Antisense oligo, t
	93	17.4	0.5	20	1	AAH56611	Streptococcus pyog
c	94	17.4	0.5	20	1	AAC89537	Human HDAC-2 PCR p
	95	17.4	0.5	20	1	AAC89546	Human HDAC-2 antis
c	96	17.4	0.5	20	1	ABZ86068	Human oligonucleot
	97	17.4	0.5	20	1	ABZ85596	Human oligonucleot
c	98	17.4	0.5	20	1	ABZ86071	Human oligonucleot
	99	17.4	0.5	20	1	ABZ86075	Human oligonucleot
c	100	17.4	0.5	20	1	ABD22298	Human stanniocalci
	101	17.4	0.5	20	1	ABD22301	Human stanniocalci
c	102	17.4	0.5	20	1	ABD22305	Human stanniocalci
	103	17.4	0.5	20	1	ABD21826	Human stanniocalci
c	104	17.4	0.5	20	1	ADP20520	Transcription fact
	105	17.4	0.5	21	1	AAZ37188	Human PRO1315 forw
c	106	17.4	0.5	21	1	AAZ73260	SNP flanking seque

c 107	17.4	0.5	21	1	AAF54275	Primer #26 used in	c 180	16.8	0.4	20	1	ADH66495	Human glucocortico
c 108	17.4	0.5	21	1	ACD68312	Novel human secret	c 181	16.8	0.4	20	1	ADH66562	Human glucocortico
c 109	17.4	0.5	21	1	ACH04414	Human secreted/tra	c 182	16.8	0.4	20	1	ADH64132	Human glucocortico
c 110	17.4	0.5	21	1	ACD67958	Novel human secret	c 183	16.8	0.4	20	1	ADJ60872	Oligonucleotide as
c 111	17.4	0.5	21	1	ADC17974	Human PRO PCR prim	c 184	16.8	0.4	20	1	ADJ60872	Human G protein-co
c 112	17.4	0.5	21	1	ADD70620	Human secreted/tra	c 185	16.8	0.4	20	1	ADO46361	Human oligonucleot
c 113	17.4	0.5	21	1	ADD39697	Human secreted/tra	c 186	16.8	0.4	20	1	ADO32574	Antisense 2'-MOE 9
c 114	17.4	0.5	21	1	ADD70143	Human secreted/tra	c 187	16.8	0.4	20	1	ADO32574	HOXB1 RT-PCR prime
c 115	17.4	0.5	21	1	ADD38264	Human secreted/tra	c 188	16.8	0.4	20	1	ADQ26559	Primer HOX11:857L2
c 116	17.4	0.5	21	1	ADD39220	Human secreted/tra	c 189	16.8	0.4	21	1	AAV40968	Human gene single
c 117	17.4	0.5	21	1	ADD38743	Human secreted/tra	c 190	16.8	0.4	21	1	AAV40968	Human polymorphic
c 118	17.4	0.5	21	1	ADD40174	Human secreted/tra	c 191	16.8	0.4	21	1	AAH89072	Synthetic antisens
c 119	17.4	0.5	21	1	ADE50395	Human secreted/tra	c 192	16.8	0.4	21	1	ABK70314	Synthetic antisens
c 120	17.4	0.5	21	1	ADE20007	Human secreted/tra	c 193	16.8	0.4	21	1	ABK70358	Plant AMP-binding
c 121	17.4	0.5	21	1	ADE49918	Human secreted/tra	c 194	16.8	0.4	21	1	ADL23446	Arabidopsis thalia
c 122	17.4	0.5	21	1	ADE21476	Human secreted/tra	c 195	16.8	0.4	21	1	ADL72332	Human ADAM19 gene
c 123	17.4	0.5	21	1	ADP29901	Human secreted/tra	c 196	16.8	0.4	21	1	ADP75370	PCR primer 2 used
c 124	17.4	0.5	21	1	ADP55794	Human secreted/tra	c 197	16.8	0.4	21	1	ADP45615	Forward primer #48
c 125	17.4	0.5	21	1	ADH99298	Human secreted/tra	c 198	16.4	0.4	18	1	AAF26668	Human Smad7 phosph
c 126	17.4	0.5	21	1	ADP25789	Human secreted/tra	c 199	16.4	0.4	18	1	AAAF26668	Simple sequence re
c 127	17.4	0.5	21	1	ADP25789	Human secreted/tra	c 200	16.4	0.4	18	1	AAAF26668	GAGA-B receptor la
c 128	17.4	0.5	21	1	ADP24688	Human secreted/tra	c 201	16.4	0.4	18	1	ABA933493	Huntington's disea
c 129	17.4	0.5	21	1	ADP29424	Human secreted/tra	c 202	16.4	0.4	18	1	ABZ81757	Huntington's disea
c 130	17.4	0.5	21	1	ADH02993	Human secreted/tra	c 203	16.4	0.4	18	1	ABZ81780	Huntington's disea
c 131	17.4	0.5	21	1	ADH03947	Human secreted/tra	c 204	16.4	0.4	18	1	ABZ81779	Human ADAM19 gene
c 132	17.4	0.5	21	1	ADH04424	Human secreted/tra	c 205	16.4	0.4	18	1	ADN75262	Primer of the inve
c 133	17.4	0.5	21	1	ADH04424	Human secreted/tra	c 206	16.4	0.4	18	1	ADN75298	Synthetic leader s
c 134	17.4	0.5	21	1	ADH61425	Human secreted/tra	c 207	16.4	0.4	18	1	ADO26670	Synthetic leader s
c 135	17.4	0.5	21	1	ADL94624	Human secreted/tra	c 208	16.4	0.4	18	1	ADO26672	Synthetic leader s
c 136	17.4	0.5	21	1	ADL94624	Human secreted/tra	c 209	16.4	0.4	18	1	ADO26640	Synthetic leader s
c 137	17.4	0.5	21	1	ADG611397	Human AMLP1a scann	c 210	16.4	0.4	18	1	ADO26630	Synthetic leader s
c 138	17.4	0.5	21	1	ADC37823	Human AMLP1a scann	c 211	16.4	0.4	18	1	ADO26642	PCR primer for the
c 139	17.4	0.5	21	1	ADC37821	Human AMLP1a scann	c 212	16.4	0.4	20	1	AAA66287	Dog genomic marker
c 140	17.4	0.5	21	1	ADC37818	Human AMLP1a scann	c 213	16.4	0.4	20	1	AAH56692	Streptococcus pyog
c 141	17.4	0.5	21	1	ADC37819	Human AMLP1a scann	c 214	16.4	0.4	20	1	ABK30537	Human glioma-asso
c 142	17.4	0.5	21	1	ADC37820	Human AMLP1a scann	c 215	16.4	0.4	20	1	ACC46964	Human phospholip
c 143	17.4	0.5	21	1	ADC37822	Human AMLP1a scann	c 216	16.4	0.4	20	1	ACC46964	Human phospholip
c 144	17.4	0.5	21	1	AAV30172	Protein kinase cat	c 217	16.4	0.4	20	1	ADP75418	Human ephrin-A2 CD
c 145	17.4	0.5	21	1	AAH19623	Oligonucleotide co	c 218	16.4	0.4	20	1	ADP75418	Human ephrin-A2 CD
c 146	17.4	0.5	21	1	AAH19624	Complementary olig	c 219	16.4	0.4	20	1	ADH5705	Human NRC2 gene ex
c 147	17.4	0.5	21	1	ABK111198	Oligonucleotide #1	c 220	16.4	0.4	20	1	ADH5705	Human glucocortico
c 148	17.4	0.5	21	1	ABK111198	Oligonucleotide #2	c 221	16.4	0.4	20	1	ADN06173	Human SP2 specif
c 149	17.4	0.5	21	1	ADK67650	Huntington's disea	c 222	16.4	0.4	20	1	ABL46975	Human GRD zinzyme
c 150	17.4	0.5	21	1	ADK67650	Huntington's disea	c 223	16.4	0.4	17	1	ABL46975	Huntington's disea
c 151	17.4	0.5	21	1	ADSI6437	Allele A oligo #2	c 224	16.4	0.4	17	1	ADC37824	Human AMLP1a scann
c 152	17.4	0.5	21	1	ADSI6437	Allele A oligo #1	c 225	16.4	0.4	17	1	ADC37824	Human AMLP1a scann
c 153	17.4	0.5	21	1	ABZ85595	Human oligonucleot	c 226	16.4	0.4	17	1	ADMS4298	Human AMLP1a scann
c 154	17.4	0.5	21	1	ABD21825	Human oligonucleot	c 227	16.4	0.4	17	1	ADMS4298	Human GRD mRNA su
c 155	17.4	0.5	21	1	AAV72522	5-Cys-encoding oli	c 228	16.4	0.4	18	1	ADSI6440	Allele A oligo #3
c 156	16.8	0.4	20	1	AAV72522	SCA2 gene CAG repe	c 229	16.4	0.4	18	1	AAH57033	Human oestrogen re
c 157	16.8	0.4	20	1	AAV30272	SNP typing-related	c 230	16.4	0.4	20	1	AAH57033	Chimeric phosphoro
c 158	16.8	0.4	20	1	ADH68486	Human oligonucleot	c 231	15.8	0.4	19	1	AAH82617	cdk2 ribozyme bind
c 159	16.8	0.4	20	1	ABZ86069	Human oligonucleot	c 232	15.8	0.4	19	1	AAH82617	Cell-cycle depende
c 160	16.8	0.4	20	1	ABZ85597	Human oligonucleot	c 233	15.8	0.4	30	1	ADQ62508	Anti-TOP2A siRNA S
c 161	16.8	0.4	20	1	ABZ85597	Human oligonucleot	c 234	15.6	0.4	30	1	ABZ81777	Huntington's disea
c 162	16.8	0.4	20	1	ABZ86062	Human oligonucleot	c 235	15.6	0.4	33	1	ABX79926	Mouse flk-1 VEGF r
c 163	16.8	0.4	20	1	ABZ86061	Human oligonucleot	c 236	15.4	0.4	17	1	AAH72851	Human EGF-R target
c 164	16.8	0.4	20	1	ABZ86070	Human PDE4A oligon	c 237	15.4	0.4	17	1	AAH72851	Human EGF-R target
c 165	16.8	0.4	20	1	ABZ86070	Human oligonucleot	c 238	15.4	0.4	17	1	AAV97395	Human GRD zinzyme
c 166	16.8	0.4	20	1	ABZ86077	Human oligonucleot	c 239	15.4	0.4	17	1	ABL46976	Human GRD NCH rib
c 167	16.8	0.4	20	1	ACC62133	Human oligonucleot	c 240	15.4	0.4	17	1	ABL46976	Human GRD NCH rib
c 168	16.8	0.4	20	1	ABZ84008	Toxicologically re	c 241	15.4	0.4	17	1	ABL46728	Human GRD NCH rib
c 169	16.8	0.4	20	1	ABD22299	Human stannioalcali	c 242	15.4	0.4	17	1	ABL46728	Human GRD NCH rib
c 170	16.8	0.4	20	1	ABD22300	Human stannioalcali	c 243	15.4	0.4	17	1	ABL46730	Human GRD NCH rib
c 171	16.8	0.4	20	1	ABD22301	Human stannioalcali	c 244	15.4	0.4	17	1	ABT38591	Tumour suppression
c 172	16.8	0.4	20	1	ABD22307	Human stannioalcali	c 245	15.4	0.4	17	1	ACC67653	Murine oligonucleo
c 173	16.8	0.4	20	1	ABD32020	Human PDE4A-deri	c 246	15.4	0.4	17	1	ADC37825	Tumour suppression
c 174	16.8	0.4	20	1	ABD28786	Human stannioalcali	c 247	15.4	0.4	17	1	ADC37825	Tumour suppression
c 175	16.8	0.4	20	1	ABD21827	Human stannioalcali	c 248	15.4	0.4	17	1	ADMS4087	Human GRD mRNA su
c 176	16.8	0.4	20	1	ABD22292	Human stannioalcali	c 249	15.4	0.4	17	1	ADMS4085	Human GRD mRNA su
c 177	16.8	0.4	20	1	ADH18033	2'-MOE gapmer anti	c 250	15.4	0.4	17	1	ADMS4086	Human GRD mRNA su
c 178	16.8	0.4	20	1	ADH65922	Human glucocortico	c 251	15.4	0.4	17	1	ADMS4299	Human GRD mRNA su
c 179	16.8	0.4	20	1	ADH64974	Human glucocortico	c 252	15.4	0.4	18	1	AAQ91051	HHV-6 associated M

253	15.4	0.4	18	1	AAV94830	Human IL-2 recepto	326	14.4	0.4	17	1	ACN04426	WNV Zinzyme subatr
c 254	15.4	0.4	18	1	AAAI0553	Smad2 antisense ol	c 327	14.4	0.4	17	1	ABT34779	Tumour suppression
c 255	15.4	0.4	18	1	AAAS07309	CPS1/TESI genomic	c 328	14.4	0.4	17	1	ADB05069	Human MD212 scanni
c 256	15.4	0.4	18	1	ABL40838	P. putida exbB and	c 329	14.4	0.4	17	1	ADB05010	Human MD212 scanni
c 257	15.4	0.4	18	1	ABS68433	Sequencing primer	c 330	14.4	0.4	17	1	ADC62073	HCV minus strand D
c 258	15.4	0.4	18	1	ADG88997	Pseudomonas putida	c 331	14.4	0.4	17	1	ACC54185	Murine oligonucleo
c 259	15.4	0.4	19	1	AAAB2737	cdk3 ribozyme bind	c 332	14.4	0.4	17	1	ADC37846	Human AMLPla scann
c 260	15.4	0.4	19	1	AAAB2738	cdk3 ribozyme bind	c 333	14.4	0.4	17	1	ADB45768	Tumour suppression
c 261	15.4	0.4	19	1	AAH57900	Cell-cycle depende	c 334	14.4	0.4	17	1	ADI50387	Human tumour suppr
c 262	15.4	0.4	19	1	AAH57899	Cell-cycle depende	c 335	14.4	0.4	17	1	ADI49572	Human tumour suppr
c 263	15.4	0.4	19	1	AAH54283	Mouse Cbfal PCR pr	c 336	14.4	0.4	17	1	ADI51822	Human tumour suppr
c 264	15.4	0.4	19	1	ADN342019	Upper strand of cy	c 337	14.4	0.4	17	1	ACC53755	Human tumour suppr
c 265	15.4	0.4	19	1	ADN34258	Lower strand of cy	c 338	14.4	0.4	17	1	ACC52683	Human tumour suppr
c 266	15.4	0.4	19	1	ADH01571	Protein tyrosine p	c 339	14.4	0.4	17	1	ADL47232	Human NOGO recepto
c 267	15.4	0.4	19	1	ADR80899	Human glucose-6-ph	c 340	14.4	0.4	17	1	ADL46972	Human NOGO recepto
c 268	15.4	0.4	19	1	ADR80898	Human glucose-6-ph	c 341	14.4	0.4	17	1	ADM54108	Human GRID mRNA su
c 269	15	0.4	17	1	ACD82527	Nucleic acid cloni	c 342	14.4	0.4	17	1	ADI85415	HCV DNzyme subatr
c 270	15	0.4	17	1	ADC37816	Human AMLPla scann	c 343	14.4	0.4	17	1	ADR27873	Murine VR-statin b
c 271	15	0.4	17	1	ADI50157	Human tumour suppr	c 344	14.4	0.4	17	1	ACN70300	Human GDMPLP-1 prob
c 272	15	0.4	18	1	ADC40522	Human G-protein co	c 345	14.4	0.4	17	1	ACN71565	Human GDMPLP-1 prob
c 273	15	0.4	18	1	ADN08161	Human S9-RNA RT-PC	c 346	14.4	0.4	17	1	ACN70299	Human GDMPLP-1 prob
c 274	15	0.4	31	1	AAQ98457	Sense probe CAG-30	c 347	14.4	0.4	17	1	ACN71566	Human GDMPLP-1 prob
c 275	15	0.4	31	1	AAZ24995	Oligonucleotide CA	c 348	14.4	0.4	18	1	AAV51900	Zea mays genome re
c 276	14.8	0.4	18	1	AAQ90869	hMLH1 gene exon 9	c 349	14.4	0.4	18	1	AAV51900	Human biallelic po
c 277	14.8	0.4	18	1	AAQ71721	Human KDR VEGF rec	c 350	14.4	0.4	18	1	AAV51900	Human AKT-1 phosph
c 278	14.8	0.4	18	1	AAZ59187	Reverse primer for	c 351	14.4	0.4	18	1	AAZ41191	Human Akt-1 mRNA 1
c 279	14.8	0.4	18	1	AAZ48499	Human TNFR1 mRNA i	c 352	14.4	0.4	18	1	AAZ48769	Human G-alpha-16 a
c 280	14.8	0.4	18	1	AAZ48498	Human TNFR1 mRNA i	c 353	14.4	0.4	18	1	AAH02259	aph(3')-VIA resist
c 281	14.8	0.4	18	1	AAZ86831	Human Smad1 antise	c 354	14.4	0.4	18	1	ABV72657	Human RISC forward
c 282	14.8	0.4	18	1	AAZ89196	Human riboprotein	c 355	14.4	0.4	18	1	ABL57876	Human ABCA7 gene p
c 283	14.8	0.4	18	1	AAAF8307	C. officinalis cal	c 356	14.4	0.4	18	1	ADK95201	Primer of the inve
c 284	14.8	0.4	18	1	AAAS20963	PCR primer Igf2r-I	c 357	14.4	0.4	18	1	ADM69867	Plant gene polymor
c 285	14.8	0.4	18	1	ABT04994	TNFR1 expression m	c 358	14.4	0.4	18	1	ADN06360	Human FIAP related
c 286	14.8	0.4	18	1	ABT04995	TNFR1 expression m	c 359	14.4	0.4	18	1	ADN06360	Oligonucleotide of
c 287	14.8	0.4	18	1	ABL01690	Human MLH1 (hMLH1)	c 360	14.4	0.4	18	1	ADS94379	Human 5-lipoxygena
c 288	14.8	0.4	18	1	ABX80015	EST polymorphic DN	c 361	14.4	0.4	26	1	ABS71093	Human GPCR ligand
c 289	14.8	0.4	18	1	AAZ56267	Hepatitis E virus	c 362	14.4	0.4	26	1	ADD69029	Angiogenesis inhib
c 290	14.8	0.4	18	1	AAZ56287	Hepatitis E virus	c 363	14	0.4	17	1	ACA99718	G-protein coupled
c 291	14.8	0.4	18	1	ADC65962	Primer oligo used	c 364	14	0.4	17	1	ACA99717	G-protein coupled
c 292	14.8	0.4	18	1	ADD28828	Escherichia coli 0	c 365	14	0.4	17	1	ACA99716	G-protein coupled
c 293	14.8	0.4	18	1	ADD28830	Escherichia coli 0	c 366	14	0.4	17	1	ACA99715	G-protein coupled
c 294	14.8	0.4	18	1	ADD28831	Escherichia coli 0	c 367	14	0.4	17	1	ADC37815	Human AMLPla scann
c 295	14.8	0.4	18	1	ADD28829	Escherichia coli 0	c 368	14	0.4	17	1	ADF78423	Chromosomal abnorm
c 296	14.8	0.4	18	1	ABZ97839	Human etaxin olig	c 369	14	0.4	17	1	ADH53228	Human APC (adenoma
c 297	14.8	0.4	18	1	ADM95270	SNP-containing car	c 370	14	0.4	17	1	ADI50862	Human tumour suppr
c 298	14.8	0.4	18	1	ADM95272	SNP-containing car	c 371	14	0.4	17	1	ADI47898	Human tumour suppr
c 299	14.8	0.4	18	1	ADM77392	Human fibrocytein	c 372	14	0.4	17	1	ADR97999	Human APC DNA frag
c 300	14.8	0.4	18	1	ABD30870	Human etaxin-deri	c 373	14	0.4	17	1	ADS08683	Human DNA oligonuc
c 301	14.8	0.4	18	1	ADJ59713	Concatemer of Bota	c 374	14	0.4	30	1	AAZ44310	Human SCA7 primer
c 302	14.8	0.4	18	1	ADJ59712	Oligonucleotide as	c 375	14	0.4	30	1	AAZ44310	Simple sequence re
c 303	14.8	0.4	18	1	ADO45203	Human oligonucleot	c 376	13.8	0.4	17	1	AAV81598	Oligonucleotide us
c 304	14.8	0.4	18	1	ADO45202	Human oligonucleot	c 377	13.8	0.4	17	1	AAV81598	Rabbit stromelysin
c 305	14.8	0.4	18	1	ADO45202	Human oligonucleot	c 378	13.8	0.4	17	1	AAV81598	Rabbit stromelysin
c 306	14.8	0.4	18	1	ADO45202	Human oligonucleot	c 379	13.8	0.4	17	1	AAV81598	Human flt1 VEGF re
c 307	14.6	0.4	30	1	ADN97224	AGC1 locus. Undie	c 380	13.8	0.4	17	1	AAV81598	Human flt1 VEGF re
c 308	14.4	0.4	17	1	AAZ53479	Rat ICAM hammerhea	c 381	13.8	0.4	17	1	AAV81598	Mouse flt-1 VEGF r
c 309	14.4	0.4	17	1	AAZ33778	Primer/probe (CTA)	c 382	13.8	0.4	17	1	AAV81598	Human KDR VEGF rec
c 310	14.4	0.4	17	1	AAZ71238	Human KDR VEGF rec	c 383	13.8	0.4	17	1	AAV81598	Human flt1 VEGF re
c 311	14.4	0.4	17	1	AAZ20589	Integrin alpha 6 s	c 384	13.8	0.4	17	1	AAV81598	Human flt1 VEGF re
c 312	14.4	0.4	17	1	AAZ25734	Oestrogen receptor	c 385	13.8	0.4	17	1	AAV81598	Mouse flt-1 VEGF r
c 313	14.4	0.4	17	1	AAZ25735	Oestrogen receptor	c 386	13.8	0.4	17	1	AAV81598	Mouse flt-1 VEGF r
c 314	14.4	0.4	17	1	ABK00234	Human NOGO Hamme	c 387	13.8	0.4	17	1	AAV81598	Mouse flt-1 VEGF r
c 315	14.4	0.4	17	1	ABK00235	Human NOGO Hamme	c 388	13.8	0.4	17	1	AAV81598	Pentaplex tc-PROBE
c 316	14.4	0.4	17	1	ABL46891	Human GRID G-cleav	c 389	13.8	0.4	17	1	AAV81598	Mouse IL-2 recepto
c 317	14.4	0.4	17	1	ABL46891	Human GRID G-cleav	c 390	13.8	0.4	17	1	AAV81598	Mouse IL-2 recepto
c 318	14.4	0.4	17	1	AAZ04520	Lactococcus lactis	c 391	13.8	0.4	17	1	AAV81598	Primer ACP/BRB for
c 319	14.4	0.4	17	1	ABN08476	Human GDMPLP-1 17-m	c 392	13.8	0.4	17	1	AAV81598	Primer ACP/BRB for
c 320	14.4	0.4	17	1	ABN07209	Human GDMPLP-1 17-m	c 393	13.8	0.4	17	1	AAV81598	Integrin subunit b
c 321	14.4	0.4	17	1	ABN07210	Human GDMPLP-1 17-m	c 394	13.8	0.4	17	1	AAV81598	Integrin subunit b
c 322	14.4	0.4	17	1	ABN07211	Human GDMPLP-1 17-m	c 395	13.8	0.4	17	1	AAV81598	Human ACE regulato
c 323	14.4	0.4	17	1	ABV89862	Human POSHL1 scann	c 396	13.8	0.4	17	1	AAV81598	Human ACE regulato
c 324	14.4	0.4	17	1	ABV89861	Human POSHL1 scann	c 397	13.8	0.4	17	1	AAV81598	Oestrogen receptor
c 325	14.4	0.4	17	1	ACN12567	WNV minus strand 2	c 398	13.8	0.4	17	1	AAV81598	Human ACE, AGT and

399	13.8	0.4	17	1	AAC61245	Human ACE, AGT and Hammerhead ribozym	c 472	13.8	0.4	17	1	ABT37737	Tumour suppression
c 400	13.8	0.4	17	1	AAF07477	Hammerhead ribozym	473	13.8	0.4	17	1	ACA06321	NFKB sub-unit modu
401	13.8	0.4	17	1	AAF05460	Hammerhead ribozym	474	13.8	0.4	17	1	ACA06547	NFKB sub-unit modu
c 402	13.8	0.4	17	1	AAF04887	Hammerhead ribozym	475	13.8	0.4	17	1	ACA06556	NFKB sub-unit modu
c 403	13.8	0.4	17	1	AAF04439	Hammerhead ribozym	c 476	13.8	0.4	17	1	ACA07772	Human MDZ12b scannin
404	13.8	0.4	17	1	AACT73225	Forward primer #39	477	13.8	0.4	17	1	ADB05972	Human MDZ2 scannin
c 405	13.8	0.4	17	1	AAAD09710	Cryptosporidium pa	c 478	13.8	0.4	17	1	ADB00149	Human MDZ4 scannin
c 406	13.8	0.4	17	1	AAH94700	Human Chk1 ribozym	c 479	13.8	0.4	17	1	ADB02404	Human MDZ3 scannin
c 407	13.8	0.4	17	1	AAH95053	Human Chk1 ribozym	c 480	13.8	0.4	17	1	ADA99981	Human MDZ3 scannin
c 408	13.8	0.4	17	1	AAH95442	Human Chk1 ribozym	c 481	13.8	0.4	17	1	ADA99394	Human MDZ3 scannin
c 409	13.8	0.4	17	1	ABK01103	Human NOGO Inozyme	c 482	13.8	0.4	17	1	ADB00150	Human MDZ3 scannin
c 410	13.8	0.4	17	1	ABK00766	Human NOGO Inozyme	c 483	13.8	0.4	17	1	ADB00152	Human MDZ3 scannin
c 411	13.8	0.4	17	1	ABK02892	Human CD20 Hammerh	c 484	13.8	0.4	17	1	ADA99390	Human MDZ4 scannin
c 412	13.8	0.4	17	1	ABK02895	Human CD20 Hammerh	c 485	13.8	0.4	17	1	ADB02405	Human MDZ3 scannin
413	13.8	0.4	17	1	ABK00767	Human NOGO Inozyme	c 486	13.8	0.4	17	1	ADA99395	Human H-Ras DNazym
414	13.8	0.4	17	1	ABK01792	Human NOGO Zinzyme	c 487	13.8	0.4	17	1	ACD51476	HBV Hammerhead rib
415	13.8	0.4	17	1	ABK02456	Human NOGO G-Cleav	c 488	13.8	0.4	17	1	ACD51476	HCV DNazyme substr
416	13.8	0.4	17	1	ABK01549	Human NOGO Amberzy	c 489	13.8	0.4	17	1	ACD1082	HBV DNazyme substr
417	13.8	0.4	17	1	ABK02456	Human NOGO Amberzy	c 490	13.8	0.4	17	1	ACD54845	HBV DNazyme substr
418	13.8	0.4	17	1	ABL46974	Human GRID zinzyme	c 491	13.8	0.4	17	1	ACD73351	Mycobacterium gast
419	13.8	0.4	17	1	ABL46825	Human GRID NCH rib	c 492	13.8	0.4	17	1	ACC65076	Murine oligonucleo
c 420	13.8	0.4	17	1	ABA93692	GAPDH CDNA PCR pri	c 493	13.8	0.4	17	1	ACC65169	Murine oligonucleo
421	13.8	0.4	17	1	ABN00672	Human GDMPLP-1 17-m	c 494	13.8	0.4	17	1	ACC65169	Murine oligonucleo
422	13.8	0.4	17	1	ABN00673	Human GDMPLP-1 17-m	c 495	13.8	0.4	17	1	ACC65917	Murine oligonucleo
423	13.8	0.4	17	1	ABN01880	Human GDMPLP-1 17-m	c 496	13.8	0.4	17	1	ACC65917	Murine oligonucleo
424	13.8	0.4	17	1	ABN01881	Human GDMPLP-1 17-m	c 497	13.8	0.4	17	1	ACC65917	Murine oligonucleo
425	13.8	0.4	17	1	ABN01881	Human GDMPLP-1 17-m	c 498	13.8	0.4	17	1	ADA15895	Primer for amplifi
426	13.8	0.4	17	1	ABN01255	Human GDMPLP-1 17-m	c 499	13.8	0.4	17	1	ADB43213	Tumour suppression
427	13.8	0.4	17	1	ABN02741	Human GDMPLP-1 17-m	c 500	13.8	0.4	17	1	ADB41766	Tumour suppression
428	13.8	0.4	17	1	ABN07811	Human GDMPLP-1 17-m	c 501	13.8	0.4	17	1	ADB40208	Tumour suppression
c 429	13.8	0.4	17	1	ABK25807	Stress tolerance c	c 502	13.8	0.4	17	1	ADB41665	Tumour suppression
430	13.8	0.4	17	1	ABK25808	Stress tolerance c	c 503	13.8	0.4	17	1	ADB43678	Tumour suppression
431	13.8	0.4	17	1	ABK27200	Reduced linolenic	c 504	13.8	0.4	17	1	ADB42015	Tumour suppression
c 432	13.8	0.4	17	1	ABK27199	Reduced linolenic	c 505	13.8	0.4	17	1	ADC70444	Tumour suppression
c 433	13.8	0.4	17	1	ABK25787	Stress tolerance c	c 506	13.8	0.4	17	1	ADC38460	TrisO-T PCR primer
434	13.8	0.4	17	1	ABK25788	Stress tolerance c	507	13.8	0.4	17	1	ADB44767	Human AMLF1b scann
435	13.8	0.4	17	1	ABK97699	Human NEDD-1 scann	508	13.8	0.4	17	1	ADB45671	Tumour suppression
436	13.8	0.4	17	1	ABN97700	Human NEDD-1 scann	c 509	13.8	0.4	17	1	ADB45324	Tumour suppression
437	13.8	0.4	17	1	ABN97698	Human NEDD-1 scann	c 510	13.8	0.4	17	1	ADB45499	Tumour suppression
438	13.8	0.4	17	1	ABN97696	Human NEDD-1 scann	c 511	13.8	0.4	17	1	ADD69451	5' anchored (ISSR)
439	13.8	0.4	17	1	ABN97697	Human NEDD-1 scann	c 512	13.8	0.4	17	1	ADD44223	Carboxypeptidase G
440	13.8	0.4	17	1	ABN90854	Human FAPP-Ea asso	c 513	13.8	0.4	17	1	ADD44239	Carboxypeptidase G
c 441	13.8	0.4	17	1	ABV90854	Human POSHL1 scann	c 514	13.8	0.4	17	1	ADF64073	Human PCCP1 DNA fr
c 442	13.8	0.4	17	1	ABV90854	Human POSHL1 scann	c 515	13.8	0.4	17	1	ADI48470	Human tumour suppr
c 443	13.8	0.4	17	1	ABV90268	Human POSHL1 scann	c 516	13.8	0.4	17	1	ADI48618	Human tumour suppr
c 444	13.8	0.4	17	1	ABV98859	Human POSHL1 gene e	517	13.8	0.4	17	1	ADI48748	Human tumour suppr
c 445	13.8	0.4	17	1	ABK56440	Human CLCA1 gene e	518	13.8	0.4	17	1	ADI49729	Human tumour suppr
446	13.8	0.4	17	1	ABK55961	Human CLCA1 gene e	519	13.8	0.4	17	1	ADI49390	Human tumour suppr
447	13.8	0.4	17	1	AAD36054	Human CHLCK DNA am	c 520	13.8	0.4	17	1	ADI49542	Human tumour suppr
c 448	13.8	0.4	17	1	ACN01188	WNV Inozyme substr	c 521	13.8	0.4	17	1	ADI49656	Human tumour suppr
c 449	13.8	0.4	17	1	ACN01188	WNV Hammerhead Rib	c 522	13.8	0.4	17	1	ADI49672	Human tumour suppr
c 450	13.8	0.4	17	1	ACN05943	WNV minus strand A	c 523	13.8	0.4	17	1	ADI52660	Human tumour suppr
451	13.8	0.4	17	1	ACN014376	WNV Inozyme substr	c 524	13.8	0.4	17	1	ADI47871	Human tumour suppr
452	13.8	0.4	17	1	ACN01465	WNV minus strand Z	c 525	13.8	0.4	17	1	ACC54207	Human tumour suppr
c 453	13.8	0.4	17	1	ACN02785	WNV Inozyme substr	c 526	13.8	0.4	17	1	ACC51702	Human tumour suppr
454	13.8	0.4	17	1	ACN02990	WNV minus strand I	c 527	13.8	0.4	17	1	ADL51684	Human PKR substrat
c 455	13.8	0.4	17	1	ACN09716	WNV Amberzyme subs	c 528	13.8	0.4	17	1	ADL48748	Human IKK-gamma su
c 456	13.8	0.4	17	1	ACN09847	WNV minus strand I	c 529	13.8	0.4	17	1	ADL49592	Human NOGO recepto
c 457	13.8	0.4	17	1	ACN01051	WNV minus strand I	c 530	13.8	0.4	17	1	ADL46971	Human PTGDR substr
c 458	13.8	0.4	17	1	ACN06089	WNV Amberzyme subs	c 531	13.8	0.4	17	1	ADL51912	Human PTGDR substr
c 459	13.8	0.4	17	1	ACN07144	WNV Hammerhead Rib	c 532	13.8	0.4	17	1	ADM54183	Human GRID mRNA su
c 460	13.8	0.4	17	1	ACN01189	WNV minus strand I	533	13.8	0.4	17	1	ADM54088	Human GRID mRNA su
c 461	13.8	0.4	17	1	ACN11320	WNV Amberzyme subs	534	13.8	0.4	17	1	ADM54297	Signature sequence
462	13.8	0.4	17	1	ACN05400	WNV minus strand H	535	13.8	0.4	17	1	ADM43565	Primer of the inve
463	13.8	0.4	17	1	ACN11532	WNV minus strand I	c 536	13.8	0.4	17	1	ADK96182	Hepatitis B virus
c 464	13.8	0.4	17	1	ACN09448	WNV minus strand I	c 537	13.8	0.4	17	1	ADM60003	Hepatitis B virus
c 465	13.8	0.4	17	1	ACN11653	WNV minus strand H	c 538	13.8	0.4	17	1	ADN45890	Mutant cell identi
466	13.8	0.4	17	1	ACN00549	G-protein coupled	c 539	13.8	0.4	17	1	ADN45891	Mutant cell identi
c 467	13.8	0.4	17	1	ABT37547	Tumour suppression	540	13.8	0.4	17	1	ADN44479	Mutant cell identi
c 468	13.8	0.4	17	1	ABT37547	Tumour suppression	541	13.8	0.4	17	1	ADN44478	Mutant cell identi
c 469	13.8	0.4	17	1	ABT37508	Tumour suppression	c 542	13.8	0.4	17	1	ADN44478	Mutant cell identi
c 470	13.8	0.4	17	1	ABT37508	Tumour suppression	c 543	13.8	0.4	17	1	ADN44478	Mutant cell identi
c 471	13.8	0.4	17	1	ABT35272	Tumour suppression	544	13.8	0.4	17	1	ADN44499	Mutant cell identi

545 13.8 0.4 17 1 ACN64970 Human GDMPLP-1 prob
 546 13.8 0.4 17 1 ACN70900 Human GDMPLP-1 prob
 547 13.8 0.4 17 1 ACN65831 Human GDMPLP-1 prob
 548 13.8 0.4 17 1 ACN63763 Human GDMPLP-1 prob
 549 13.8 0.4 17 1 ACN70901 Human GDMPLP-1 prob
 550 13.8 0.4 17 1 ACN63762 Human GDMPLP-1 prob
 551 13.8 0.4 17 1 ACN73845 Human GDMPLP-1 prob
 552 13.8 0.4 17 1 ACN64971 Human GDMPLP-1 prob
 553 13.8 0.4 17 1 ACN73345 Human GDMPLP-1 prob

ALIGNMENTS

RESULT 1
 ID ABX79926 standard; cDNA; 33 BP.
 XX
 AC ABX79926;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE EST polymorphic DNA repeat polynucleotide #251.
 XX
 KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Fredeich's ataxia; myotonic dystrophy; hyperandrogenemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
 XX
 OS Homo sapiens.
 XX
 PN US6472154-B1.
 XX
 PD 29-OCT-2002.
 XX
 PF 31-DEC-1999; 99US-00475947.
 XX
 PR 31-DEC-1999; 99US-00475947.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX
 DR WPI; 2003-208818/20.
 XX
 PT Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.
 XX
 PS Example; Col 1089; 588pp; English.
 XX
 SS The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Fredeich's ataxia,
 CC myotonic dystrophy, hyperandrogenemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 SQ Sequence 33 BP; 11 A; 10 C; 11 G; 1 T; 0 U; 0 Other;
 Query Match 0.8%; Score 30.4; DB 1; Length 33;

Best Local Similarity 96.9%; Pred. No. 5.5;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 1440
 DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGTAGCAGCA 32
 RESULT 2
 ID AAZ44310 standard; DNA; 30 BP.
 XX
 AC AAZ44310;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE Human SCA7 primer 1.
 XX
 KW SCA7; human; spinocerebellar ataxia type 7; SCA1; SCA2; SCA3; SCA6;
 KW repeat expansion detection; RED analysis; detection; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN CA2245310-A.
 XX
 PD 19-FEB-1999.
 XX
 PF 19-AUG-1998; 98CA-02245310.
 XX
 PR 19-AUG-1997; 97US-0056170P.
 XX
 PA (MINU) UNIV MINNESOTA.
 XX
 PI Koob MD, Ranum LP;
 XX
 DR WPI; 2000-098181/09.
 XX
 PT Identifying individuals at risk of developing spinocerebellar ataxia type
 PT 7 by analyzing trinucleotide repeat regions of spinocerebellar ataxia
 PT type 7 gene.
 XX
 PS Disclosure; Page 43; 66pp; English.
 XX
 SS This invention describes a novel method for identifying individuals at
 CC risk for developing spinocerebellar ataxia type 7 (SCA7). The method
 CC comprises analyzing the CAG repeat region of a SCA7 gene to detect CAG
 CC repeats, where individuals at risk have at least 30 CAG repeats and those
 CC not at risk have less than 19 CAG repeats. The method is useful for
 CC identifying individuals at risk of developing SCA7 and also those at risk
 CC of developing SCA1, 2, 3 or 6. The use of genomic DNA in the repeat
 CC expansion detection (RED) analysis allows isolation of any potential
 CC trinucleotide repeat expansion regardless of the expression pattern.
 CC Utilization of different oligonucleotides in the RED assay allows any of
 CC the possible trinucleotide repeats to be detected, and the cyclized nature
 CC of the reaction makes it extremely sensitive. This sequence represents a
 CC primer used to amplify the human SCA7 gene which is described in the
 CC method of the invention.
 XX
 SQ Sequence 30 BP; 10 A; 10 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.8%; Score 30; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
 DB 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 3
 ID AAS13781 standard; DNA; 30 BP.
 XX

CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing

CC Revised record issued on 04-NOV-2004 : Correction to Feature Table Key

XX SQ Sequence 31 BP; 16 A; 10 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 0.8%; Score 29.4; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 6.5;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1561 GCAGCAGCAGCAGCAACCAACAGCAACAA 1591
 Db 1 GCAGCAGCAGCAGCAACCAACCAACAA 31

RESULT 8

ABZ81777
 ID ABZ81777 standard; DNA; 30 BP.

XX AC ABZ81777;

XX DT 11-JUN-2003 (first entry)

XX DE Huntington's disease gene mutated exon 1 region.

XX KW Huntington's disease; nontropic; anticonvulsant; huntingtin; human;
 KW gene therapy; mutant; ds.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT mutation replace(5,A)

FT /*tag= a

XX PN WO2003013437-A2.

XX PD 20-FEB-2003.

XX PF 07-AUG-2002; 2002WO-US025352.

XX PR 07-AUG-2001; 2001US-0310757P.

XX PR 08-AUG-2001; 2001US-0310770P.

XX PR 08-AUG-2001; 2001US-0310889P.

XX PR 04-DEC-2001; 2001US-0337219P.

XX (UYDE) UNIV DELAWARE.

XX PI Kmiec EB, Parekh-Olmedo H;

XX WPI; 2003-256478/25.

XX New single stranded oligonucleotides comprising a DNA domain having at
 PT least one mismatch with respect to the genetic sequence of the
 PT Huntington's disease gene to be altered, useful for treating or
 PT preventing Huntington's disease.

XX Example 4; Fig 14; 13pp; English.

XX The present sequence is that of a portion of a mutated glutamine (CAG)
 CC triplet repeat region of exon 1 of the human Huntington's disease (HD)
 CC gene (see also ABZ81760). The triplet repeat region (see ABZ81770) is
 CC mutated following liposome transfection of neuronal PC12 cells bearing an
 CC HD gene exon 1-GFP fusion gene with phosphorothioate-modified single-
 CC stranded oligonucleotide HD3T/52 (see ABZ81774), which causes a CAG (Gln)
 CC to CAG (Ileu) gene alteration in the HD exon 1 repeats. HD3T/52 is an
 CC example of oligonucleotides of the invention for targeted alteration of

CC the HD gene. Such oligonucleotides can be used for the treatment or
 CC prevention of HD

XX SQ Sequence 30 BP; 9 A; 10 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 28.4; DB 1; Length 30;

Best Local Similarity 96.7%; Pred. No. 8.3;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1438

Db 1 CAGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 9

ABA00946/c

ID ABA00946 standard; DNA; 28 BP.

XX AC ABA00946;

XX DT 28-APR-2003 (first entry)

XX DE MECT1-MAML2 chimeric protein detection primer, MAML2 Exon 2 antisense.

XX KW Consensus sequence; NOTCH; Mastermind-like; gene family; screening; t(11;
 KW 19)(q14-21; p12-13); translocation; MECT1-MAML2 chimera; MECT1; MAML2;
 KW cancer; mucoepidermoid carcinoma; malignant; salivary gland; tumour; PCR;
 KW primer; amplify; ss.

XX OS Homo sapiens.

XX PN WO2003004645-A1.

XX PD 16-JAN-2003.

XX PF 03-JUL-2002; 2002WO-US021344.

XX PR 03-JUL-2001; 2001US-0302788P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Kaye FJ, Tonon G;

XX WPI; 2003-210364/20.

XX Screening a tissue sample from a subject for a t(11;19)(q14-21;p12-13)
 PT translocation, useful for treating mucoepidermoid carcinoma comprises
 PT detecting the presence of MECT1-MAML2 chimeric nucleic acid or protein in
 PT a tissue sample.

XX Example 4; Page 36; 65pp; English.

XX The sequences given in ABA00945-46 are primers which were used to detect
 CC specific MECT1/MAML2 fusion mRNA in mucoepidermoid tumours. The method of
 CC the invention allows for screening of a tissue sample from a subject for
 CC a t(11;19)(q14-21;p12-13) translocation and comprises detecting the
 CC presence of MECT1-MAML2 chimeric nucleic acid or protein in a tissue
 CC sample. The method is useful for diagnosing and treating cancer.
 CC including cancer that involves the NOTCH pathway, particularly cancer of
 CC mucoepidermoid carcinoma, the most common malignant salivary gland tumour

XX SQ Sequence 28 BP; 3 A; 6 C; 11 G; 8 T; 0 U; 0 Other;

Query Match 0.7%; Score 28; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 7.6;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 CTCCTGCCAACAGCAAGCGACCCCAATGG 210

Db 28 CTCCTGCCAACAGCAAGCGACCCCAATGG 1

RESULT 10

XX 11-JUN-2003 (first entry)
 XX Huntington's disease gene targeting oligonucleotide.
 DE Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
 XX gene therapy; ds.
 KW Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH misc_binding 1..25
 FT /*tag= a
 FT /bound_motety= "HD gene exon 1 triplet repeat"
 FT /note="hybridises to bases 1-25 of sequence given in
 FT ABZ81767"
 XX
 XX WO2003013437-A2.
 PN
 XX 20-FEB-2003.
 XX
 XX 07-AUG-2002; 2002WO-US025352.
 XX
 XX 07-AUG-2001; 2001US-0310757P.
 PR 08-AUG-2001; 2001US-0310770P.
 PR 08-AUG-2001; 2001US-0310889P.
 PR 04-DEC-2001; 2001US-0337219P.
 XX
 XX (UYDE) UNIV DELAWARE.
 PA
 XX Kmiec EB, Parekh-Olmedo H;
 PI
 XX WPI; 2003-256478/25.
 DR
 XX New single stranded oligonucleotides comprising a DNA domain having at
 PT least one mismatch with respect to the genetic sequence of the
 PT Huntington's disease gene to be altered, useful for treating or
 PT preventing Huntington's disease.
 XX
 XX Example 1; Fig 6a; 133pp; English.
 PS
 XX The present sequence is that of a portion of a 52-mer RNA/DNA chimeric
 CC oligonucleotide of the glutamine (CAG) that is targeted to triplet
 CC repeat region (see ABZ81767) of exon 1 of the human Huntington's disease
 CC (HD) gene. This targeting results in a CAG to TAG (stop codon) nucleotide
 CC exchange due to sliding of the repeat region, a phenomenon that can occur
 CC with the methods of this invention. The oligonucleotide is an example of
 CC claimed oligonucleotides of the invention for targeted alteration of the
 CC HD gene. Such oligonucleotides can be used for the treatment or
 CC prevention of HD
 XX
 XX Sequence 25 BP; 0 A; 8 C; 9 G; 0 T; 8 U; 0 Other;
 SQ
 Query Match 0.7%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred.No. 16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCAGC 1433
 DB |||||||||||||||||||||||||
 25 CAGCAGCAGCAGCAGCAGCAGC 1
 RESULT 13
 ABN87602
 ID ABN87602 standard; DNA; 24 BP.
 XX
 XX ABN87602;
 AC
 XX 07-AUG-2002 (first entry)
 DT
 XX Human copine I27.5 PCR primer 1 SEQ ID NO:3.
 DE
 XX Human; copine I27.5; cell membrane protein function disorder; PCR primer;

KW ss.
 XX Homo sapiens.
 OS
 XX CN1331112-A.
 PN
 XX 16-JAN-2002.
 PD
 XX 30-JUN-2000; 2000CN-00116931.
 PF
 XX 30-JUN-2000; 2000CN-00116931.
 PR
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA
 XX Mao Y, Xie Y;
 PI
 XX WPI; 2002-316396/36.
 DR
 XX Copine I27.5 polypeptide and its encoding polynucleotide, for treating
 XX e.g. cell membrane protein function disorder.
 PT
 XX Example 2; Page 18 (Disclosure); 35pp; Chinese.
 PS
 XX The present invention describes human copine I27.5 (I). Also described is
 CC a method for producing (I) using DNA recombination technology. (I) can be
 CC used in the treatment of cell membrane protein function disorders. The
 CC present sequence represents a PCR primer for (I), which is used in an
 CC example from the present invention
 CC
 XX Sequence 24 BP; 12 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred.No. 20;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2281 GAATCAATTGACCCACACAGAGAA 2304
 DB |||||||||||||||||||||||||
 1 GAATCAATTGACCCACACAGAGAA 24
 RESULT 14
 ADN97255
 ID ADN97255 standard; DNA; 24 BP.
 XX
 XX ADN97255;
 AC
 XX 01-JUL-2004 (first entry)
 DT
 XX Primer of the invention #57.
 DE
 XX DNA fingerprinting; Cannabis sativa; short tandem repeat marker;
 XX forensic identification; marijuana; primer; ss.
 KW
 XX Unidentified.
 OS
 XX WO2004008841-A2.
 PN
 XX 29-JAN-2004.
 PD
 XX 21-JUL-2003; 2003WO-US022887.
 PF
 XX 19-JUL-2002; 2002US-0397179P.
 PR
 XX (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P S.
 PA (ZINN/) ZINNAMON K.
 XX
 XX Keim PS, Zinamon K;
 PI
 XX WPI; 2004-143139/14.
 DR
 XX New isolated nucleic acid for amplification of a short tandem repeat
 PT located in DNA isolated from Cannabis sativa L species, useful for

PT forensic identification of marijuana or for linking a marijuana sample to
 XX its plant source.

XX Example 11; SEQ ID NO 122; 79pp; English.

XX The present invention relates to DNA fingerprinting for Cannabis Sativa
 CC using short tandem repeat markers. The nucleic acid is useful for
 CC forensic identification of marijuana or for linking a marijuana sample to
 CC its plant source. The present sequence represents a primer of the
 CC invention.

XX Sequence 24 BP; 8 A; 8 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 24; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGC 1433

DB 1 AGCAGCAGCAGCAGCAGCAGC 24

RESULT 15

ADN97164
 ID ADN97164 standard; DNA; 24 BP.

XX AC ADN97164;

XX AC (first entry)

DT 01-JUL-2004

XX Primer of the invention #3.

XX DNA fingerprinting; Cannabis sativa; short tandem repeat marker;

KW forensic identification; marijuana; primer; ss.

XX Synthetic.

XX WO2004008841-A2.

XX 29-JAN-2004.

XX 21-JUL-2003; 2003WO-US022887.

XX 19-JUL-2002; 2002US-0397179P.

XX (UYAR-) UNIV ARIZONA.

XX (KEIM/) KEIM P. S.

XX (ZINN/) ZINNAMON K.

XX Keim PS, Zinamon K;

XX WPI; 2004-143139/14.

XX New isolated nucleic acid for amplification of a short tandem repeat
 PT located in DNA isolated from Cannabis sativa L species, useful for
 PT forensic identification of marijuana or for linking a marijuana sample to
 PT its plant source.

XX Disclosure; SEQ ID NO 31; 79pp; English.

XX The present invention relates to DNA fingerprinting for Cannabis Sativa
 CC using short tandem repeat markers. The nucleic acid is useful for
 CC forensic identification of marijuana or for linking a marijuana sample to
 CC its plant source. The present sequence represents a primer of the
 CC invention.

XX Sequence 24 BP; 8 A; 8 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 24; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGC 1433

DB 1 AGCAGCAGCAGCAGCAGCAGC 24

RESULT 16

ADR68635/c

ID ADR68635 standard; DNA; 24 BP.

XX AC ADR68635;

XX 04-NOV-2004 (first entry)

XX DNA G-quadruplex structure-fixing compound-related oligonucleotide #12.

XX G-quadruplex structure; isomer; racemate; enantiomer; diastereoisomer;
 KW cytotatic; muscular-Gen; dermatological; vasotropic; endocrine-Gen;
 KW telomerase inhibitor; anticancer agent; genetic disorder;
 KW Bloom's syndrome; Werner's syndrome; Rothmund-Thomson syndrome;
 KW ataxia telangiectasia; ss.

XX Unidentified.

XX FR2850970-A1.

XX 13-AUG-2004.

XX 07-FEB-2003; 2003FR-00001478.

XX 07-FEB-2003; 2003FR-00001478.

XX (AVET) AVENTIS PHARMA SA.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX (MUSE-) MUSEUM NAT HISTOIRE NATURELLE.

XX (CURI-) INST CURIE.

XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

XX (UYRE-) UNIV REIMS CHAMPAGNE-ARDENNE.

XX Hittinger A, Caulfield T, Maillet P, Bouchard H, Mandine B;

PI Belmokhtar C, Mergny JL, Guittat L, Riou JF, Gomez D;

XX WPI; 2004-583573/57.

XX New quaternary aromatic nitrogen heterocycle derivatives that fix the G-
 PT quadruplex structure of DNA or RNA are telomerase inhibitors, useful in
 PT the treatment of cancers and some genetic disorders.

XX Disclosure; Page 25; 57pp; French.

XX This invention relates to novel compounds that fix the G-quadruplex
 CC structure of DNA or RNA, their isomers, racemates, enantiomers,
 CC diastereoisomers, and their salts. The invention may be useful for the
 CC production of compounds with a cytostatic, muscular-Gen, dermatological,
 CC vasotropic or endocrine-Gen activity acting as telomerase inhibitors. The
 CC compounds are useful as anticancer agents and for treatment of genetic
 CC disorders such as Bloom's syndrome, Werner's syndrome, Rothmund-Thomson
 CC syndrome and ataxia telangiectasia. The present sequence is that of an
 CC oligonucleotide which is related to the novel compounds of the invention.

XX Sequence 24 BP; 0 A; 8 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 24; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAGC 1432

DB 24 CAGCAGCAGCAGCAGCAGCAGC 1

RESULT 17

ADM48412/c

ID ADM48412 standard; DNA; 29 BP.

XX

```
AC ADM48412;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE Probe #7 used to illustrate the method of the invention.
XX
XX KW Detection; protein-protein interaction; protein-drug interaction; probe;
XX ss.
XX
XX OS Unidentified.
XX
XX PN US2003215825-A1.
XX
XX PD 20-NOV-2003.
XX
XX PF 12-NOV-2002; 2002US-00291986.
XX
XX PR 09-APR-2002; 2002AU-00001597.
XX
XX PA (TONG/) TONG S.
XX
XX PI Tong S;
XX
XX DR WPI; 2004-106890/11.
XX
XX PT Detecting molecular target in sample utilizing molecular interaction
XX between molecular targets, bead-bound probes and support-bound probes,
XX useful for detecting interaction between protein and drug.
XX
XX PS Disclosure; Fig 13C; 41pp; English.
XX
XX CC The present invention relates to a novel method of detecting a molecular
XX target in a sample by attaching to bead a first molecular probe to form a
XX bead-bound probe, attaching to support at predefined area a second
XX molecular probe to form support-bound probe, introducing sample to the
XX bead-bound probe and support-bound probe so that the molecular target is
XX sandwiched between support and beads and detecting presence of beads at
XX predefined area on support which indicates the presence of the molecular
XX target in the sample. The method is useful for detecting interaction
XX between two proteins. It is useful for detecting interaction between a
XX protein and a drug. The method is also useful for detecting the
XX interactions between several drugs and several proteins. The present
XX sequence is a probe used to illustrate the method of the invention.
XX
XX SQ Sequence 29 BP; 0 A; 7 C; 13 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 23.4; DB 1; Length 29;
Best Local Similarity 96.0%; Pred. No. 44;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1424 CAGCAGCAGCAGCAGCAGCAGCAGC 1448
Db 29 CAGCAGCAGCAGCAGCAGCAGCAGC 5

RESULT 18
ABAO0945
ID ABA00945 standard; DNA; 23 BP.
XX
XX AC ABA00945;
XX
XX DT 28-APR-2003 (first entry)
XX
XX DE MECT1-MAML2 chimeric protein detection primer, MECT1 Exon 1 Sense.
XX
XX KW Consensus sequence; NOTCH; Mastermind-like; gene family; screening; t(11;
XX q14-q21; p12-13); translocation; MECT1-MAML2 chimera; MECT1; MAML2;
XX cancer; mucoepidermoid carcinoma; malignant; salivary gland; tumour; PCR;
XX primer; amplify; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO2003004645-A1.

XX
XX 16-JAN-2003.
XX
XX PD 03-JUL-2002; 2002WO-US021344.
XX
XX PF 03-JUL-2001; 2001US-0302788P.
XX
XX PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PA Kaye FJ, Tonon G;
XX
XX PI WPI; 2003-210364/20.
XX
XX DR Screening a tissue sample from a subject for a t(11;19)(q14-q21;p12-q13)
XX translocation, useful for treating mucoepidermoid carcinoma comprises
XX detecting the presence of MECT1-MAML2 chimeric nucleic acid or protein in
XX a tissue sample.
XX
XX PS Example 4; Page 36; 65pp; English.
XX
XX CC The sequences given in ABA00945-46 are primers which were used to detect
XX specific MECT1/MAML2 fusion mRNA in mucoepidermoid tumours. The method of
XX the invention allows for screening of a tissue sample from a subject for
XX a t(11;19)(q14-q21;p12-q13) translocation and comprises detecting the
XX presence of MECT1-MAML2 chimeric nucleic acid or protein in a tissue
XX sample. The method is useful for diagnosing and treating cancer,
XX including cancer that involves the NOTCH pathway, particularly cancer of
XX mucoepidermoid carcinoma, the most common malignant salivary gland tumour
XX
XX SQ Sequence 23 BP; 8 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGAGAGATGCGGACTTCGAACA 32
Db 1 CGAGAGATGCGGACTTCGAACA 23

RESULT 19
ADC59319
ID ADC59319 standard; DNA; 23 BP.
XX
XX AC ADC59319;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Oligonucleotide, #1, based on human polynucleotide #1.
XX
XX KW Human; ss; polyglutamine disease; genealogical polyglutamine disease;
XX nootropic; anticonvulsant.
XX
XX OS Homo sapiens.
XX
XX PN JF2002360268-A.
XX
XX PD 17-DEC-2002.
XX
XX PF 03-AUG-2001; 2001JP-00236788.
XX
XX PR 04-AUG-2000; 2000JP-00236839.
XX
XX PR 06-APR-2001; 2001JP-00108723.
XX
XX PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
XX (DAUC ) DAICHI PHARM CO LTD.
XX
XX DR WPI; 2003-516153/49.
XX
XX PT A genealogical line diagnostic marker for polyglutamine disease, useful
XX in the diagnosis, prevention and/or treatment, comprises a polyglutamine
XX related gene and its encoded polypeptide.
XX
```


PS Claim 3; SEQ ID NO 11; 72pp; Japanese.

XX

CC The invention discloses polyglutamine disease related genes and their
 CC encoded polypeptides. Also claimed is a recombinant vector,
 CC transformants, preparation of the polynucleotides and resultant
 CC polypeptides, diagnostic methods and a kit. The genes and encoded
 CC polypeptides are useful in the diagnosis, prevention and treatment of
 CC genealogical polyglutamine disease. The sequence presented is an
 CC oligonucleotide which is based on one of theDNAs encoding a polypeptide
 CC of the invention.

XX

SQ Sequence 23 BP; 4 A; 12 C; 1 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 23; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1369 GCCTTCTCTCTACTACACCC 1391
 |||||||
 DB 1 GCCTTCTCTCTACTACACCC 23

RESULT 20

AD043735/c

ID ADO43735 standard; DNA; 27 BP.

XX

AC ADO43735;

XX

XX

DT 29-JUL-2004 (first entry)

XX

DE PCR primer used to amplify SEAP for cloning into pFerX8 and pFerX9.

XX

XX transfection; eukaryotic cell; eukaryotic locus;

KW ferritin heavy chain locus; PCR; primer; ss;

KW secreted alkaline phosphatase; SEAP.

XX

OS Synthetic.

XX

XX WO2004037982-A2.

PN

XX

PD 06-MAY-2004.

XX

XX

PF 22-OCT-2003; 2003WO-US033433.

XX

XX

PR 24-OCT-2002; 2002US-0421252P.

XX

PA (BIOJ) BIOGEN INC.

XX

PI Prentice H;

XX

XX WPI; 2004-357431/33.

DR

XX

XX New genetic vector comprising distal 5' flanking sequences and proximal
 PT 5' regulatory sequences, an insertion site and proximal 3' regulatory
 PT sequences, useful for transfecting and expressing a protein within
 PT eukaryotic cells.

XX

XX

PS Example 2; Page 23; 51pp; English.

XX

XX The specification describes a genetic vector for stable transfection and
 CC expression of a desired protein within eukaryotic cells. The vector
 CC comprises distal 5' flanking sequences of a eukaryotic locus, proximal 5'
 CC regulatory sequences of a eukaryotic locus, at least a first insertion
 CC site for a first heterologous coding sequence, and proximal 3' regulatory
 CC sequences effective for transcription termination of a eukaryotic locus.
 CC These sequences are operably joined in a 5' to 3' orientation, with
 CC optional linker sequences between adjacent sequences. The distal flanking
 CC sequences and proximal 5' regulatory sequences and the proximal 3'
 CC regulatory sequences are derived from a ferritin heavy chain locus, and
 CC have a total length of between 1000 and 10000 bases. The genetic vector
 CC is useful for stably transfecting and expressing a desired protein within
 CC eukaryotic cells. PCR primers ADO43734-ADO43735 were used to amplify
 CC secreted alkaline phosphatase (SEAP) for insertion into pFerX8 and

```
XX 18-DEC-2003 (first entry)
DT Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:536.
DE human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
PN 08-MAY-2003.
PD 01-NOV-2002; 2002WO-US035129.
PF 01-NOV-2001; 2001US-0334773P.
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 536; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
Db ||||| ||||| ||||| ||||| |||||
1 GCAGCAGCAGCAACAGCAGCAG 22

RESULT 23
ADC38189
ID ADC38189 standard; DNA; 25 BP.
XX
AC ADC38189;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:538.
XX human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
PN 08-MAY-2003.
PD 01-NOV-2002; 2002WO-US035129.
PF 01-NOV-2001; 2001US-0334773P.
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 536; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
Db ||||| ||||| ||||| ||||| |||||
3 GCAGCAGCAGCAACAGCAGCAG 24

RESULT 23
ADC38189
ID ADC38189 standard; DNA; 25 BP.
XX
AC ADC38189;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:538.
XX human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
PN 08-MAY-2003.
PD 01-NOV-2002; 2002WO-US035129.
PF 01-NOV-2001; 2001US-0334773P.
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 535; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
PR 01-NOV-2001; 2001US-0334773P.
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 538; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
Db ||||| ||||| ||||| ||||| |||||
1 GCAGCAGCAGCAACAGCAGCAG 22

RESULT 24
ADC38186
ID ADC38186 standard; DNA; 25 BP.
XX
AC ADC38186;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:535.
XX human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
PN 08-MAY-2003.
PD 01-NOV-2002; 2002WO-US035129.
PF 01-NOV-2001; 2001US-0334773P.
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
PA Shannon M, Phan T;
PI WPI; 2003-430501/40.
XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX Example 2; SEQ ID NO 535; 172pp; English.
PS The present invention describes the human angiominotin-like protein 1
XX (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.

XX SQ Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGCAG 1450

Db 4 GCAGCAGCAGCAACAGCAGCAG 25

RESULT 25

ADC38188

ID ADC38188 standard; DNA; 25 BP.

XX AC ADC38188;

XX DT 18-DEC-2003 (first entry)

XX DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:537.

XX KW human; angiominotin-like protein 1; AMLP1; cytosstatic; gene therapy;
XX KW AMLP1a; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX XX WO2003037931-A2.

XX PD 08-MAY-2003.

XX PF 01-NOV-2002; 2002WO-US035129.

XX PR 01-NOV-2001; 2001US-0334773P.

XX PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.

XX PI Shannon M, Phan T;

XX XX WPI; 2003-430501/40.

XX PT New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.

XX PS Example 2; SEQ ID NO 537; 172pp; English.

XX CC The present invention describes the human angiominotin-like protein 1
CC (AMLP1). human AMLP1 has cytosstatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.

XX SQ Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAGCAGCAG 1450

Db 2 GCAGCAGCAGCAACAGCAGCAG 23

RESULT 26

ABS71093/c

ID ABS71093 standard; DNA; 26 BP.

XX AC ABS71093;

XX DT 27-NOV-2002 (first entry)

XX DE Human GPCR ligand Bv8 cDNA PCR primer hBv8-F1.

XX KW G-protein coupled receptor; GPCR; ZAQ; human; ZAQ; ZAQ; rat; ZAQ1;
KW ZAQ1; ZAQ2; mouse; 15E receptor; m15E; GPR73; Bv8 protein;
KW digestive disorder; central nervous system disorder; CNS; diarrhoea;
KW bowel inflammation; constipation; food absorption disorder; nootropic;
KW Alzheimer's disease; Parkinson's disease; schizophrenia; laxative;
KW antiinflammatory; antidiarrhoeic; neuroleptic; neuroprotective; PCR;
KW primer; ss.

XX OS Homo sapiens.

XX PN WO200262944-A2.

XX PD 15-AUG-2002.

XX PF 01-FEB-2002; 2002WO-JP000852.

XX PR 02-FEB-2001; 2001JP-00026820.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
XX PI Hinuma S;

XX DR WPI; 2002-627537/67.

XX PT Screening of compounds modifying the binding of G-protein coupled
PT receptor protein ZAQ and related proteins to their ligands for use in
PT treatment and diagnosis of digestive disorders.

XX PS Example 3; Page 117; 197pp; Japanese.

XX CC The present invention relates to a screening method for compounds for
CC their ability to modify the binding of G-protein coupled receptor (GPCR)
CC protein ZAQ and related proteins (human ZAQ, human ZAQ, rat ZAQ1
CC (-ZQAQ1), ZQAQ2, human and mouse 15E (m15E) receptor, and mouse GPR73) to
CC their ligands (the mature form of human, mouse or rat Bv8 protein). The
CC receptor protein and ligand are contacted in the presence or absence of
CC the test compound. The compounds are useful in a drug composition for the
CC treatment, and prevention of digestive and central nervous system (CNS)
CC disorders, including bowel inflammation, diarrhoea, constipation, food
CC absorption disorders, Alzheimer's disease, Parkinson's disease and
CC schizophrenia. The present sequence represents a PCR primer used in the
CC examples of the present invention

XX SQ Sequence 26 BP; 1 A; 9 C; 6 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 69;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1407 AACAGCAGCAGCAGCAGCAGCAG 1432

Db 26 AACAGCAGCAGCAGCAGCAGCAGTAG 1

RESULT 27

ABZ30010/c

ID ABZ30010 standard; DNA; 26 BP.

XX AC ABZ30010;

XX DT 30-JAN-2003 (first entry)

XX XX


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PR 27-SEP-1999; 99US-0156135P.
XX 23-AUG-2000; 2000US-0227436P.
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX Krieg AM, Schetter C, Vollmer J;
XX WPI; 2001-273485/28.
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX Claim 101; Page 53; 338pp; English.
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 30
ABS78296/c
ID ABS78296 standard; DNA; 21 BP.
XX AC ABS78296;
XX 13-DEC-2002 (first entry)
XX Angiogenesis inhibitory oligonucleotide #780.
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX rubosis; Osler-Webber Syndrome; myocardial angiogenesis;
XX plaque neovascularisation; telangiectasia; haemophilic joint;
XX angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
XX scleroderma; hypertrophic scar.
XX Synthetic.
XX WO200253141-A2.
XX 11-JUL-2002.
XX 14-DEC-2001; 2001WO-US048458.
XX 14-DEC-2000; 2000US-0255534P.
XX (COLE-) COLEY PHARM GROUP INC.
XX Bratzler RL;

WPI; 2002-566690/60.
XX Inhibiting angiogenesis in a subject, involves administering at least one
XX antiangiogenic nucleic acid molecule to the subject.
XX Claim 2; Page 33; 276pp; English.
XX The invention relates to inhibiting angiogenesis in a subject, comprising
XX administering at least one antiangiogenic nucleic acid molecule. Also
XX included is a kit comprising a first container housing the antiangiogenic
XX nucleic acids, and instructions for administering them to a subject
XX having a condition characterised by unwanted angiogenesis. The method is
XX useful for inhibiting angiogenesis associated with solid tumour growth,
XX tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
XX diabetic retinopathy, retinopathy of prematurity, macular degeneration,
XX corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
XX rubosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
XX neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
XX wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
XX hypertrophic scars. The present sequence is an antiangiogenic nucleic
XX acid of the invention
XX
SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 31
ABL38849/c
ID ABL38849 standard; DNA; 21 BP.
XX AC ABL38849;
XX 16-APR-2002 (first entry)
XX Immunostimulatory nucleic acid SEQ ID NO: 240.
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..21
XX /tag= a
XX /mod_base= OTHER
XX /note= "phosphorothioate backbone"
XX WO200197843-A2.
XX 27-DEC-2001.
XX 22-JUN-2001; 2001WO-US020154.
XX 22-JUN-2000; 2000US-0213346P.
XX (IOWA ) UNIV IOWA RES FOUND.
XX Weiner G, Hartmann G;
XX WPI; 2002-154611/20.
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
XX administering immunostimulatory nucleic acids that induce expression of
XX cell surface antigens and antibodies to a subject having or at risk of
XX developing cancer.

```

XX Disclosure; Page 156; 312pp; English.

PS The present invention relates to methods for treating or preventing

CC cancer, involving immunostimulating to a subject having or at risk of

CC developing cancer immunostimulatory nucleic acids that induce expression

CC of cell surface antigens and antibodies. The methods are useful for

CC treating or preventing cancer such as basal cell carcinoma, bladder

CC cancer, bone cancer, brain and central nervous system (CNS) cancer,

CC breast cancer, cervical cancer, colon and rectum cancer, connective

CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx

CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-

CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian

CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin

CC cancer, stomach cancer, testicular cancer, and uterine cancer. The

CC present sequence is an immunostimulatory oligonucleotide described in the

CC exemplification of the invention

XX

SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429

Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 32

ABK10202/c

ID ABK10202 standard; DNA; 21 BP.

XX

AC ABK10202;

XX

DT 21-MAY-2002 (first entry)

XX

DE Double stranded DNA isolation (CTG)7 repeat sequence.

XX

KW Single stranded DNA isolation; DNA purification; CTG repeat; ds.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT repeat_region 1..21

FT /*tag= a

FT /rpt_type= TANDEM

FT repeat_unit 1..3

FT /*tag= b

FT /note= "CTG type repeat"

XX

PN WO200210182-A2.

XX

PD 07-FEB-2002.

XX

PF 18-JUL-2001; 2001WO-US022782.

XX

PR 02-AUG-2000; 2000US-0222686P.

XX

PA (PEKE) PE CORP NY.

XX

PI Chiesa C, Schroth GP, Egholm M;

XX

DR WPI; 2002-188719/24.

XX

XX Isolating one strand of double-stranded nucleic acid, by contacting

PT double stranded nucleic acid having first and second strands with

PT competitor oligo to form first strand-oligo complex and isolating the

PT complex.

XX

PS Disclosure; Page 12; 61pp; English.

XX

CC This invention relates to a novel method for isolating one strand of

CC double-stranded target nucleic acid. The method comprises contacting a

CC double stranded target DNA molecule with a competitor oligonucleotide

CC capable of hybridizing to the first strand of the double stranded

CC molecule. The method is performed under conditions in which the first

CC strand dissociates from the second and hybridizes with the competitor

CC oligonucleotide to form a heteroduplex. The method of the invention is

CC useful for separating a strand from a double-stranded target nucleic

CC acid. The method is rapid, efficient and specific for isolating a single

CC strand from a double-stranded nucleic acid. Because the method provides

CC easy and efficient recovery of the single strand from a double-stranded

CC advantageously used to purify a first strand from a double-stranded

CC nucleic acid that is a polymerase chain reaction (PCR) amplification

CC product from a pool of related or unrelated sequences in high yield for

CC subsequent use. The method also permits capture and/or recovery of the

CC first strand of a double-stranded target nucleic acid from biological

CC samples or other samples containing large molecule contaminants. The

CC present sequence represents a double stranded (CTG)7 DNA molecule used to

CC isolate double stranded DNA molecules in an example of a similar method

CC to that of the invention

XX

SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429

Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 33

ACH03118/c

ID ACH03118 standard; DNA; 21 BP.

XX

AC ACH03118;

XX

DT 25-SEP-2003 (first entry)

XX

DE Immunostimulatory nucleic acid #753.

XX

KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;

KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;

KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX

OS Synthetic.

XX

PN US2003050268-A1.

XX

PD 13-MAR-2003.

XX

PF 29-MAR-2002; 2002US-00112653.

XX

PR 29-MAR-2001; 2001US-0279642P.

XX

PA (KRIE/) KRIEG A M.

PA (BERG/) BERG D J.

XX

PI Krieg AM, Berg DJ;

XX

DR WPI; 2003-521815/49.

XX

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,

PT allergic contact dermatitis, latex dermatitis or inflammatory bowel

PT disease by administering an immunostimulatory nucleic acid.

XX

PS Disclosure; Page 29; 229pp; English.

XX

CC The invention describes a method of treating non-allergic inflammatory

CC disease comprising administering to a subject having or at risk of

CC developing a non-allergic inflammatory disease an immunostimulatory

CC nucleic acid for prevention or treatment of the disease. The method is

CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
 DB 21 CAGCAGCAGCAGCAGCAGCAG 1
 RESULT 34
 ADB37082/c
 ID ADB37082 standard; DNA; 21 BP.
 XX
 AC ADB37082;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #696.
 XX
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX
 OS Synthetic.
 XX
 PN US2003087848-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 02-FEB-2001; 2001US-00776479.
 XX
 PR 03-FEB-2000; 2000US-0179991P.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 XX
 DR WPI; 2003-657977/62.
 XX
 PT Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 PS Disclosure; Page 16; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.6%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
 DB 21 CAGCAGCAGCAGCAGCAGCAG 1
 RESULT 35
 ADC38190
 ID ADC38190 standard; DNA; 25 BP.

XX
 AC ADC38190;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:539.
 XX
 KW human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1a; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003037931-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 01-NOV-2002; 2002WO-US035129.
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX
 PI Shannon M, Phan T;
 XX
 DR WPI; 2003-430501/40.
 XX
 PT New isolated nucleic acid molecule encoding a human angiomotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 PS Example 2; SEQ ID NO 539; 172pp; English.
 XX
 CC The present invention describes the human angiomotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1a, which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.6%; Score 21; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1430 CAGCAGCAGCAGCAGCAGCAG 1450
 DB 1 CAGCAGCAGCAGCAGCAGCAG 21
 RESULT 36
 ADC38185
 ID ADC38185 standard; DNA; 25 BP.
 XX
 AC ADC38185;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:534.
 XX
 KW human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1a; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003037931-A2.
 XX
 PD 08-MAY-2003.
 XX

```

PF 01-NOV-2002; 2002WO-US035129.
XX
PR 01-NOV-2001; 2001IUS-0334773P.
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Shannon M, Phan T;
XX
DR WPI; 2003-430501/40.
XX
PT New isolated nucleic acid molecule encoding a human angiotensin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
PS Example 2; SEQ ID NO 534; 172pp; English.
XX
CC The present invention describes the human angiotensin-like protein 1
CC (AMLPL1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX
SQ Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.6%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 66; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;
QY 1429 GCAGCAGCAGCAACAGCAGCA 1449
DB 5 GCAGCAGCAGCAACAGCAGCA 25
RESULT 37
ABL61611
ID ABL61611 standard; DNA; 24 BP.
XX
AC ABL61611;
XX
DT 13-MAY-2002 (first entry)
XX
DE Porcine GPR8-related PCR primer #3.
XX
KW Anorectic; GPR8 ligand; central nervous system; obesity; pig;
KW appetite-stimulating agent; prolactin; porcine; PCR primer; ss.
XX
OS Sus scrofa.
XX
PN WO200198494-A1.
XX
PD 27-DEC-2001.
XX
PF 20-JUN-2001; 2001WO-JP005257.
XX
PR 21-JUN-2000; 2000JP-00191089.
PR 06-SEP-2000; 2000JP-00275013.
PR 13-APR-2001; 2001JP-00116000.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Harada M, Kurihara M, Kitada C, Asami T;
PI Mateumoto Y, Adachi Y, Watanabe T, Sugo T, Abe M;
XX
DR WPI; 2002-139790/18.
XX
Ligand to GPR8 and encoded gene, useful in developing receptor-binding
PT assay system, diagnosis and screening candidate compounds for central
PT nervous system function-regulating drugs to treat e.g. obesity.
XX
PS Example 30; Page 184; 221pp; Japanese.
XX
XX The present invention relates to GPR8 ligands. The ligands as well as
CC their precursor proteins and DNAs are useful in developing receptor-
CC binding assay systems, diagnosis and screening candidate compounds for
CC central nervous system function-regulating drugs as preventives or
CC remedies for obesity, appetite-stimulating agents and prolactin
CC production promoters or inhibitors. The present PCR primer was used to
CC illustrate the invention
XX
SQ Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1418 CAGCAGCAGCAGCAGCAGCA 1441
DB 1 CAGCGCAGCAGCAGCAGTAA 24
RESULT 38
ABK94601
ID ABK94601 standard; DNA; 24 BP.
XX
AC ABK94601;
XX
DT 28-AUG-2002 (first entry)
XX
DE G-protein-coupled receptor DNA PCR primer #17.
XX
KW Human; rat; primer; ss; G protein-coupled receptor; anorectic; anabolic;
KW obesity; appetite enhancement; prolactin production; eating disorder;
KW PCR; pig; mouse.
XX
OS Sus scrofa.
XX
PN WO200244368-A1.
XX
PD 06-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-JP010418.
XX
PR 30-NOV-2000; 2000JP-00364801.
PR 26-MAR-2001; 2001JP-00087482.
PR 15-MAY-2001; 2001JP-00145434.
PR 06-SEP-2001; 2001JP-00270838.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Terao Y, Shintani Y, Harada M, Shimomura Y, Mori M;
XX
DR WPI; 2002-471832/50.
XX
PT New rat and mouse brain-originated G protein-coupled receptor proteins
PT TGR26, useful in diagnosis and developing drugs for prevention or
PT treatment of obesity or an eating disorder.
XX
PS Example 11; Page 244; 312pp; Japanese.
XX
CC The invention relates to G protein-coupled receptor proteins and their
CC associated nucleic acids. The sequences are used in diagnosis of diseases
CC relating to function of the protein and can be used for treating obesity,
CC enhancing appetite or inhibiting prolactin production by administering
CC the compounds or their salts that can alter binding of the G protein-
CC coupled receptors. The proteins and encoded DNAs are useful in diagnosis
CC of and developing drugs for prevention or treatment of obesity and eating
CC disorders. This sequence represents a PCR primer used in production of
CC DNA encoding a G protein-coupled receptor protein
XX
SQ Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 62;

```



```

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1418 CAGCAGCAGCAGCAGCAGCA 1441
    |||||
Db 1 CAGCGGCAGCAGCAGCAGTAA 24

RESULT 39
ABX92931
ID ABX92931 standard; DNA; 24 BP.
XX AC ABX92931;
XX DE
DT 14-MAY-2003 (first entry)
XX DE
DE Screening method related primer #13.
KW G protein-coupled receptor; GPR7; primer; ss; anorectic; cibophobia;
KW anorexia; appetite loss; excessive appetite; obesity-related disorder;
KW adipocyte malignancy; obesity; excessive insulin; blood volume change;
KW thyroid disorder; paediatric obesity; upper body obesity;
KW dietary obesity; cardiac obesity; whole body adipocyte disorder.
XX OS Synthetic.
XX FN WO200293161-A1.
XX PD 21-NOV-2002.
XX PF 14-MAY-2002; 2002WO-JP004635.
XX PR 15-MAY-2001; 2001JP-00145411.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Mori M, Shimomura Y, Goto M;
XX DR WPI; 2003-129320/12.
XX PT Screening compounds that modify the binding of G-protein coupled receptor
XX GPR7 to its ligands for treatment of obesity and cibophobia.
XX PS Disclosure; Page 176; 222pp; Japanese.
XX SQ Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1418 CAGCAGCAGCAGCAGCAGCA 1441
    |||||
Db 1 CAGCGGCAGCAGCAGCAGTAA 24

RESULT 40
ABZ58841
ID ABZ58841 standard; DNA; 24 BP.
XX AC ABZ58841;
XX DE
DT 14-MAY-2003 (first entry)
XX DE
DE Screening method related primer #13.
KW G protein-coupled receptor; GPR7; primer; ss; anorectic; cibophobia;
KW anorexia; appetite loss; excessive appetite; obesity-related disorder;
KW adipocyte malignancy; obesity; excessive insulin; blood volume change;
KW thyroid disorder; paediatric obesity; upper body obesity;
KW dietary obesity; cardiac obesity; whole body adipocyte disorder.
XX OS Synthetic.
XX FN WO200293161-A1.
XX PD 21-NOV-2002.
XX PF 14-MAY-2002; 2002WO-JP004635.
XX PR 15-MAY-2001; 2001JP-00145411.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PI Mori M, Shimomura Y, Goto M;
XX DR WPI; 2003-129320/12.
XX PT Screening compounds that modify the binding of G-protein coupled receptor
XX GPR7 to its ligands for treatment of obesity and cibophobia.
XX PS Disclosure; Page 176; 222pp; Japanese.
XX SQ Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1418 CAGCAGCAGCAGCAGCAGCA 1441
    |||||
Db 1 CAGCGGCAGCAGCAGCAGTAA 24

RESULT 41
ADC51835
ID ADC51835 standard; DNA; 24 BP.
XX AC ADC51835;
XX DT 18-DEC-2003 (first entry)
XX DE GPR8 PCR primer, SEQ ID 46.
XX KW Body weight; GPR8L; brain; hyperphagia; obesity; anorectic; GPR8; PCR;
XX KW primer; ss.
XX OS Unidentified.
XX FN WO2003057236-A1.
XX PD 17-JUL-2003.

```

```

DT 28-APR-2003 (first entry)
XX DE Histidine tag encoding DNA.
XX KW Genetic information; glyph; molecular biology; histidine tag; ds.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT CDS 1..24
FT /*tag= a
XX PN WO200282264-A2.
XX PD 17-OCT-2002.
XX PF 05-APR-2002; 2002WO-US010825.
XX PR 06-APR-2001; 2001US-0282022P.
XX PA (SEED/) SEED B.
XX PI Seed B;
XX DR WPI; 2003-058588/05.
XX DR P-PSDB; ABP71241.
XX PT Displaying genetic information represented by set of glyphs, by receiving
XX entered command to display glyphs, identifying glyph assigned to the
XX entered command, and displaying identified glyph.
XX PS Example 3; Page 37; 50pp; English.
XX SQ The invention relates to displaying genetic information represented by a
    set of glyphs. The method involves receiving an entered command to
    display one of the set of glyphs, identifying the glyph of the set
    assigned to the entered command, and displaying the identified glyph,
    where the glyph is displayed at a location on a display screen with a
    cursor. Another method for displaying a double-stranded codon and an
    amino acid encoded by the codon is also provided. The methods provide
    simple and quick way for displaying and genetic information that has been
    modified by a standard molecular biology technique. The present sequence
    represents a DNA fragment encoding a histidine tag
    Sequence 24 BP; 8 A; 12 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 977 CAGCAGCAGCAGCAGCAGCAGCAG 1000
    |||||
Db 1 CAGCAGCAGCAGCAGCAGCAGCAG 24

RESULT 41
ADC51835
ID ADC51835 standard; DNA; 24 BP.
XX AC ADC51835;
XX DT 18-DEC-2003 (first entry)
XX DE GPR8 PCR primer, SEQ ID 46.
XX KW Body weight; GPR8L; brain; hyperphagia; obesity; anorectic; GPR8; PCR;
XX KW primer; ss.
XX OS Unidentified.
XX FN WO2003057236-A1.
XX PD 17-JUL-2003.

```

```
XX 27-DEC-2002; 2002WO-JP013781.
XX
XX
XX 28-DEC-2001; 2001JP-00403260.
PR
XX 28-MAR-2002; 2002JP-00093096.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX
XX Mateumoto H, Noguchi J, Harada M, Mori M;
PI
XX WPI; 2003-569538/53.
XX
XX Composition comprising peptide of brain origin binding to orphan G-
PT
PT protein coupled receptor GPR8 for treatment and prevention of obesity and
PT hyperphagia.
XX
XX Example 30; SEQ ID NO 46; 277pp; Japanese.
XX
XX The present invention relates to novel compositions for inhibiting body
CC weight gain, for lowering body weight, for inhibiting fat weight gain,
CC and for suppressing appetite, which contain as active component a peptide
CC ligand (GPR8L, ADC51805) of brain origin. The compositions can be used
CC for treatment and prevention of hyperphagia and obesity (including
CC malignant mastocytosis, exogenous obesity, hyperinsulinemic obesity,
CC hyperplasmic obesity, hypophyseal obesity, hypoplasmic obesity,
CC hypothyroid obesity, hypothalamic obesity, symptomatic obesity, infant
CC obesity, upper body obesity, alimentary obesity, hypogonadal obesity,
CC systemic mastocytosis, simple obesity and central obesity). The present
CC sequence was used to illustrate the invention.
XX
XX Sequence 24 BP; 8 A; 7 C; 8 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 62;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1418 CAGCAGCAGCAGCAGCAGCAGCA 1441
DB 1 CAGCGGCAGCAGCAGCAGCAGTAA 24
|||||
|||||

RESULT 42
ID ABK88725/c
XX
XX ABK88725 standard; DNA; 22 BP.
AC
XX
XX 07-OCT-2002 (first entry)
DT
XX
XX Human Pur alpha anti-sense strand, phosphorothioate oligonucleotide #4.
DE
XX
XX Human; apoptotic cell death; proteinaceous transcription factor;
KW regulation of gene transcription; apoptosis; p53; CD95; TRA;
KW transcriptional regulator of apoptosis; Y-box family; YB-1; cancer;
KW tumour cell; embryonic cell; nervous system; intracellular pathogen;
KW DNA-damaging agent; retroviral infection; neurodegenerative disorder;
KW immune system dysfunction; anti-tumour; cytostatic; Pur alpha;
KW phosphorothioate; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..22
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate internucleotide linkages"
XX
XX WO200244363-A1.
XX
XX 06-JUN-2002.
PD
XX
XX 28-NOV-2001; 2001WO-NZ000287.
XX
XX
XX 28-NOV-2000; 2000US-00724809.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Lasham A, Watson JD;
PI
XX WPI; 2002-557540/59.
XX
XX Modulating p53-mediated apoptotic cell death in a population of cells, by
PT modulating the amount of a transcriptional regulator of apoptosis
PT available to bind to a target polynucleotide in the cells.
XX
XX Example 2; Page 57; 62pp; English.
XX
XX The present invention relates to methods for modulating apoptotic cell
CC death using proteinaceous transcription factors that regulate the
CC transcription of genes encoding proteins involved in apoptosis (e.g. CD95
CC and p53). The methods involve modulating the amount of a transcriptional
CC regulator of apoptosis (TRA) available to bind to a target polynucleotide
CC in the cells, where TRA is a member of the Y-box nucleic acid binding
CC family of polypeptides (e.g. YB-1). The methods of the invention are
CC useful for modulating apoptotic cell death in a population of cells,
CC where the cells are selected from tumour cells, cells of the immune
CC system, embryonic cells, cells of the nervous system, or cells infected
CC with intracellular pathogens. The methods are also useful for increasing
CC the sensitivity of tumour cells to a DNA-damaging agent, and for
CC increasing sensitivity to apoptosis in a population of cells harbouring
CC intracellular pathogens. The methods are useful for screening an
CC apoptosis modulatory agent that modulates the binding of TRA. The methods
CC for regulating apoptosis can be used therapeutically and prophylactically
CC for various disorders such as cancer, viral and retroviral infections,
CC neurodegenerative disorders, and immune system dysfunction. The present
CC sequence represents a phosphorothioate oligonucleotide to the anti-sense
CC strand of human Pur alpha
XX
XX Sequence 22 BP; 0 A; 5 C; 9 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 56;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1397 CAACAGCAGCAGCAGCAGCAGC 1418
DB 22 CACCAGCAGCAGCAGCAGCAGC 1
|||||
|||||

RESULT 43
ID AAD37201 standard; DNA; 20 BP.
XX
XX AAD37201;
AC
XX
XX 21-AUG-2002 (first entry)
DT
XX
XX Human MEKK4 antisense oligonucleotide, ISIS #123136.
DE
XX
XX Human; MEKK4 modulation; mitogen-activated protein kinase kinase 4; MTK1;
KW MAP3K4; MAP three kinase 1; MAP/ERK kinase kinase 4; MAPKKK4; cytostatic;
KW prophylaxis; immunological; hyperproliferative disorder; cancer; therapy;
KW antisense; inflammatory; phosphorothioate backbone; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl nucleotides"
XX
```


ID AB231489 standard; DNA; 20 BP.
AC AB231489;
XX
DT 30-JAN-2003 (first entry)
XX
DE Candida albicans GRACE strain PCR primer SEQ ID NO 5708.
XX
KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
XX
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-0259128P.
PR 20-FEB-2001; 2001US-0079202A.
PR 22-AUG-2001; 2001US-0314050P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX
DR WPI; 2002-566694/60.
XX
PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
PS Claim 36; SEQ ID NO 5708; 167pp + Sequence Listing; English.
XX
CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office
XX
SQ Sequence 20 BP; 0 A; 5 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1555 ACAACAGCAGCAGCAGCAGC 1574
|||||
Db 20 ACAACAGCAGCAGCAGCAGC 1
|||||

RESULT 46

AAQ14196
ID AAQ14196 standard; DNA; 21 BP.
XX
AC AAQ14196;
XX
DT 02-JAN-1992 (first entry)
XX
DE Oligonucleotide probe incorporating disulphide linker.
XX
KW ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 8
FT /*tag= a
FT /note= "n = O2-P-O-CH2-CH2-O-CH2-CH2-S-S-CH2-CH2-O- CH2-
FT CH2-O-P-O3"
XX
PN WO9114696-A.
XX
PD 03-OCT-1991.
XX
PF 29-MAR-1990; 90US-00502361.
XX
PR 29-MAR-1990; 90US-00502361.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Latham JA, Lin KY, Matteucci M;
XX
DR WPI; 1991-310523/42.
XX
PT New oligo:nucleotide- transport agent di:sulphide conjugate(s) - for
PT inhibiting nucleotide expression in therapy and diagnosis of endogenous
PT nucleotide sequences in cells.
XX
PS Example; Page 37; 67pp; English.
XX
CC The oligonucleotide has a disulphide linker incorporated into the probe
CC which acts as a hybridisation-triggered crosslinking agent. This will
CC permit novel diagnostic assay modifications such as the use of
CC crosslinker to increase probe discrimination and incorporation of a
CC denaturing wash step to reduce background. Also carrying out
CC hybridisation and crosslinking at or near the melting temperature of the
CC hybrid DNA will reduce secondary structure in the target DNA and increase
CC probe specificity. See also AAQ14195
XX
SQ Sequence 21 BP; 6 A; 7 C; 7 G; 0 T; 0 U; 1 Other;

Query Match 0.5%; Score 20; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1429
|||||
Db 1 CAGCAGCAGCAGCAGCAGCAG 21
|||||

RESULT 47

ADC38191
ID ADC38191 standard; DNA; 25 BP.
XX
AC ADC38191;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:540.
XX
KW human; angiotensin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX
OS Synthetic.


```
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGCAG 1432
DB 1 AGCAGCAGCAGCAGCAGCAGGAG 23

RESULT 50
ABZ81769
ID ABZ81769 standard; DNA; 21 BP.
XX AC
XX ABZ81769;
XX
DT 11-JUN-2003 (first entry)
XX
DE Huntington's disease gene mutated exon 1 region.
XX
KW Huntington's disease; nontropic; anticonvulsant; huntingtin; human;
KW gene therapy; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation replace(10,C)
FT /*tag= a
XX
PN WO2003013437-A2.
XX
PD 20-FEB-2003.
XX
PF 07-AUG-2002; 2002WO-US025352.
XX
PR 07-AUG-2001; 2001US-0310757P.
PR 08-AUG-2001; 2001US-0310770P.
PR 08-AUG-2001; 2001US-0310889P.
PR 04-DEC-2001; 2001US-0337219P.
XX
XX (UYDE ) UNIV DELAWARE.
XX
XX Kmiec BB, Parekh-Olmedo H;
XX WPI; 2003-256478/25.
XX
XX New single stranded oligonucleotides comprising a DNA domain having at
XX least one mismatch with respect to the genetic sequence of the
XX Huntington's disease gene to be altered, useful for treating or
XX preventing Huntington's disease.
XX
XX Example 1; Fig 6b; 133pp; English.
XX
XX The present sequence is that of a portion of a mutated glutamine (CAG)
XX triplet repeat region of exon 1 of the human Huntington's disease (HD)
XX gene (see also ABZ81760). The triplet repeat region (see ABZ81767) is
XX mutated following treatment with an RNA/DNA chimeric oligonucleotide (see
XX CC ABZ81768) that causes a CAG (Gln) to TAG (stop) gene alteration in the HD
XX exon 1 repeats due to sliding of the repeat region, a phenomenon that can
XX occur with the methods of this invention. The RNA/DNA chimeric
XX oligonucleotide is an example of oligonucleotides of the invention for
XX targeted alteration of the HD gene. Such oligonucleotides can be used for
XX the treatment or prevention of HD
XX
XX Sequence 21 BP; 7 A; 6 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 69;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
DB 1 CAGCAGCAGTAGCAGCAGCAG 21

RESULT 51
AAF76808
ID AAF76808 standard; DNA; 22 BP.
XX AC
XX AAF76808;
XX
DT 14-MAY-2001 (first entry)
XX
DE Codon-optimised HPV6 E2 fragment 6PM.
XX
KW Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1; E2; E7; E1;
KW antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX
XX Human papillomavirus.
OS Synthetic.
XX
PN WO200114416-A2.
XX
PD 01-MAR-2001.
XX
PF 21-AUG-2000; 2000WO-US022932.
XX
PR 25-AUG-1999; 99US-0150728P.
PR 07-JUN-2000; 2000US-0210143P.
XX
XX (MERI ) MERCK & CO INC.
XX
XX Neepser MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
XX WPI; 2001-218428/22.
XX
XX Novel synthetic polynucleotide encoding human papillomavirus (HPV)
XX protein or mutated HPV protein useful as anti-HPV vaccines, comprises
XX optimized-codons for expression of the viral proteins in human host
XX cells.
XX
XX Example 6; Fig 23; 119pp; English.
XX
XX The present sequence is an oligomer which was used in the assembly of one
XX of a number of synthetic polynucleotides that encode a human
XX papillomavirus (HPV) protein, or a mutated form of a HPV protein. The
XX mutated HPV proteins have reduced protein function as compared to wild
XX type proteins but maintain immunogenicity. The proteins comprise codons
XX for optimised expression in humans. The polynucleotides are useful as a
XX vaccine which provides effective immunoprophylaxis against papillomavirus
XX infection through stimulation of neutralising antibody and cell-mediated
XX immunity
XX
XX Sequence 22 BP; 9 A; 9 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1497 CTCAACACAGCAGCAGCAGCAGC 1517
DB 2 CGCAACACAGCAGCAGCAGCAGC 22

RESULT 52
ABX03797/C
ID ABX03797 standard; cDNA; 24 BP.
XX AC
XX ABX03797;
XX
DT 09-JAN-2003 (first entry)
XX
DE DNA encoding secreted protein signal peptide sequence #6.
XX
KW Differential display method; leucine-rich motif; transmembrane protein;
KW secreted protein; secreted protein signal peptide; ss.
XX
XX Unidentified.
```

```

XX PN WO200259259-A2.
XX PD 01-AUG-2002.
XX PF 23-JAN-2002; 2002WO-IL000071.
XX PR 23-JAN-2001; 2001US-0263158P.
XX PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX PI Wreschner DH;
XX XX WPI; 2002-599769/64.
XX DR P-PSDB; ABG98326.
XX PT Differential display method for identifying secreted or transmembrane
XX PT protein, comprises contacting a DNA with a first primer that hybridizes
XX PT to a sequence coding for a leucine-rich motif and with a second
XX PT oligonucleotide primer.
XX PS Disclosure; Fig 2; 37pp; English.
XX CC The invention relates to a differential display comprising contacting
XX CC cDNA with a first primer that hybridises to an oligonucleic sequence
XX CC coding for a leucine-rich motif, and with a second oligonucleotide primer
XX CC to form a cDNA-hybrid molecule. The method comprises obtaining mRNA from
XX CC at least 2 samples, synthesising cDNA from the RNA of each sample,
XX CC contacting the cDNA with a first primer that hybridises to an
XX CC oligonucleic sequence coding for a leucine-rich motif, and with a second
XX CC oligonucleotide primer to form cDNA-hybrid molecules, amplifying the cDNA
XX CC -hybrid molecules, detecting amplified products and comparing the
XX CC amplified products from each sample to identify distinctive amplified
XX CC products coding for at least one secreted or transmembrane protein. The
XX CC method is useful for discovering novel secreted and/or transmembrane
XX CC proteins which are important for cell processes and play an important
XX CC role in determining its phenotype, and which act as mediators for the
XX CC transfer of signals from external environment into the cell itself, thus
XX CC modulating gene expression. Sequences ABX03792-ABX03869 represent DNA
XX CC encoding secreted protein signal peptide sequences
XX SQ Sequence 24 BP; 0 A; 9 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1403 CAGCAGCAGCAGCAGCAG 1423
DB 21 CAGCAGCAGCAGCAGCAGCG 1
RESULT 53
ADN06499
ID ADN06499 standard; DNA; 24 BP.
XX AC ADN06499;
XX DT 15-JUL-2004 (first entry)
XX DE Human FLAP related microsatellite marker SEQ ID NO:147.
XX KW leukotriene synthesis inhibitor; myocardial infarction;
XX KW acute coronary syndrome; antiatherosclerotic; cardiant; antianginal;
XX KW leukotriene biosynthesis inhibitor; leukotriene receptor antagonist;
XX KW 5-lipoxygenase activating protein; FLAP; human; chromosome 13;
XX KW chromosome 13q12; polymorphism; 5-lipoxygenase gene promoter;
XX KW 5-LO gene promoter; diabetes; hypertension; hypercholesterolaemia;
XX KW obesity; inflammatory marker; low density lipoprotein; cholesterol;
XX KW high density lipoprotein; angina; atherosclerosis; microsatellite marker;
XX KW ss.
XX OS Homo sapiens.
OS Synthetic.
XX PN WO2004035741-A2.
XX PD 29-APR-2004.
XX PF 16-OCT-2003; 2003WO-US032556.
XX PR 17-OCT-2002; 2002US-0419433P.
XX PR 21-FEB-2003; 2003US-0449331P.
XX PA (DECO-) DECODE GENETICS EHF.
XX PI Helgadottir A, Gurney ME, Gulcher JR;
XX XX WPI; 2004-357211/33.
XX DR Use of leukotriene synthesis inhibitor for manufacture of a medicament
XX PT for treatment of myocardial infarction or susceptibility to myocardial
XX PT infarction in individual.
XX PS Disclosure; SEQ ID NO 147; 306pp; English.
XX CC The present invention describes using a leukotriene synthesis inhibitor
XX CC (I) for the manufacture of a medicament for the treatment of myocardial
XX CC infarction or susceptibility to myocardial infarction in an individual.
XX CC Also described is a method (M1) for the treatment of acute coronary
XX CC syndrome (ACS) in an individual comprising administering (I). (I) has
XX CC antiatherosclerotic, cardiant and antianginal activities, and can be used
XX CC as a leukotriene biosynthesis inhibitor, and a leukotriene receptor
XX CC antagonist. (I) can be used for the manufacture of a medicament for the
XX CC treatment of myocardial infarction or susceptibility to myocardial
XX CC infarction in an individual who has at least one risk factor chosen from
XX CC an at-risk haplotype for myocardial infarction, an at-risk haplotype in
XX CC the 5-lipoxygenase activating protein (FLAP) gene, a polymorphism in a
XX CC FLAP nucleic acid and an at-risk polymorphism in the 5-lipoxygenase (5-
XX CC LO) gene promoter; in an individual who has at least one risk factor
XX CC chosen from diabetes, hypertension, hypercholesterolaemia, elevated
XX CC lip(a), obesity, past or current smoker; in an individual having elevated
XX CC inflammatory marker chosen from C-reactive protein (CRP), serum amyloid
XX CC A, fibrinogen, leukotriene, leukotriene metabolite, interleukin-6, tissue
XX CC necrosis factor-alpha, soluble vascular cell adhesion molecule (sVCAM),
XX CC soluble intervascular adhesion molecule (sICAM), E-selectin, matrix
XX CC metalloproteinase type-1, matrix metalloproteinase type-2, matrix
XX CC metalloproteinase type-3 and matrix metalloproteinase type-9; in an
XX CC individual having increased low density lipoprotein (LDL) cholesterol
XX CC and/or decreased high density lipoprotein (HDL) cholesterol; in an
XX CC individual having increased leukotriene synthesis; in an individual
XX CC having previous myocardial infarction or acute coronary syndrome (ACS)
XX CC event, stable angina; or in an individual who has atherosclerosis or who
XX CC requires treatment to restore blood flow in arteries. (M1) is useful for
XX CC treating an individual suffering from acute coronary syndrome chosen from
XX CC unstable angina, non-ST-elevation myocardial infarction (NSTEMI) and ST-
XX CC elevation myocardial infarction (STEMI). The human FLAP gene is located
XX CC on chromosome 13, more specifically to 13q12. The present sequence
XX CC represents a microsatellite marker used in the exemplification of the
XX CC present invention.
XX SQ Sequence 24 BP; 16 A; 7 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 0.5%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1570 GCAGCAACACACACAGCAGCAACA 1593
DB 1 GAAACAACACACACACACACACA 24
RESULT 54
ADN94518
ID ADN94518 standard; DNA; 24 BP.
XX XX

```

```

AC ADS94518;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human 5-lipoxygenase activating protein (FLAP) gene PCR primer #144.
XX
XX human; 5-lipoxygenase activating protein; FLAP; chromosome 13q12;
KW single nucleotide polymorphism; SNP; myocardial infarction; PCR; primer;
KW microsatellite marker; ss.
XX
XX Homo sapiens.
OS
XX WO2004035746-A2.
FN
XX
XX 29-APR-2004.
PD
XX
XX 16-OCT-2003; 2003WO-US032805.
PF
XX
XX 17-OCT-2002; 2002US-0419432P.
PR
XX
XX (DECO-) DECODE GENETICS EHF.
PA
XX Helgadottir A, Gulcher JR, Manolescu A;
PI
XX
XX WPI; 2004-348442/32.
DR
XX
XX Novel FLAP (5-lipoxygenase activating protein) nucleic acid useful for
PT diagnosing myocardial infarction and for identifying agent that is useful
PT for treating myocardial infarction.
XX
XX Example; SEQ ID NO 147; 230pp; English.
PS
XX
XX The invention comprises nucleic acid sequences of the human 5-
CC lipoxygenase activating protein (FLAP) gene - present on chromosome
CC 13q12. In particular the invention relates to polymorphisms identified
CC within this gene. The DNA sequences of the invention are useful for
CC diagnosing susceptibility to myocardial infarction and identifying agents
CC that alter expression of FLAP. The present DNA sequence represents a PCR
CC primer that is used to amplify a microsatellite marker from the human
CC FLAP gene.
XX
XX Sequence 24 BP; 16 A; 7 C; 1 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1570 GCAGCAACACACAGCAACCAACA 1593
DB 1 GAAACACACACACACACACCAACA 24
RESULT 55
AAK97150/c
ID AAK97150 standard; DNA; 20 BP.
XX
XX AAK97150;
AC
XX
XX 13-SEP-1999 (first entry)
DT
XX
XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
DE
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
XX Synthetic.
OS
XX Chlamydia pneumoniae.
OS
XX WO99271105-A2.
PN
XX
XX 03-JUN-1999.
XX
XX

```

```

PF 20-NOV-1998; 98WO-IB001890.
XX
XX 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
XX (GEST ) GENSET.
PA
XX Griffais R;
PI
XX
XX WPI; 1999-357842/30.
DR
XX
XX Genome sequence of Chlamydia pneumoniae.
PT
XX
XX Page 1881; Disclosure; 1912pp; English.
PS
XX
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
XX Sequence 20 BP; 1 A; 3 C; 7 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1454 CAGCAACAGCAACAGCAAC 1472
DB 19 CAGCAACAGCAACAGCAAC 1
RESULT 56
AAF76807/c
ID AAF76807 standard; DNA; 23 BP.
XX
XX AAF76807;
AC
XX
XX 14-MAY-2001 (first entry)
DT
XX
XX Codon-optimised HPV6 E2 fragment 6PL.
DE
XX
XX Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1; E2; E7; E1;
KW antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX
XX Human papillomavirus.
OS
XX Synthetic.
OS
XX WO200114416-A2.
PN
XX
XX C1-MAR-2001.
PD
XX
XX 21-AUG-2000; 2000WO-US022932.
PF
XX
XX 25-AUG-1999; 99US-0150728P.
PR C7-JUN-2000; 2000US-0210143P.
XX
XX (MERI ) MERCK & CO INC.
PA
XX
XX Neoper MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
PI
XX WPI; 2001-218428/22.
DR
XX
XX Novel synthetic polynucleotide encoding human papillomavirus (HPV)
PT protein or mutated HPV protein useful as anti-HPV vaccines, comprises
PT optimized-codons for expression of the viral proteins in human host
PT cells.
XX

```


XX Example 6; Fig 23; 119pp; English.

XX The present sequence is an oligomer which was used in the assembly of one

CC of a number of synthetic polynucleotides that encode a human

CC papillomavirus (HPV) protein, or a mutated form of a HPV protein. The

CC mutated HPV proteins have reduced protein function as compared to wild

CC type proteins but maintain immunogenicity. The proteins comprise codons

CC for optimised expression in humans. The polynucleotides are useful as a

CC vaccine which provides effective immunoprophylaxis against papillomavirus

CC infection through stimulation of neutralising antibody and cell-mediated

CC immunity

XX

SQ Sequence 23 BP; 0 A; 5 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 19; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1499 CAACAACAGCAACAGCAGC 1517

Db 22 CAACAACAGCAACAGCAGC 4

RESULT 57

AAA54149/c

ID AAA54149 standard; cDNA; 22 BP.

XX

AC AAA54149;

AC

DT 08-FEB-2001 (first entry)

XX

XX Antisense oligonucleotide (WH6) directed against preproendothelin-1.

DE

XX

XX Preproendothelin; endothelin; antisense oligonucleotide; therapy;

KW treatment; inhibition; synthesis; lung disease; pulmonary hypertension;

KW obliterative bronchiolitis; asthma; obstructive pulmonary disease; human;

KW ss.

XX

OS Homo sapiens.

XX

XX WO200055314-A2.

XX

PD 21-SEP-2000.

XX

PF 17-MAR-2000; 2000WO-US040074.

XX

XX

PR 18-MAR-1999; 99US-0125000P.

XX

PA (UNTH-) UNITED THERAPEUTICS CORP.

XX

XX Corder R, Smith APL, Higenbottam TW, Rothblatt M, Vane SJ;

PI Lees DDM;

PI

XX WPI; 2000-647072/62.

XX

XX Antisense oligonucleotides complementary to human preproendothelin-1 mRNA

PT and capable of inhibiting synthesis of preproendothelin-1 useful for

PT treating lung diseases such as pulmonary hypertension and asthma.

XX

PS Claim 26; Fig 19; 54pp; English.

XX

XX Antisense oligonucleotides directed against human preproendothelin-1 can

CC be used to inhibit the synthesis of preproendothelin-1 and endothelin-1.

CC Combinations of active antisense oligonucleotides achieve a greater

CC effect than individual antisense oligonucleotides. The antisense

CC oligonucleotides have applications for treating lung disease such as

CC pulmonary hypertension, obliterative bronchiolitis, asthma or chronic

CC obstructive pulmonary disease, they are also useful for treating diseases

CC caused or aggravated by excess production of endothelin. The antisense

CC oligonucleotides are described in GENESQ records AAA54136-A54157 and

CC AAA54192-A54205. This antisense oligonucleotide is designated WH6 and

CC corresponds to nucleotides 939-960 of preproendothelin-1

XX SQ Sequence 22 BP; 5 A; 4 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.8; DB 1; Length 22;

Best Local Similarity 90.9%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 807 TGGCCAACTCTGCCCTCTCCAC 828

Db 22 TGGCCGACTCTGCACTCTCCAC 1

RESULT 58

AAC85525/c

ID AAC85525 standard; cDNA; 23 BP.

XX

AC AAC85525;

XX

DT 16-MAY-2001 (first entry)

XX

DE Primer ZC21.076.

XX

KW Splice variant; zdtint2; mammalian adhesion protease peptide; MAPP;

KW testis; ovary; prostate; small intestine; colon; stomach; thyroid;

KW spinal cord; lymph node; trachea; heart; wound healing; apoptosis;

KW neurogenesis; tumor proliferation; ischemia reperfusion; inflammation;

KW immunologic recognition; gamete maturation; platelet aggregation;

KW infarction; brain; cancer; Alzheimer's disease; multiple sclerosis;

KW congestive heart failure; PCR; polymerase chain reaction; amplify;

KW primer; ss.

XX

OS Synthetic.

XX

PN WO200109293-A2.

XX

PD 08-FEB-2001.

XX

PF 02-AUG-2000; 2000WO-US021085.

XX

PR 03-AUG-1999; 99US-00368070.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

XX Sheppard PO, Baindur N, Bishop PD;

XX

XX WPI; 2001-202662/20.

XX

XX Mammalian adhesion protease peptides useful for delivery of therapeutic

PT agents, for identifying agonists and antagonists and treating disorders

PT of brain, heart tissue and platelet aggregation.

XX

PS Example 1; Page 105; 106pp; English.

XX

CC This primer sequence was used to clone the full length cDNA encoding

CC mammalian adhesion protease peptide (MAPP). Analysis of tissue

CC distribution of MAPP cDNA showed a transcript of approx. 4.4kb with a

CC strong signal in testes, ovary, prostate, small intestine and colon, and

CC a fainter signal in stomach, thyroid, spinal cord, lymph node and

CC trachea. Also there were two transcripts, approx. 4kb and 4.4kb, both

CC showing medium strength signal in heart tissue

XX

SQ Sequence 23 BP; 2 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.8; DB 1; Length 23;

Best Local Similarity 90.9%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1421 CAGCAGCAGCAGCAGCAGCAAC 1442

Db 23 CAGTAGTAGCAGCAGCAGCAAC 2

RESULT 59

```
ABV72153/c
ID ABV72153 standard; DNA; 23 BP.
XX
AC ABV72153;
XX
DT 05-DEC-2002 (first entry)
XX
DE PCR primer ZC21076 used to amplify cDNA encoding zdint2.
XX
KW Human; isoform; zdint2; mammalian adhesion protease peptide; MAPP;
KW disintegrin-like family member; disintegrin protease; DP; PCR; primer;
KW anticoagulation; fertilization; muscle fusion; neurogenesis; ss.
XX
OS Homo sapiens.
XX
PN US6420154-B1.
XX
PD 16-JUL-2002.
XX
PF 02-AUG-2000; 2000US-00632098.
XX
PR 03-AUG-1999; 99US-0146968P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sheppard PO, Baidur N, Bishop PD;
XX
DR WPI; 2002-626081/67.
XX
PT New Isolated Mammalian Adhesion Protease Peptides (zdint2), which have
PT homology to disintegrin-like family members, useful for preventing,
PT diagnosing and treating fertility, muscular and neurogenic disorders.
XX
PS Example 1; Col 81-82; 42pp; English.
XX
CC PCR primers ABV72153-54 were used to amplify cDNA encoding human zdint2.
CC zdint2 is a mammalian adhesion protease peptide (MAPP), and has homology
CC to disintegrin-like family members (ADAMs, SVMPs and MDCs), referred to
CC as disintegrin proteases (Dps). MAPPs have been found to be involved in
CC anticoagulation, fertilization, muscle fusion, and neurogenesis. Zdint2
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate MAPP expression. The proteins may be
CC administered to treat disorders associated with decreased expression by
CC rectifying mutations or deletions in a patient's genome that affect the
CC activity of MAPP by expressing inactive proteins or to supplement the
CC patients own production of MAPPs
XX
SQ Sequence 23 BP; 2 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 0.5%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1421 CAGCAGCAGCAGCAGCAGCAAC 1442
DB 23 CAGTAGTAGCAGCAGCAGCAAC 2
RESULT 60
AAV52748/c
ID AAV52748 standard; DNA; 20 BP.
XX
AC AAV52748;
XX
DT 02-NOV-1998 (first entry)
XX
DE Angiotensin-converting enzyme PCR 5'-primer SEQ ID NO:1.
XX
KW Angiotensin-converting enzyme; ACE; human; heart; PCR primer; detection;
KW screening; cardiovascular disease; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN US5800990-A.
XX
PD 01-SEP-1998.
XX
PF 06-DEC-1995; 95US-00568271.
XX
PR 06-DEC-1995; 95US-00568271.
XX
PA (COLS ) UNIV COLORADO.
XX
PI Perryman MB, Raynolds MV;
XX
DR WPI; 1998-494763/42.
XX
PT Detecting mutation(s) in angiotensin-converting enzyme gene - to assess
PT cardiovascular disease risk.
XX
PS Example 1; Col 9; 12pp; English.
XX

ABV72153/c
ID ABV72153 standard; DNA; 23 BP.
XX
AC ABV72153;
XX
DT 05-DEC-2002 (first entry)
XX
DE PCR primer ZC21076 used to amplify cDNA encoding zdint2.
XX
KW Human; isoform; zdint2; mammalian adhesion protease peptide; MAPP;
KW disintegrin-like family member; disintegrin protease; DP; PCR; primer;
KW anticoagulation; fertilization; muscle fusion; neurogenesis; ss.
XX
OS Homo sapiens.
XX
PN US6420154-B1.
XX
PD 16-JUL-2002.
XX
PF 02-AUG-2000; 2000US-00632098.
XX
PR 03-AUG-1999; 99US-0146968P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Sheppard PO, Baidur N, Bishop PD;
XX
DR WPI; 2002-626081/67.
XX
PT New Isolated Mammalian Adhesion Protease Peptides (zdint2), which have
PT homology to disintegrin-like family members, useful for preventing,
PT diagnosing and treating fertility, muscular and neurogenic disorders.
XX
PS Example 1; Col 81-82; 42pp; English.
XX
CC PCR primers ABV72153-54 were used to amplify cDNA encoding human zdint2.
CC zdint2 is a mammalian adhesion protease peptide (MAPP), and has homology
CC to disintegrin-like family members (ADAMs, SVMPs and MDCs), referred to
CC as disintegrin proteases (Dps). MAPPs have been found to be involved in
CC anticoagulation, fertilization, muscle fusion, and neurogenesis. Zdint2
CC may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate MAPP expression. The proteins may be
CC administered to treat disorders associated with decreased expression by
CC rectifying mutations or deletions in a patient's genome that affect the
CC activity of MAPP by expressing inactive proteins or to supplement the
CC patients own production of MAPPs
XX
SQ Sequence 23 BP; 2 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 0.5%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1421 CAGCAGCAGCAGCAGCAGCAAC 1442
DB 23 CAGTAGTAGCAGCAGCAGCAAC 2
RESULT 60
ADH62525/c
ID ADH62525 standard; DNA; 23 BP.
XX
AC ADH62525;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human MAPP DNA specific PCR primer, ZC21076.
XX
KW MAPP; disintegrin protease; diagnosis; tumour; gene therapy; PCR; primer;
KW mammalian adhesion protease peptide; ss.
XX
OS Homo sapiens.
XX
```

CC The following methods have been developed for detecting small deletions,
 CC insertions or point mutations in an angiotensin-converting enzyme (ACE)
 CC gene of a human patient: (1) a method comprising: (a) isolating an ACE
 CC genomic DNA sequence from the patient, where the sequence spans intron
 CC 25, using oligonucleotide primers in the 3' region of exon 25 and the 5',
 CC region of exon 26; (b) hybridising the genomic sequence with a detectable
 CC probe specific for the corresponding sequence with no mutations; and (c)
 CC detecting mismatches between the genomic sequence and the probe; (2) a
 CC method comprising: (a) isolating an ACE genomic DNA sequence as in (1);
 CC (b) amplifying the sequence; (c) hybridising the amplification products
 CC with a probe as in (1); and (d) detecting mismatches between the
 CC amplification products and the probe; (3) a method comprising: (a)
 CC isolating an ACE genomic DNA sequence as in (1); (b) denaturing the
 CC genomic sequence to obtain single-stranded DNA; (c) hybridising the
 CC single-stranded DNA with a probe as in (1); and (d) detecting mismatches
 CC between the single-stranded DNA and the probe; (4) a method comprising:
 CC (a) isolating an ACE genomic DNA sequence as in (1); (b) amplifying the
 CC sequence; (c) denaturing the amplification products to obtain single-
 CC stranded DNA; (d) hybridising the single-stranded DNA with a probe as in
 CC (1); and (e) detecting mismatches between the single-stranded DNA and the
 CC probe. The methods are used for assessing the patient's risk of
 CC developing cardiovascular disease. The present sequence represents a PCR
 CC primer for ACE

XX SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 84;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1402 GCAGCAACAGCAGCAGCAGC 1421
 DB 20 GCAGCAACAGCAGCAGCAGC 1

RESULT 62
 AAA55806/c
 ID AAA55806 standard; DNA; 20 BP.

XX AC AAA55806;

XX DT 01-SEP-2000 (first entry)

XX DE Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:51.

XX KW Human; DNA methyltransferase; DNA Methylase; antisense oligonucleotide;
 KW modulation; inhibition; gene expression; combination therapy; p16;
 KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
 KW antiinflammatory; inflammation; asthma; ss.

XX OS Homo sapiens.

XX PN WO200023112-A1.

XX PD 27-APR-2000.

XX PF 19-OCT-1999; 99WO-US024278.

XX PR 19-OCT-1998; 98US-0104804P.

XX PA (METH-) METHYLGENE INC.

XX PI Besterman JM, Macleod AR, Siders WM;

XX DR WPI; 2000-339532/29.

XX PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
 PT with a synergistic amount of antisense oligonucleotide and protein
 PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
 PT of e.g. tumors.

XX PS Disclosure; Page 29; 99pp; English.

XX CC The present invention describes a method for inhibiting the expression of
 CC a gene in a cell comprising contacting the cell with an effective
 CC synergistic amount of an antisense oligonucleotide which inhibits
 CC expression of the gene, and an effective synergistic amount of a protein
 CC effector of a product of the gene. Also described are: (1) a method for
 CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
 CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
 CC comprising an antisense oligonucleotide which inhibits expression of the
 CC gene in operable association with a protein effector of a gene product;
 CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
 CC methods and compositions are useful as analytical tools for transgenic
 CC studies and as therapeutic tools, e.g. as gene therapy tools for human
 CC diseases including benign and malignant tumours, inflammation or asthma.
 CC The methods, inhibitors and compositions of the invention that inhibit
 CC expression or activity of a gene or gene product may be used to treat
 CC patients having, or predisposed to developing, a disease responsive to
 CC inhibition of the gene. These may also be used to activate silenced genes
 CC to provide missing gene functions and improve a given condition.
 CC Furthermore, the methods and compositions are useful as probes of the
 CC physiological function of a gene product in an experimental cell culture
 CC or animal system; and to evaluate the effect of inhibiting gene activity
 CC or expression. AAA55758 to AAA55842 represent oligonucleotide sequences
 CC which are used in the exemplification of the present invention

XX SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 84;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
 DB 20 CGCAGCAGCAGCAGCAGCA 1

RESULT 63

AAH43116/c

ID AAH43116 standard; DNA; 20 BP.

XX AC AAH43116;

XX DT 19-SEP-2001 (first entry)

XX DE Antisense oligo, target HDAC-2 121-141.

XX KW Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
 KW cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
 KW fungal infections; ss.

XX OS Synthetic.

XX PN WO200138322-A1.

XX PD 31-MAY-2001.

XX PF 22-NOV-2000; 2000WO-IB001881.

XX PR 23-NOV-1999; 99US-0167035P.

XX PA (METH-) METHYLGENE INC.

XX PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;

XX DR WPI; 2001-432601/46.

XX PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
 PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
 PT restenosis or fungal infections.

XX PS Disclosure; Page 40; 147pp; English.

XX CC The sequences given in AAH43115-21 are oligonucleotides which are

CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
CC may be used in combination with an inhibitor of histone deacetylase
CC enzyme function, to given an improved inhibitory effect, thereby reducing
CC the amount of inhibitor required to obtain a given inhibitory effect.
CC Compounds containing these oligonucleotides may be used to treat cell
CC proliferation conditions such as cancer, restenosis or psoriasis. They
CC can also be used to treat protozoal and fungal infections
XX
SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 64
AAC89545/c
ID AAC89545 standard; DNA; 20 BP.
XX
AC AAC89545;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human HDAC-2 antisense sequence SEQ ID NO: 15.
XX
KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200071703-A2.
XX
PD 30-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-IB001252.
XX
PR 03-MAY-1999; 99US-0132287P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Macleod AR, Li Z, Besterman JM;
XX
DR WPI; 2001-016407/02.
XX

PT Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
PS Example 1; Page 24; 125pp; English.
XX
CC The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 65
AAC89536/c
ID AAC89536 standard; DNA; 20 BP.
XX
AC AAC89536;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human HDAC-2 PCR primer SEQ ID NO: 6.
XX
KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200071703-A2.
XX
PD 30-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-IB001252.
XX
PR 03-MAY-1999; 99US-0132287P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Macleod AR, Li Z, Besterman JM;
XX
DR WPI; 2001-016407/02.
XX

PT Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
PS Disclosure; Page 12; 125pp; English.
XX
CC The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 66
AAS20967/c
ID AAS20967 standard; DNA; 20 BP.
XX
AC AAS20967;
XX
DT 09-APR-2002 (first entry)
XX
DE PCR primer Snrpn-U relating to gene imprinting invention.
XX
KW Human; genomic imprinting; pluripotent mouse embryonic germ cell line;
KW EG; methylated CpG island; DNA methylation; gene imprinting;
KW post-translational modification of histone; cancer; birth defect;
KW diabetes; aberrant imprinting; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200190313-A2.
XX

```
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US016253.
XX
PR 22-MAY-2000; 2000US-0206158P.
XX
PR 22-MAY-2000; 2000US-0206161P.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Feinberg A, Strichman-Almashanu L, Jiang S;
XX WPI; 2002-083100/11.
XX
PT Forming embryonic germ cells useful as model system to study imprinting
PT involves mating genetically divergent male and female mammal of same
PT species, dissecting and dissociating embryo obtained from pregnant
PT mammal.
XX
PS Disclosure; Page 54; 125pp; English.
XX
CC The present invention relates to a model system for genomic imprinting
CC using pluripotent mouse embryonic germ (EG) cell lines derived from an
CC interspecific cross. Also disclosed is a library containing methylated
CC CpG islands and a method for assaying methylation in one or more
CC imprintable genes. The gene imprinting assay is carried out by single-
CC strand conformation polymorphism (SSCP), quantitative sequencing, single
CC nucleotide primer extension or hot stop PCR. The assays are carried out
CC to determine the post-translational modification of histones. The method
CC further involves identifying a test substance as a candidate drug for
CC treating cancer if the test substance enhances imprinting of a gene whose
CC imprinting is lost in cancer, or if the test substance inhibits
CC imprinting of a gene whose imprinting is gained in cancer. The methylated
CC CpG islands are useful for providing an assessment of the risk of
CC developing cancer, or for providing diagnostic information relative to
CC cancer which involves determining the methylation status of the CpG
CC island in a patient's DNA. The EG cells allow the accession of imprinted
CC genes which are useful for detecting birth defects, diabetes and cancers
CC associated with aberrant imprinting. The EG cell lines represent the
CC first in vitro model system in which genomic imprinting can be followed
CC dynamically and the two alleles can be distinguished. AAS20953-AAS20969
CC represent PCR primers described in the present invention
XX
SQ Sequence 20 BP; 1 A; 5 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1430 CAGCAGCAGCAGCAGCAGCA 1449
Db |||||
20 CAGTAGCAGCAGCAGCAGCA 1
RESULT 67
ABZ86076/c
ID ABZ86076 standard; DNA; 20 BP.
XX
AC ABZ86076;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytosolic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
OS Homo sapiens.
XX
PN W0200285308-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US016253.
XX
PR 22-MAY-2000; 2000US-0206158P.
XX
PR 22-MAY-2000; 2000US-0206161P.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Feinberg A, Strichman-Almashanu L, Jiang S;
XX WPI; 2002-083100/11.
XX
PT Forming embryonic germ cells useful as model system to study imprinting
PT involves mating genetically divergent male and female mammal of same
PT species, dissecting and dissociating embryo obtained from pregnant
PT mammal.
XX
PS Disclosure; Page 54; 125pp; English.
XX
CC The present invention relates to a model system for genomic imprinting
CC using pluripotent mouse embryonic germ (EG) cell lines derived from an
CC interspecific cross. Also disclosed is a library containing methylated
CC CpG islands and a method for assaying methylation in one or more
CC imprintable genes. The gene imprinting assay is carried out by single-
CC strand conformation polymorphism (SSCP), quantitative sequencing, single
CC nucleotide primer extension or hot stop PCR. The assays are carried out
CC to determine the post-translational modification of histones. The method
CC further involves identifying a test substance as a candidate drug for
CC treating cancer if the test substance enhances imprinting of a gene whose
CC imprinting is lost in cancer, or if the test substance inhibits
CC imprinting of a gene whose imprinting is gained in cancer. The methylated
CC CpG islands are useful for providing an assessment of the risk of
CC developing cancer, or for providing diagnostic information relative to
CC cancer which involves determining the methylation status of the CpG
CC island in a patient's DNA. The EG cells allow the accession of imprinted
CC genes which are useful for detecting birth defects, diabetes and cancers
CC associated with aberrant imprinting. The EG cell lines represent the
CC first in vitro model system in which genomic imprinting can be followed
CC dynamically and the two alleles can be distinguished. AAS20953-AAS20969
CC represent PCR primers described in the present invention
XX
SQ Sequence 20 BP; 1 A; 5 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1430 CAGCAGCAGCAGCAGCAGCA 1449
Db |||||
20 CAGTAGCAGCAGCAGCAGCA 1
RESULT 68
ABZ22306/c
ID ABZ22306 standard; DNA; 20 BP.
XX
AC ABZ22306;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human stannocalcin-derived oligo SEQ ID 1318.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
OS Homo sapiens.
XX
PN W0200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 1318; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytosolic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 1 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db |||||
20 CTGCAGCAGCAGCAGCAGCA 1
RESULT 69
ABD22306/c
ID ABD22306 standard; DNA; 20 BP.
XX
AC ABD22306;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human stannocalcin-derived oligo SEQ ID 1318.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
OS Homo sapiens.
XX
PN W0200285308-A2.
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XX WO200285309-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013143.
XX 24-APR-2001; 2001US-0286036P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX Claim 15; SEQ ID NO 1318; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX Sequence 20 BP; 1 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
DB 20 CTGCAGCAGCAGCAGCAGCA 1

RESULT 69
ADP20499
ID ADP20499 standard; DNA; 20 BP.
XX AC
XX ADP20499;
XX 26-AUG-2004 (first entry)
DT
KW

DE Transcription factor AP-2 antisense oligonucleotide seqid 46.
XX cytosolic; AP-2-Inhibitor-Alpha; AP-2 alpha; AP-2 alpha modulator;
KW AP-2 alpha associated disorder; hyperproliferative disorder; human;
KW transcription factor; antisense oligonucleotide; antisense technology;
KW ss.
XX Homo sapiens.
XX OS
XX US2004109848-A1.
XX 10-JUN-2004.
XX 09-DEC-2002; 2002US-00315962.
XX 09-DEC-2002; 2002US-00315962.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dean NM, Freier SM, Dobie KW;
XX WPI; 2004-440306/41.
XX New compounds targeted to nucleic acid molecules encoding AP-2 alpha and
PT inhibits the expression of AP-2 alpha, useful for treating AP-2 alpha-
PT associated disease or condition, particularly a hyperproliferative
PT disorder.
XX Example 15; SEQ ID NO 46; 58pp; English.
XX The invention describes a compound (1) 8-80 nucleobases in length
CC targeted to a nucleic acid molecule encoding AP-2 alpha. The compound
CC specifically hybridises with a nucleic acid molecule encoding AP-2 alpha
CC (19868 bp, SEQ ID NO: 4), and inhibits the expression of AP-2 alpha. Also
CC described are: inhibiting the expression of AP-2 alpha in cells or tissues
CC comprising contacting the cells or tissues with (1); screening for a
CC modulator of AP-2 alpha by contacting a preferred target segment of a
CC nucleic acid molecule encoding AP-2 alpha with one or more candidate
CC modulators of AP-2 alpha, and identifying one or more modulators of AP-2
CC alpha expression, which modulate the expression of AP-2 alpha; a
CC diagnostic method for identifying a disease state, and a kit or assay
CC device comprising (1). The compound is useful for treating an animal
CC having a disease or condition associated with AP-2 alpha, particularly a
CC hyperproliferative disorder. The compounds may be used for diagnostics,
CC therapeutics prophylaxis and as research reagents; or as tools in
CC differential and/or combinatorial analyses to elucidate expression
CC patterns of a portion or the entire complement of genes expressed within
CC cells and tissues. This sequence represents a human transcription factor
CC AP-2 antisense oligonucleotide.
XX Sequence 20 BP; 6 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
SQ Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 84;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1411 GCAGCAGCAGCAGCAGCAGC 1430
DB 1 GCAGCAGCAGCAGCAGTAGC 20

RESULT 70
AAA63144/C
ID AAA63144 standard; DNA; 18 BP.
XX AC
XX AAA63144;
XX 07-DEC-2000 (first entry)
DT
XX Antisense oligonucleotide for use in RNase H mapping assay SEQ ID NO: 48.
KW Immunoregulator; antisense oligonucleotide; cancer; tumour cell vaccine;
KW rheumatoid arthritis; autoimmune disease; diabetes mellitus; thyroiditis;

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KW XX ss.
XX OS Mus sp.
XX FN WO200034467-A1.
XX PD 15-JUN-2000.
XX XX 24-NOV-1999; 99WO-US028096.
XX PF 04-DEC-1998; 98US-00205995.
XX PR (ANTI-) ANTIGEN EXPRESS INC.
XX PA Xu M, Qiu G, Humphreys R;
XX PI WPI; 2000-423417/36.
XX XX Cancer cell vaccine for treating malignancies, autoimmune disorders and
XX PT isolating autodeterminant peptides comprises a regulator of invariant
XX PT chain protein expression or immunoregulatory function.
XX PS Claim 21; Page 47; 94pp; English.
XX CC The present sequence is an antisense oligonucleotide which was used in an
XX CC RNase mapping experiment. This enables the identification of sites within
XX CC the 11 RNA strand which hybridise to antisense DNA. These sites can then
XX CC be used as targets for antisense strands which may, using gene therapy,
XX CC be used as tumour cell vaccines (for example to treat carcinomas,
XX CC melanoma, leukaemia, lymphomas, stomach, breast, colon or rectum, lung,
XX CC prostate, bladder, pancreas, brain and ovarian cancers), or they can be
XX CC used to treat autoimmune diseases including rheumatoid arthritis,
XX CC diabetes mellitus and thyroiditis
XX SQ Sequence 18 BP; 0 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAG 1417
Db 18 CAGCAGCAACAGCAGCAG 1

RESULT 71
AAS13717/c
ID AAS13717 standard; DNA; 18 BP.
XX AC AAS13717;
XX DT 08-MAY-2002 (first entry)
XX DE Simple sequence repeat, SSR, #14.
XX KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
XX KW cereal profiling; grass profiling; seed batch purity testing.
XX OS Poae.
XX FN NZ509193-A.
XX XX 25-MAY-2001.
XX PD 03-JAN-2001; 2001NZ-00509193.
XX PF 24-DEC-1999; 99AU-00004906.
XX PR 04-MAY-2000; 2000AU-00007310.
XX XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
XX PA (UYSC-) UNIV SOUTHERN CROSS.
XX PI (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
XX PA (UYAD-) UNIV ADELAIDE.

PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
XX Forster JW, Jones ES;
XX DR WPI; 2001-512563/56.
XX XX New simple sequence repeats having 2 or more tandemly repeated nucleotide
XX PT core elements isolated from ryegrass and fescue, useful for selecting of
XX PT genes in grass or cereal breeding or profiling grass or cereal species
XX XX varieties.
XX PS Claim 6; Page 51; 72pp; English.
XX CC The invention relates to a substantially purified or isolated nucleic
XX CC acid (I) from ryegrass or fescue species including a simple sequence
XX CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
XX CC 2-6 nucleotides in length. Also included are a nucleic acid primer
XX CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
XX CC library of ryegrass or fescue genomic DNA enriched for SSRs and
XX CC identifying clones in the library containing SSRs, a library of ryegrass
XX CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
XX CC a gene in grass or cereal breeding by identifying an SSR that is closely
XX CC associated with the gene such that the SSR and the gene are
XX CC preferentially co-inherited, and selecting for the SSR in the breeding, a
XX CC method for DNA profiling grass or cereal species varieties by assessing
XX CC variation between SSR varieties and testing the purity of grass or cereal
XX CC seed batches by assessing variation within seed batch of an SSR. The SSRs
XX CC may be used in the selection of genes in grass or cereal breeding, for
XX CC profiling grass or cereal species varieties, for testing the purity of
XX CC grass or cereal seed batches, and for DNA profiling to establish the
XX CC distinct identity, uniformity and/or stability of a cultivar. The present
XX CC sequence is a ryegrass or fescue SSR
XX SQ Sequence 18 BP; 0 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1411 GCAGCAGCAGCAGCAGCA 1428
Db 18 GCAGCAGCAGCAGCAGCA 1

RESULT 72
ADN97239
ID ADN97239 standard; DNA; 18 BP.
XX AC ADN97239;
XX DT 01-JUL-2004 (first entry)
XX DE Primer of the invention #47.
XX KW DNA fingerprinting; Cannabis sativa; short tandem repeat marker;
XX KW forensic identification; marijuana; primer; ss.
XX OS Unidentified.
XX FN WO2004008841-A2.
XX PD 29-JAN-2004.
XX PF 21-JUL-2003; 2003WO-US022887.
XX PR 19-JUL-2002; 2002US-0397179P.
XX XX (UYAR-) UNIV ARIZONA.
XX PA (KEIM/) KEIM P S.
XX PA (ZINN/) ZINNAMON K.
XX XX Keim PS, Zinamon K;
XX XX

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DR WPI; 2004-143139/14.

XX New isolated nucleic acid for amplification of a short tandem repeat

PT located in DNA isolated from Cannabis sativa L species, useful for

PT forensic identification of marijuana or for linking a marijuana sample to

PT its plant source.

PS Example 9; SEQ ID NO 106; 79pp; English.

XX The present invention relates to DNA fingerprinting for Cannabis Sativa

CC using short tandem repeat markers. The nucleic acid is useful for

CC forensic identification of marijuana or for linking a marijuana sample to

CC its plant source. The present sequence represents a primer of the

CC invention.

XX Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGC 1427

|||||

Db 1 AGCAGCAGCAGCAGCAGC 18

RESULT 73

ADO26674/c

ID ADO26674 standard; DNA; 18 BP.

XX ADO26674;

AC ADO26674;

XX 12-AUG-2004 (first entry)

DT Synthetic leader sequence encoding DNA SEQ ID NO:67.

DE phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

OS WO2004042059-A1.

PN 21-MAY-2004.

PD 10-NOV-2003; 2003WO-AU001487.

PF 08-NOV-2002; 2002US-0425163P.

PR (UYQU) UNIV QUEENSLAND.

PA Frazer IH;

PI WPI; 2004-411519/38.

DR P-PSDB; ADO26675.

XX Constructing synthetic polynucleotide for modulating the quality of a

PT selected phenotype displayed by an organism comprises replacing a first

PT codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 67; 86pp; English.

PS The present invention describes a method for constructing a synthetic

CC polynucleotide from which a polypeptide is producible to confer a

CC selected phenotype to an organism of interest or part in a different

CC quality than that conferred by a parent polynucleotide that encodes the

CC same polypeptide. The method comprises: (a) selecting a first codon of

CC the parent polynucleotide for replacement with a synonymous codon, where

CC the synonymous codon is selected on the basis that it exhibits a

CC different phenotypic preference than the first codon in a comparison of

CC phenotypic preferences in test organisms or parts, where the test

CC organism are selected from organisms of the same species as the organism

CC of interest and organisms that are related to the organisms of interest;

CC and (b) replacing the first codon with the synonymous codon to construct

CC the synthetic polynucleotide. Also described: (1) a method for

CC determining the phenotypic preference of a first codon in an organism of

CC interest or its parts; (2) a synthetic polynucleotide constructed from

CC the method above; (3) an organism or interest or part containing a

CC synthetic polynucleotide constructed from the method above; (4) an

CC organism or interest or part containing a synthetic construct that

CC comprises a regulatory polynucleotide operably linked to a tandem repeat

CC of a first codon fused in frame with a reporter polynucleotide that

CC encodes a reporter protein, which produces, or is predicted to produce a

CC phenotype in the organism or part; (5) a method of modulating the quality

CC of a selected phenotype that is displayed by an organism of interest or

CC part and that results from the expression of a parent polynucleotide that

CC encodes the polypeptide; (6) a method of enhancing the quality of a

CC and that results from the expression of a parent polynucleotide that

CC encodes the polypeptide; and (7) a method of reducing the quality of a

CC selected phenotype that is displayed by an organism of interest or part

CC and that results from the expression of a parent polynucleotide that

CC encodes the polypeptide. The method is useful for constructing a

CC synthetic polynucleotide from which a polypeptide is producible to confer

CC a selected phenotype to an organism of interest or part in a different

CC quality than that conferred by a parent polynucleotide that encodes the

CC same polypeptide. It is useful for modulating the quality of a selected

CC phenotype displayed by an organism or part. The present sequence encodes

CC a synthetic leader sequence, which is used in an example from the present

CC invention.

XX Sequence 18 BP; 0 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAG 1426

|||||

Db 18 CAGCAGCAGCAGCAGCAG 1

RESULT 74

ADO26644

ID ADO26644 standard; DNA; 18 BP.

XX ADO26644;

AC ADO26644;

XX 12-AUG-2004 (first entry)

DT Synthetic leader sequence encoding DNA SEQ ID NO:37.

DE phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

OS WO2004042059-A1.

PN 21-MAY-2004.

PD 10-NOV-2003; 2003WO-AU001487.

PF 08-NOV-2002; 2002US-0425163P.

PR (UYQU) UNIV QUEENSLAND.

PA Frazer IH;

PI WPI; 2004-411519/38.

DR P-PSDB; ADO26645.

XX Constructing synthetic polynucleotide for modulating the quality of a

PT selected phenotype displayed by an organism comprises replacing a first

PT codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 37; 86pp; English.

XX The present invention describes a method for constructing a synthetic
 CC polynucleotide from which a polypeptide is producible to confer a
 CC selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. The method comprises: (a) selecting a first codon of
 CC the parent polynucleotide for replacement with a synonymous codon, where
 CC the synonymous codon is selected on the basis that it exhibits a
 CC different phenotypic preference than the first codon in a comparison of
 CC phenotypic preferences in test organisms or parts, where the test
 CC organism are selected from organisms of the same species as the organism
 CC of interest and organisms that are related to the organisms of interest;
 CC and (b) replacing the first codon with the synonymous codon to construct
 CC the synthetic polynucleotide. Also described: (1) a method for
 CC determining the phenotypic preference of a first codon in an organism of
 CC interest or its parts; (2) a synthetic polynucleotide constructed from
 CC the method above; (3) an organism or interest or part containing a
 CC synthetic polynucleotide constructed from the method above; (4) an
 CC organism or interest or part containing a synthetic construct that
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat
 CC of a first codon fused in frame with a reporter polynucleotide that
 CC encodes a reporter protein, which produces, or is predicted to produce a
 CC selected phenotype or a phenotype of the same class as the selected
 CC phenotype in the organism or part; (5) a method of modulating the quality
 CC of a selected phenotype that is displayed by an organism of interest or
 CC part and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; (6) a method of enhancing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; and (7) a method of reducing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide. The method is useful for constructing a
 CC synthetic polynucleotide from which a polypeptide is producible to confer
 CC a selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. It is useful for modulating the quality of a selected
 CC phenotype displayed by an organism or part. The present sequence encodes
 CC a synthetic leader sequence, which is used in an example from the present
 CC invention.

XX
 SQ Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 0.5%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAG 1426
 DB 1 CAGCAGCAGCAGCAGCAG 18
 |||||

RESULT 75
 ADO26638/c
 ID ADO26638 standard; DNA; 18 BP.

XX ADO26638;
 AC
 XX 12-AUG-2004 (first entry)

DE Synthetic leader sequence encoding DNA SEQ ID NO:31.

XX phenotype; phenotypic preference; phenotype modulation; leader; ds.

OS Synthetic.

XX WO2004042059-A1.

XX 21-MAY-2004.

XX 10-NOV-2003; 2003WO-AU001487.

XX 08-NOV-2002; 2002US-0425163P.

XX (UYQU) UNIV QUEENSLAND.

XX Frazer IH;

XX WPI; 2004-411519/38.

XX P-PSDB; ADO26639.

XX Constructing synthetic polynucleotide for modulating the quality of a
 PT selected phenotype displayed by an organism comprises replacing a first
 PT codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 31; 86bp; English.

XX The present invention describes a method for constructing a synthetic
 CC polynucleotide from which a polypeptide is producible to confer a
 CC selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. The method comprises: (a) selecting a first codon of
 CC the parent polynucleotide for replacement with a synonymous codon, where
 CC the synonymous codon is selected on the basis that it exhibits a
 CC different phenotypic preference than the first codon in a comparison of
 CC phenotypic preferences in test organisms or parts, where the test
 CC organism are selected from organisms of the same species as the organism
 CC of interest and organisms that are related to the organisms of interest;
 CC and (b) replacing the first codon with the synonymous codon to construct
 CC the synthetic polynucleotide. Also described: (1) a method for
 CC determining the phenotypic preference of a first codon in an organism of
 CC interest or its parts; (2) a synthetic polynucleotide constructed from
 CC the method above; (3) an organism or interest or part containing a
 CC synthetic polynucleotide constructed from the method above; (4) an
 CC organism or interest or part containing a synthetic construct that
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat
 CC of a first codon fused in frame with a reporter polynucleotide that
 CC encodes a reporter protein, which produces, or is predicted to produce a
 CC selected phenotype or a phenotype of the same class as the selected
 CC phenotype in the organism or part; (5) a method of modulating the quality
 CC of a selected phenotype that is displayed by an organism of interest or
 CC part and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; (6) a method of enhancing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide. The method is useful for constructing a
 CC synthetic polynucleotide from which a polypeptide is producible to confer
 CC a selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. It is useful for modulating the quality of a selected
 CC phenotype displayed by an organism or part. The present sequence encodes
 CC a synthetic leader sequence, which is used in an example from the present
 CC invention.

XX Sequence 18 BP; 0 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428
 DB 18 GCAGCAGCAGCAGCAGCA 1
 |||||

RESULT 76
 ADO26610
 ID ADO26610 standard; DNA; 18 BP.

XX ADO26610;

XX 12-AUG-2004 (first entry)

XX

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DE Synthetic leader sequence encoding DNA SEQ ID NO:3.
XX phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX Synthetic.
OS
XX WO2004042059-A1.
XX 21-MAY-2004.
XX 10-NOV-2003; 2003WO-AU001487.
XX 08-NOV-2002; 2002US-0425163P.
XX (UYQU ) UNIV QUEENSLAND.
XX Frazer IH;
XX WPI; 2004-411519/38.
XX P-PSDB; ADO26611.
XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
XX Example 1; SEQ ID NO 3; 86pp; English.
XX
XX The present invention describes a method for constructing a synthetic
XX polynucleotide from which a polypeptide is producible to confer a
XX selected phenotype to an organism of interest or part in a different
XX quality than that conferred by a parent polynucleotide that encodes the
XX same polypeptide. The method comprises: (a) selecting a first codon of
XX the parent polynucleotide for replacement with a synonymous codon, where
XX the synonymous codon is selected on the basis that it exhibits a
XX different phenotypic preference than the first codon in a comparison of
XX phenotypic preferences in test organisms or parts, where the test
XX organism are selected from organisms of the same species as the organism
XX of interest and organisms that are related to the organisms of interest;
XX and (b) replacing the first codon with the synonymous codon to construct
XX the synthetic polynucleotide. Also described: (1) a method for
XX determining the phenotypic preference of a first codon in an organism of
XX interest or its parts; (2) a synthetic polynucleotide constructed from
XX the method above; (3) an organism or interest or part containing a
XX synthetic polynucleotide constructed from the method above; (4) an
XX organism or interest or part containing a synthetic construct that
XX comprises a regulatory polynucleotide operably linked to a tandem repeat
XX of a first codon fused in frame with a reporter polynucleotide that
XX encodes a reporter protein, which produces, or is predicted to produce a
XX selected phenotype or a phenotype of the same class as the selected
XX phenotype in the organism or part; (5) a method of modulating the quality
XX of a selected phenotype that is displayed by an organism of interest or
XX part and that results from the expression of a parent polynucleotide that
XX encodes the polypeptide; (6) a method of enhancing the quality of a
XX selected phenotype that is displayed by an organism of interest or part
XX and that results from the expression of a parent polynucleotide that
XX encodes the polypeptide; and (7) a method of reducing the quality of a
XX selected phenotype that is displayed by an organism of interest or part
XX and that results from the expression of a parent polynucleotide that
XX encodes the polypeptide. The method is useful for constructing a
XX synthetic polynucleotide from which a polypeptide is producible to confer
XX a selected phenotype to an organism of interest or part in a different
XX quality than that conferred by a parent polynucleotide that encodes the
XX same polypeptide. It is useful for modulating the quality of a selected
XX phenotype displayed by an organism or part. The present sequence encodes
XX a synthetic leader sequence, which is used in an example from the present
XX invention.
XX
XX Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.5%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 71;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1411 GCAGCAGCAGCAGCA 1428
DB 1 GCAGCAGCAGCAGCA 18
|||||
AC ADO26696;
XX 12-AUG-2004 (first entry)
XX Synthetic leader sequence encoding DNA SEQ ID NO:89.
XX phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX Synthetic.
XX WO2004042059-A1.
XX 21-MAY-2004.
XX 10-NOV-2003; 2003WO-AU001487.
XX P-PSDB; ADO26697.
XX WPI; 2004-411519/38.
XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
XX Example 1; SEQ ID NO 89; 86pp; English.
XX
XX The present invention describes a method for constructing a synthetic
XX polynucleotide from which a polypeptide is producible to confer a
XX selected phenotype to an organism of interest or part in a different
XX quality than that conferred by a parent polynucleotide that encodes the
XX same polypeptide. The method comprises: (a) selecting a first codon of
XX the parent polynucleotide for replacement with a synonymous codon, where
XX the synonymous codon is selected on the basis that it exhibits a
XX different phenotypic preference than the first codon in a comparison of
XX phenotypic preferences in test organisms or parts, where the test
XX organism are selected from organisms of the same species as the organism
XX of interest and organisms that are related to the organisms of interest;
XX and (b) replacing the first codon with the synonymous codon to construct
XX the synthetic polynucleotide. Also described: (1) a method for
XX determining the phenotypic preference of a first codon in an organism of
XX interest or its parts; (2) a synthetic polynucleotide constructed from
XX the method above; (3) an organism or interest or part containing a
XX synthetic polynucleotide constructed from the method above; (4) an
XX organism or interest or part containing a synthetic construct that
XX comprises a regulatory polynucleotide operably linked to a tandem repeat
XX of a first codon fused in frame with a reporter polynucleotide that
XX encodes a reporter protein, which produces, or is predicted to produce a
XX selected phenotype or a phenotype of the same class as the selected
XX phenotype in the organism or part; (5) a method of modulating the quality
XX of a selected phenotype that is displayed by an organism of interest;
XX part and that results from the expression of a parent polynucleotide that
XX encodes the polypeptide; (6) a method of enhancing the quality of a
XX selected phenotype that is displayed by an organism of interest or part
XX and that results from the expression of a parent polynucleotide that
XX encodes the polypeptide; and (7) a method of reducing the quality of a
XX selected phenotype that is displayed by an organism of interest or part
XX and that results from the expression of a parent polynucleotide that
XX encodes the polypeptide. The method is useful for constructing a
XX synthetic polynucleotide from which a polypeptide is producible to confer
```

CC a selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. It is useful for modulating the quality of a selected
 CC phenotype displayed by an organism or part. The present sequence encodes
 CC a synthetic leader sequence, which is used in an example from the present
 CC invention.

XX SQ Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGC 1427
 |||||
 Db 1 AGCAGCAGCAGCAGCAGC 18

RESULT 78
 ADO26614/c
 ID ADO26614 standard; DNA; 18 BP.

XX AC ADO26614;
 XX DT 12-AUG-2004 (first entry)
 XX DE Synthetic leader sequence encoding DNA SEQ ID NO:7.
 XX KW phenotype; phenotypic preference; phenotype modulation; leader; ds.
 XX OS Synthetic.
 XX PN WO2004042059-A1.
 XX PD 21-MAY-2004.
 XX PF 10-NOV-2003; 2003WO-AU001487.
 XX PR 08-NOV-2002; 2002US-0425163P.
 XX PA (UYQU) UNIV QUEENSLAND.
 XX PI Frazer IH;
 XX WPI; 2004-411519/38.
 XX P-PSDB; ADO26615.

XX Constructing synthetic polynucleotide for modulating the quality of a
 PT selected phenotype displayed by an organism comprises replacing a first
 PT codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 7; 86pp; English.

XX The present invention describes a method for constructing a synthetic
 CC polynucleotide from which a polypeptide is producible to confer a
 CC selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. The method comprises: (a) selecting a first codon of
 CC the parent polynucleotide for replacement with a synonymous codon, where
 CC the synonymous codon is selected on the basis that it exhibits a
 CC different phenotypic preference than the first codon in a comparison of
 CC phenotypic preferences in test organisms or parts, where the test
 CC organism are selected from organisms of the same species as the organism
 CC of interest and organisms that are related to the organisms of interest;
 CC and (b) replacing the first codon with the synonymous codon to construct
 CC the synthetic polynucleotide. Also described: (1) a method for
 CC determining the phenotypic preference of a first codon in an organism of
 CC interest or its parts; (2) a synthetic polynucleotide constructed from
 CC the method above; (3) an organism of interest or part containing a
 CC synthetic polynucleotide constructed from the method above; (4) an
 CC organism of interest or part containing a synthetic construct that
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat
 CC of a first codon fused in frame with a reporter polynucleotide that

CC encodes a reporter protein, which produces, or is predicted to produce a
 CC selected phenotype or a phenotype of the same class as the selected
 CC phenotype in the organism or part; (5) a method of modulating the quality
 CC of a selected phenotype that is displayed by an organism of interest or
 CC part and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; (6) a method of enhancing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; and (7) a method of reducing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide. The method is useful for constructing a
 CC synthetic polynucleotide from which a polypeptide is producible to confer
 CC a selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. It is useful for modulating the quality of a selected
 CC phenotype displayed by an organism or part. The present sequence encodes
 CC a synthetic leader sequence, which is used in an example from the present
 CC invention.

XX SQ Sequence 18 BP; 0 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGC 1427
 |||||
 Db 18 AGCAGCAGCAGCAGCAGC 1

RESULT 79
 ADR06261
 ID ADR06261 standard; DNA; 18 BP.

XX AC ADR06261;
 XX DT 04-NOV-2004 (first entry)
 XX DE Short tandem (microsatellite) repeat #1.
 XX KW amplification data; DNA marker; biological sample identification;
 KW microorganism detection; virus detection; bacteria detection;
 KW fungi detection; protozoa detection; HIV-1;
 KW human T-cell lymphotropic virus type 1; HTLV-1; Hepatitis B virus; HBV;
 KW Hepatitis C virus; HCV; Herpes Simplex virus; paternity screening;
 KW genetic screening; prenatal diagnosis; presymptomatic diagnosis;
 KW disease carrier detection; forensic chemical analysis;
 KW short tandem repeat; microsatellite repeat; ds.

XX Unidentified.

XX US2004157220-A1.
 XX 12-AUG-2004.
 XX 10-FEB-2003; 2003US-00360854.
 XX 10-FEB-2003; 2003US-00360854.
 XX (KURN/) KURNOOL P.
 XX (WUBB/) WU B.
 XX (BANK/) BANKS P.
 XX Kurnool P, Wu B, Banks P;
 XX WPI; 2004-614752/59.

XX Identifying biological sample of mammal, involves obtaining amplification
 PT data indicative of amplification of DNA markers of genomic DNA of mammal,
 PT generating indicia indicative of amplification data, associating indicia
 PT with sample.

XX

```
PS Example; Page 19; 39pp; English.
XX
XX The invention describes a method of identifying (M1) a biological sample
CC comprising a biological material of a mammal. The method involves
CC obtaining amplification data indicative of amplification of at least two
CC DNA markers of genomic DNA of the mammal, generating indicia indicative
CC of the amplification data, and associating the indicia with the
CC biological sample, where the indicia is used to identify the biological
CC sample. (M1) is useful: in identifying biological sample of a subject
CC undergoing diagnosis to determine whether the subject is afflicted with a
CC particular disease or disorder; for identifying a biological sample of a
CC subject, undergoing screening for genetic lesions or mutations; for
CC identifying a biological sample of a subject, being diagnosed for the
CC presence of target microorganism chosen from virus, bacteria, fungi or
CC protozoa, where the virus includes HIV-1, human T-cell lymphotropic
CC virus type 1 (HTLV-1), Hepatitis B virus (HBV), Hepatitis C virus (HCV)
CC and Herpes Simplex, the bacteria includes Mycobacterium tuberculosis,
CC Rickettsia rickettsii, Ehrlichia chaffeensis, Borrelia burgdorferi and
CC Yersinia pestis, the fungi includes Cryptococcus neoformans, Pneumocystis
CC carinii and Histoplasma capsulatum, and the protozoa is chosen from
CC Trypanosoma cruzi, Leishmania sp., Plasmodium, Entamoeba histolytica,
CC Babesia microti, Giardia lamblia, Cyclospora sp. and Eimeria sp.; in
CC identifying a biological sample of a subject undergoing paternity
CC screening, genetic screening, prenatal diagnosis, presymptomatic
CC diagnosis, disease carrier detection or forensic chemical analysis; in
CC identifying a biological sample during the screening of the plant to
CC detect the presence of the target microorganism, or during carrier
CC detection analysis or forensic chemical analysis of a plant; and in
CC diagnostic medicines, for identification of genetically inherited
CC diseases in humans, family relationship analysis and microbial typing.
CC (M1) enables simultaneous analysis and tracking of biological samples.
CC The molecular barcode of the genomic DNA of the sample can be determined
CC at any time during the collection or processing of a biological sample.
CC This sequence represents an example of a short tandem or microsatellite
CC repeat that can be used in DNA fingerprinting to identify a biological
CC material.
SQ Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAG 1426
DB 1 CAGCAGCAGCAGCAGCAG 18
|||||
RESULT 80
AAV68372/c
ID AAV68372 standard; DNA; 20 BP.
XX
XX AAV68372;
10-MAR-1999 (first entry)
DE Adapter primer oligonucleotide #11 for CAG repeat analysis.
XX
XX CAG repeat; human; genome analysis; adapter primer; medical diagnostic;
XX nucleic acid analysis; variation assessment; neurological disease;
XX Huntington's chorea; PCR suppression; ss.
XX
XX Synthetic.
XX WO9849345-A1.
XX 05-NOV-1998.
XX 29-APR-1998; 98WO-US008616.
XX 29-APR-1997; 97US-0045078P.
XX (UYBO-) UNIV BOSTON.
XX
XX Smith CL;
XX WPI; 1998-594983/50.

PS This sequence represents an adapter primer oligonucleotide. It was used
CC to isolate CAG repeat containing sequences from the human genome to test
CC the method of the invention. The method is for analysing nucleic acids in
CC a sample, and comprises: (a) providing a sample containing nucleic acid,
CC a first oligonucleotide primer comprising a CTG repeat, a second
CC oligonucleotide primer comprising a CAG repeat and a polymerase and PCR
CC reagents; (b) preparing said nucleic acid so that it is amplifiable; (c)
CC amplifying the nucleic acid with the first and second primers; and (d)
CC detecting the amplified product. The method is used to distinguish
CC between the expression of genes in two or more biological samples, e.g.
CC body fluids, cells, solid tissue or solid and liquid foods. It can be
CC used in medical diagnostics, e.g. to differentiate between normal and
CC diseased tissue or to assess the variation within monozygotic twin pairs.
CC The method allows the isolation and analysis of genome subsets containing
CC CAG repeats which are known to be important in a number of neurological
CC diseases including Huntington's chorea. The method uses PCR suppression,
CC in which only fragments which contain a target repeat are efficiently
CC amplified. This allows accurate identification of differentially
CC expressed genes in various cell types. Genome complexity is reduced by
CC the new method which targets genomic subsets containing CAG repeats
SQ Sequence 20 BP; 1 A; 6 C; 6 G; 6 T; 0 U; 1 Other;

Query Match 0.5%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAG 1426
DB 20 CAGCAGCAGCAGCAGCAG 3
|||||
RESULT 81
AAV68373/c
ID AAV68373 standard; DNA; 20 BP.
XX
XX AAV68373;
10-MAR-1999 (first entry)
DE Adapter primer oligonucleotide #12 for CAG repeat analysis.
XX
XX CAG repeat; human; genome analysis; adapter primer; medical diagnostic;
XX nucleic acid analysis; variation assessment; neurological disease;
XX Huntington's chorea; PCR suppression; ss.
XX
XX Synthetic.
XX WO9849345-A1.
XX 05-NOV-1998.
XX 29-APR-1998; 98WO-US008616.
XX 29-APR-1997; 97US-0045078P.
XX (UYBO-) UNIV BOSTON.
XX
XX Smith CL;
XX WPI; 1998-594983/50.
XX
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PT Analysing nucleic acid samples - using amplification primers which
 PT contain CAG or CTG trinucleotide repeats for differential display of
 PT samples from different sources.
 XX
 PS Example; Page 31; 44pp; English.
 XX
 CC This sequence represents an adapter primer oligonucleotide. It was used
 CC to isolate CAG repeat containing sequences from the human genome to test
 CC the method of the invention. The method is for analysing nucleic acids in
 CC a sample, and comprises: (a) providing a sample containing nucleic acid,
 CC a first oligonucleotide primer comprising a CTG repeat, a second
 CC oligonucleotide primer comprising a CAG repeat and a polymerase and PCR
 CC reagents; (b) preparing said nucleic acid so that it is amplifiable; (c)
 CC amplifying the nucleic acid with the first and second primers; and (d)
 CC detecting the amplified product. The method is used to distinguish
 CC between the expression of genes in two or more biological samples, e.g.
 CC body fluids, cells, solid tissue or solid and liquid foods. It can be
 CC used in medical diagnostics, e.g. to differentiate between normal and
 CC diseased tissue or to assess the variation within monozygotic twin pairs.
 CC The method allows the isolation and analysis of genome subsets containing
 CC CAG repeats which are known to be important in a number of neurological
 CC diseases including Huntington's chorea. The method uses PCR suppression,
 CC in which only fragments which contain a target repeat are efficiently
 CC amplified. This allows accurate identification of differentially
 CC expressed genes in various cell types. Genome complexity is reduced by
 CC the new method which targets genomic subsets containing CAG repeats
 XX
 SQ Sequence 20 BP; 1 A; 7 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1409 CAGCAGCAGCAGCAGCAG 1426
 Db 18 CAGCAGCAGCAGCAGCAG 1

RESULT 82
 ADC65856/c
 ID ADC65856 standard; DNA; 20 BP.
 XX
 AC ADC65856;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Mouse TGF-beta receptor II targeted antisense oligonucleotide #55.
 XX
 KW mouse; antisense oligonucleotide;
 KW transforming growth factor beta receptor II; TGF-beta receptor II;
 KW hyperproliferative disorder; breast cancer; autoimmune disorder;
 KW rheumatoid arthritis; 2'-O-methoxyethyl gapmer;
 KW phosphorothioate backbone; ss; murine.
 XX
 OS Mus musculus.
 XX
 FN WO2003000656-A2.
 XX
 PD 03-JAN-2003.
 XX
 PF 19-JUN-2002; 2002WO-US019665.
 XX
 PR 21-JUN-2001; 2001US-00888361.
 XX
 PA (ISIS-) ISIS PHARM INC.

PI Murray SF, Wyatt JR;
 XX
 DR WPI; 2003-175279/17.
 XX
 PT New compound having a sequence targeted to a nucleic acid encoding
 PT transforming growth factor beta-receptor II, useful for preparing a
 PT composition for treating hyperproliferative disorder e.g., lung, liver,

PT colon or gastric cancer.
 XX
 PS Claim 3; SEQ ID NO 152; 141pp; English.
 XX
 CC The invention comprises antisense oligonucleotides that are targeted to
 CC the nucleic acid encoding transforming growth factor beta (TGF-beta)
 CC receptor II. The antisense oligonucleotides of the invention are useful
 CC for treating: hyperproliferative disorders (e.g. breast cancer), or an
 CC autoimmune disorder (e.g. rheumatoid arthritis). The present DNA sequence
 CC represents a 2'-O-methoxyethyl gapmer oligonucleotide with a
 CC phosphorothioate backbone that is targeted to mouse TGF-beta receptor II.
 XX
 SQ Sequence 20 BP; 1 A; 4 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 0.5%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1602 AGCAGCAGCAACACCAT 1619
 Db 20 AGCAGCAGCAACACCAT 3

RESULT 83
 ADD69519/c
 ID ADD69519 standard; DNA; 20 BP.
 XX
 AC ADD69519;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE ISSR-related PCR primer 6.
 XX
 KW inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
 KW animal; Basmati rice; ss.
 XX
 OS Unidentified.

FN WO2003085133-A2.
 XX
 PD 16-OCT-2003.

PF 09-JAN-2003; 2003WO-IB000041.
 XX
 PR 08-APR-2002; 2002IN-CH000260.

PA (DNAP-) CENT DNA FINGERPRINTING & DIAGNOSTICS.

PI Nagaraju JG;

DR WPI; 2003-804317/75.

PT New set of inter-simple sequence repeats (ISSR)-PCR primers for
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
 PT animal systems.

PS Disclosure; Page 19; 60pp; English.

CC The invention relates to a novel set of inter-simple sequence repeats
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
 CC invention may be useful for genotyping diverse genomes of plant and
 CC animal systems, in particular for distinguishing Basmati rice varieties
 CC from non-Basmati rice varieties and traditional Basmati rice varieties
 CC from evolved Basmati rice varieties. The current sequence is that of the
 CC ISSR-related PCR primer of the invention.

SQ Sequence 20 BP; 1 A; 6 C; 6 G; 6 T; 0 U; 1 Other;

Query Match 0.5%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1410 AGCAGCAGCAGCAGCAGC 1427

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Db      |||||
20 AGCAGCAGCAGCAGCAGC 3

RESULT 84
ABZ75647/c
ID ABZ75647 standard; DNA; 21 BP.
XX
AC ABZ75647;
XX
DT 15-MAY-2003 (first entry)
XX
DE Template (CTGA)6-A3 for second strand synthesis by HIV RT.
XX
KW DNA polymerization; drug susceptibility; HIV; reverse transcriptase; RT;
KW ds.
XX
OS Synthetic.
XX
PN WO2002103039-A1.
XX
PD 27-DEC-2002.
XX
PF 14-JUN-2002; 2002WO-SE001155.
XX
PR 14-JUN-2001; 2001US-0297773P.
XX
PA (CAVI-) CAVIDI TECH AB.
XX
PI Kaellander C, Pettersson I, Gronowitz S, Shao X;
XX
DR WPI; 2003-167535/16.
XX
PT Measuring DNA-dependent DNA polymerization in a biological sample, useful
PT for drug susceptibility testing, comprises measuring the amount of
PT incorporated modified deoxynucleoside triphosphate with the aid of a
PT labeled antibody.
XX
PS Example 1; Page 33; 36pp; English.
XX
CC The invention relates to measuring DNA-dependent DNA polymerization in a
CC biological sample and involves measuring the amount of incorporated
CC modified deoxynucleoside triphosphate with the aid of the label of a
CC bound antibody. The method is useful in measuring DNA polymerization for
CC drug susceptibility testing. Sequences ABZ75637-647 represent different
CC templates used for second strand synthesis by HIV reverse transcriptase
CC (RT)
XX
SQ Sequence 21 BP; 3 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match      0.5%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAG 1426
Db 18 CAGCAGCAGCAGCAGCAG 1

RESULT 85
ABK70327
ID ABK70327 standard; DNA; 21 BP.
XX
AC ABK70327;
XX
DT 15-JUL-2002 (first entry)
XX
DE Synthetic antisense IGFBP-2-oligodeoxynucleotide (ODN) #15.
XX
KW Hormone-regulated cancer; antisense oligonucleotide; IGFBP-2;
KW insulin-like growth factor binding protein-2; hormone-regulated tumour;
KW breast cancer; prostate cancer; IGF-1-sensitive cancer; apoptosis;
KW hormone-responsive cancer; hormonal withdrawal; oligodeoxynucleotide;

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```

KW ODN; endocrine tumour therapy; ss.
XX Synthetic.
XX WO200222642-A1.
XX
PN 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-US028748.
XX
PR 14-SEP-2000; 2000US-0232641P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Satoshi K, Nelson C, Rennie PS;
XX
DR WPI; 2002-339861/37.
XX
PT Composition for treating hormone-regulated cancer, particularly of
PT prostate or breast, comprises oligonucleotide antisense to insulin-like
PT growth factor binding protein-2.
XX
PS Claim 3; Page 12; 36pp; English.
XX
CC The present invention relates to a new composition for treating hormone-
CC regulated cancer. The composition comprises an antisense oligonucleotide
CC that inhibits expression of IGFBP-2 (insulin-like growth factor binding
CC protein-2). The molecules of the invention are used to delay progression
CC of hormone-regulated tumours, particularly of breast or prostate, to the
CC hormone-independent state, to delay metastatic progression to the bone of
CC IGF-1-sensitive cancers and to treat hormone-responsive cancers by
CC inducing apoptosis, after hormonal withdrawal. The present nucleic acid
CC sequence represents one of a collection (ABK70313-ABK70375) of antisense
CC IGFBP-2-oligodeoxynucleotides (ODN) that were used in the invention for
CC prostate and other endocrine tumour therapy
XX
SQ Sequence 21 BP; 6 A; 6 C; 8 G; 1 T; 0 U; 0 Other;

Query Match      0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 1 CAGTAGCAGCAGCAGCAGCGG 21

RESULT 86
ABX94818
ID ABX94818 standard; DNA; 22 BP.
XX
AC ABX94818;
XX
DT 11-JUL-2003 (first entry)
XX
DE Human cysteine-rich FGF receptor (CFR) PCR primer CFR-For1.
XX
KW Human; antibody; murine antibody NM58-49/69; cysteine-rich FGF receptor;
KW glycoprotein receptor; proliferating cell; stomach carcinoma; vaccine.
KW CFR-1 protein; human antibody 103/51; immunoglobulin M; cytostatic; gut;
KW antibacterial; antiinflammatory; receptor antagonism; cancer; stomach;
KW cesophagus; rectum; liver; gall bladder; pancreas; lung; bronchus;
KW breast; cervix; prostate; heart; ovary; uterus; metaplasia of oesophagus;
KW Helicobacter pylori-associated gastritis; tubular adenoma; tumour marker;
KW villous adenoma; Barrett dysplasia; cervical intraepithelial neoplasia;
KW anticancer agent; PCR; primer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1 /+tag= a
FT /mod_base= OTHER

```

FT /note= "This nucleotide is depicted as o in the
specification"

FN WO2003011907-A2.

XX 13-FEB-2003.

XX 23-JUL-2002; 2002WO-DE002699.

XX 24-JUL-2001; 2001DE-01036009.

XX 09-MAR-2002; 2002DE-01010425.

XX (MUELLER) MUELLER-HERMELINK H K.

PA (VOLLER) VOLLMERS H.

PA (HENSEL) HENSEL F.

XX Mueller-Hermelink HK, Vollmers H, Henseel F;

XX WPI; 2003-256436/25.

XX New glycoprotein receptor on surface of cancer cells, useful for
treatment and diagnosis of cancer and for drug screening, also new
specific antibody.

XX Disclosure; Page 21; 49pp; German.

XX This invention describes a novel glycoprotein receptor, present on the
surface membrane of strongly proliferating cells, especially stomach
carcinoma, having at least one determinant that corresponds with a
determinant of CFR-1 protein and binding specifically to human antibody
103/51 and/or the murine antibody 58/47-69 (immunoglobulin M). The
products of the invention have cytostatic, antibacterial and
antiinflammatory activity and can be used in a vaccine or for receptor
antagonism. The novel receptor is used for therapeutic in vivo generation
of antibodies, for treatment and prevention of cancer (of oesophagus,
stomach, gut, rectum, liver, gall bladder, pancreas, lung, bronchi,
breast, cervix, prostate, heart, ovary and/or uterus), for treating a
wide range of precancerous states (e.g. Helicobacter pylori-associated
gastritis, tubular or villous adenoma, Barrett dysplasia/metaplasia of
oesophagus, cervical intraepithelial neoplasia etc.), for diagnosis (as a
tumour marker) and for identifying potential anticancer agents from their
ability to bind selectively to the glycoprotein receptor. This sequence
represents a PCR primer used to amplify the human cysteine-rich FGF
receptor (CFR) described in the disclosure of the invention

XX Sequence 22 BP; 7 A; 7 C; 5 G; 2 T; 0 U; 1 Other;

Query Match 0.5%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1426 GCAGCAGCAGCAGCAGCAGCA 1446
||||| ||||||| |||||||

Db 2 GCAGCTTCAGCAGCAGCAGCA 22

RESULT 87

AAT39475

XX AAT39475 standard; DNA; 19 BP.

XX AAT39475;

XX 21-MAY-1997 (first entry)

XX Steroidogenesis acute regulatory protein sense PCR primer 1.

XX Human; steroidogenesis; acute regulatory protein; hStAR; analysis;
mutation; detection; prenatal; genetic defect; congenital; protein;
lipoid adrenal hyperplasia; treatment; prevention; gene;
replacement therapy; hypercholesterolaemia; primer; PCR;
polymerase chain reaction; ss.

XX Synthetic.

XX WO9629338-A1.

XX 26-SEP-1996.

XX 22-MAR-1996; 96WO-US003896.

XX 23-MAR-1995; 95US-00410540.

XX (REGC) UNIV CALIFORNIA.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Miller WL, Lin D, Straus JF;

XX WPI; 1996-443130/44.

XX Isolated human steroidogenesis acute regulatory protein gene - used for
detection of mutation(s) of this gene that cause congenital lipoid
adrenal hyperplasia.

XX Disclosure; Page 4; 89pp; English.

XX The present sequence is a PCR primer (nt 66-84) for the human
steroidogenesis acute regulatory protein (hStAR) cDNA. The hStAR gene can
be analysed for mutations to detect (e.g. prenatally) genetic defects
associated with congenital lipoid adrenal hyperplasia (CAH), or its
transmission to children. CAH can be treated by protein or gene
replacement therapy, which can also be used to prevent or treat
hypercholesterolaemia. A human adrenal cortex cDNA library was screened
with a mouse StAR probe to isolate a 1.6 Kb insert, including an ORF for
a 285 residue protein. When it was cloned into pSPORT and expressed in
COS-1 cells cotransfected with pP450sc and pADX, it increased the level
of pregnenolone synthesis from cholesterol or 20-alpha-hydroxycholesterol

XX Sequence 19 BP; 5 A; 6 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
||||| ||||||| |||||||

Db 1 GCAGCAGCAGCAGCAGCAG 19

RESULT 88

ADH70599/c

ID ADH70599 standard; DNA; 19 BP.

XX ADH70599;

XX 25-MAR-2004 (first entry)

XX Human Vbeta gene repeat sequence #389.

XX human; T-cell associated disease; Vbeta; autoimmune disease;
degenerative nervous system disease; graft versus host disease;
hypersensitivity disease; infectious disease; neoplastic disease;
Addison's disease; atrophic gastritis;
degenerative nervous system disease; multiple sclerosis;
Alzheimer's disease; hypersensitivity; Goodpasture's syndrome;
allergy; type II hypersensitivity; infectious disease; viral infection;
type IV hypersensitivity; leprosy; parasitic infection; schistosoma;
HIV; fungal infection; Candida; parasitic infection; schistosoma;
filaria; bacterial infection; Mycobacterium; neoplastic disease;
lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;
breast cancer; ds.

XX Homo sapiens.

XX US2002150891-A1.

XX 17-OCT-2002.

XX PF 05-MAR-1999; 99US-00263959.
 XX PR 19-SEP-1994; 94US-00309335.
 XX PR 19-SEP-1995; 95US-00531241.
 XX PA (HOOD/) HOOD L E.
 XX FA (ROWE/) ROWEN L.
 XX PI Hood LE, Rowen L;
 XX WPI; 2004-059052/06.
 DR Kit for diagnosing and treating T-cell associated diseases e.g.
 XX autoimmune, degenerative nervous system and infectious disease, comprises
 PT nucleic acid primers specifically priming and allowing amplification of a
 PT Vbeta gene.
 XX Disclosure; SEQ ID NO 793; 164pp; English.
 XX The invention relates to a kit for diagnosing and treating T-cell
 CC associated diseases which comprises a panel of nucleic acid primers
 CC specifically priming and allowing amplification of each Vbeta gene,
 CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant
 CC rejection and diagnosing and treating T-cell associated diseases,
 CC including autoimmune diseases, degenerative nervous system diseases,
 CC graft versus host disease, hypersensitivity diseases, infectious diseases
 CC and neoplastic diseases. Autoimmune diseases include Addison's disease,
 CC atrophic gastritis. Degenerative nervous system diseases include multiple
 CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type
 CC I hypersensitivities such as contact with allergens that lead to
 CC allergies, Type II hypersensitivities such as those present in
 CC Goodpasture's syndrome and Type IV hypersensitivities such as those
 CC manifested in leprosy. Infectious diseases include viral infections
 CC caused by viruses such as HIV, fungal infections such as those caused by
 CC the yeast genus Candida, parasitic infections such as those caused by
 CC schistosomes, filaria and bacterial infections such as those caused by
 CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases
 CC such as leukaemias, lymphomas and cancers such as cancer of the brain,
 CC breast. The present sequence represents a Vbeta gene repeat sequence.
 XX Sequence 19 BP; 0 A; 6 C; 5 G; 8 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1410 AGCAGCAGCAGCAGCAGCA 1428
 DB ||||||| |||||||
 19 AGCAGCAGCAGCAGCAGCA 1
 RESULT 89
 AAT86505/c
 ID AAT86505 standard; DNA; 20 BP.
 AC AAT86505;
 XX 12-MAR-1998 (first entry)
 DE S-adenosylmethionine decarboxylase antisense oligonucleotide #6.
 XX S-adenosylmethionine decarboxylase; SAMDC; antisense oligonucleotide;
 KW antitumour; diagnosis; phosphorothioate; psoriasis; spermine; spermidine;
 KW ss.
 XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /tag= a
 FT /note= "nucleotides are bonded via phosphorothioate"

linkages"
 FT XX WO9605298-A1.
 XX PD 22-FEB-1996.
 XX PF 27-JUL-1995; 95WO-EP002985.
 XX PR 09-AUG-1994; 94US-00287753.
 XX PA (CIBA) CIBA GEIGY AG.
 XX PI Mett H, Haner R, Dean NM;
 XX WPI; 1996-139694/14.
 DR New oligo:nucleotide deriva. specific for S-adenosyl:methionine
 XX decarboxylase related nucleic acid- useful as anti:sense inhibitors of
 PT this enzyme, esp. for treatment of tumours but also as hybridisation
 PT probes for diagnosis.
 XX Example 6; Page 45; 81pp; English.
 XX This sequence represents a phosphorothioate analogue of an antisense
 CC oligonucleotide which targets the translated region of S-
 CC adenosylmethionine decarboxylase (SAMDC) around nucleotides at positions
 CC 979 to 998. Antisense oligonucleotide analogues (AAT86500-14) which
 CC target the SAMDC gene are used to diagnose conditions associated with
 CC expression of SAMDC by specifically hybridising to RNA or DNA derived
 CC from the SAMDC gene. These antisense molecules are useful for therapeutic
 CC modulation (especially inhibition) of SAMDC synthesis, particularly to
 CC treat tumours (e.g. leukaemia, prostatic carcinoma, colon or brain
 CC tumours, but especially bladder cancer), but also other hyper-
 CC proliferative diseases such as psoriasis. They cause tumour regression
 CC and prevent establishment/growth of (micro)metastases. Inhibition of
 CC SAMDC reduces the level of polyamines (spermine and spermidine in cells),
 CC resulting in cytosclerosis and possibly apoptosis
 XX Sequence 20 BP; 0 A; 4 C; 5 G; 11 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1545 AGCAGCAGCAACACAGCA 1563
 DB ||||||| |||||||
 19 AGAAGCAGCAACACAGCA 1
 RESULT 90
 AAA55807/c
 ID AAA55807 standard; DNA; 20 BP.
 XX AAA55807;
 AC AAA55807;
 XX 01-SEP-2000 (first entry)
 DT Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:52.
 DE Human; DNA methyltransferase; DNA Metase; antisense oligonucleotide;
 KW modulation; inhibition; gene expression; combination therapy; pl6;
 KW histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KW methylation; gene therapy; tumour; cytostatic; antiasthmatic;
 KW antiinflammatory; inflammation; asthma; ss.
 XX Homo sapiens.
 OS WO200023112-A1.
 XX 27-APR-2000.
 PD 19-OCT-1999; 99WO-US024278.
 XX PF 19-OCT-1999; 99WO-US024278.

XX The sequences given in AAH3115-21 are oligonucleotides which are
 CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
 CC may be used in combination with an inhibitor of histone deacetylase
 CC enzyme function, to give an improved inhibitory effect, thereby reducing
 CC the amount of inhibitor required to obtain a given inhibitory effect.
 CC Compounds containing these oligonucleotides may be used to treat cell
 CC proliferation conditions such as cancer, restenosis or psoriasis. They
 CC can also be used to treat protozoal and fungal infections
 XX
 SQ Sequence 20 BP; 0 A; 9 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
 Db 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 93
 AAH56611/C
 ID AAH56611 standard; DNA; 20 BP.
 XX
 AC AAH56611;
 XX
 DT 06-SEP-2001 (first entry)
 XX
 DE Streptococcus pyogenes groEL antisense oligonucleotide SEQ ID NO:259.
 XX
 KW Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KW microbial infection; ss.
 XX
 OS Streptococcus pyogenes.
 OS
 PN WO200136625-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 20-NOV-2000; 2000WO-CA001347.
 XX
 PR 18-NOV-1999; 99US-0166249P.
 XX
 PA (GENE-) GENESENSE TECHNOLOGIES INC.
 XX
 PI Wright JA, Young AH, Dugourd D;
 XX
 DR WPI; 2001-355633/37.
 XX

XX Novel antisense compounds targeting nucleic acid encoding groEL or groES
 PT gene of microorganism, which hybridize with and inhibit expression of the
 PT genes, useful to inhibit growth of microorganism having the genes.
 XX
 PS Claim 3; Page 48; 110pp; English.

XX The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or GS
 CC of a microorganism and specifically hybridises with and inhibits the
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral and
 CC antiproliferative activities, and can be used in antisense therapy and
 CC for inhibiting expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or a
 CC virus) having a GL or GS gene which involves administering to the

CC microorganism or to a cell infected with the microorganism, (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organiam
 CC having a pathological condition mediated by microorganisms having a GL or
 CC GS gene and administering (I) such that the growth of microorganism is
 CC inhibited. The antisense compounds are utilised for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention
 XX

SQ Sequence 20 BP; 1 A; 4 C; 5 G; 10 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY ,1456 GCACAGCAACAGCAACAG 1474
 Db 19 GAAACAGCAACAGCAACAG 1

RESULT 94
 AAC89537/C
 ID AAC89537 standard; DNA; 20 BP.
 XX
 AC AAC89537;
 XX
 DT 08-MAR-2001 (first entry)
 XX
 DE Human HDAC-2 PCR primer SEQ ID NO: 7.
 XX
 KW Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
 KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
 KW gene therapy; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200071703-A2.
 XX
 PD 30-NOV-2000.
 XX
 PF 03-MAY-2000; 2000WO-IB001252.
 XX
 PR 03-MAY-1999; 99US-0132287P.
 XX
 PA (METH-) METHYLGENE INC.

XX Macleod AR, Li Z, Besterman JM;
 XX
 DR WPI; 2001-016407/02.

XX Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal.

PS Disclosure; Page 12; 125pp; English.

XX The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia

SQ Sequence 20 BP; 0 A; 9 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX Homo sapiens.
 XX WO200285308-A2.
 XX 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013135.
 XX 24-APR-2001; 2001US-0286137P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX Claim 15; SEQ ID NO 838; 872pp; English.
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 0 A; 5 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1533 CCCACAGCAGCAGCAGCA 1551
 DB 19 CCCACAGCAGCAGCAGCA 1
 RESULT 98
 ABZ86071/c
 ID ABZ86071 standard; DNA; 20 BP.
 XX
 XX ABZ86071;
 XX 17-OCT-2003 (first entry)
 XX Human oligonucleotide sequence.
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX Homo sapiens.
 XX WO200285308-A2.
 XX 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013135.
 XX 24-APR-2001; 2001US-0286137P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX Claim 15; SEQ ID NO 1313; 872pp; English.
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCAGC 1427
 DB 20 CAGCAGCAGCAGCAGCAGC 2
 RESULT 99
 ABZ86075/c
 ID ABZ86075 standard; DNA; 20 BP.
 XX
 XX ABZ86075;
 XX 17-OCT-2003 (first entry)
 XX Human oligonucleotide sequence.
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX Homo sapiens.
 XX WO200285308-A2.
 XX 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013135.
 XX 24-APR-2001; 2001US-0286137P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX Claim 15; SEQ ID NO 1317; 872pp; English.
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cycostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
 Db 20 CAGCAGCAGCAGCAGCAGC 2
 RESULT 100
 ABD22298/c
 ID ABD22298 standard; DNA; 20 BP.
 XX AC ABD22298;
 XX 29-JUL-2004 (first entry)
 DT Human stanniocalcin-derived oligo SEQ ID 1310.
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;

KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 OS Homo sapiens.
 XX WO200285309-A2.
 XX 31-OCT-2002.
 XX 23-APR-2002; 2002WO-US013143.
 XX 24-APR-2001; 2001US-0286036P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-093058/08.
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX Claim 15; SEQ ID NO 1310; 763pp; English.
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic, is a
 CC analgesic, hypotensive, immunosuppressive and cycostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 1.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
 Db 20 CAGCAGCAGCAGCAGCAGC 2
 RESULT 101
 ABD22301/c

ID ABD22301 standard; DNA; 20 BP.
XX ABD22301;
XX 29-JUL-2004 (first entry)
XX Human stanniocalcin-derived oligo SEQ ID 1313.
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX Homo sapiens.
XX WO200285309-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013143.
XX 24-APR-2001; 2001US-0286036P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX Claim 15; SEQ ID NO 1313; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1409 CAGCAGCAGCAGCAGCAGC 1427
Db 20 CAGCAGCAGCAGCAGCAGC 2
RESULT 102
ID ABD22305/c
XX 29-JUL-2004 (first entry)
XX Human stanniocalcin-derived oligo SEQ ID 1317.
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytosolic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX Homo sapiens.
XX WO200285309-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013143.
XX 24-APR-2001; 2001US-0286036P.
XX (EPIG-) EPIGENESIS PHARM INC.
XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX Claim 15; SEQ ID NO 1317; 763pp; English.

This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated

This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating allergies and bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine, (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC targeted to a nucleic acid molecule encoding AP-2 alpha. The compound
CC specifically hybridises with a nucleic acid molecule encoding AP-2 alpha
CC (19868 bp, SEQ ID NO: 4), and inhibits the expression of AP-2 alpha. Also
CC described are: inhibiting the expression of AP-2 alpha in cells or tissues
CC comprising contacting the cells or tissues with (1); screening for a
CC modulator of AP-2 alpha by contacting a preferred target segment of a
CC nucleic acid molecule encoding AP-2 alpha with one or more candidate
CC modulators of AP-2 alpha, and identifying one or more modulators of AP-2
CC alpha expression, which modulate the expression of AP-2 alpha; a
CC diagnostic method for identifying a disease state; and a kit or assay
CC device comprising (1). The compound is useful for treating an animal
CC having a disease or condition associated with AP-2 alpha, particularly a
CC hyperproliferative disorder. The compounds may be used for diagnostics,
CC therapeutics prophylaxis and as research reagents; or as tools in
CC differential and/or combinatorial analyses to elucidate expression
CC patterns of a portion or the entire complement of genes expressed within
CC cells and tissues. This sequence represents a human transcription factor
CC AP-2 antisense oligonucleotide.

XX
SQ Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
Db 1 GCGGCAGCAGCAGCAGCAG 19

RESULT 105
AAA37188/c

ID AAA37188 standard; DNA; 21 BP.

XX AC AAA37188;

XX DT 08-AUG-2000 (first entry)

XX DE Human PRO1315 forward PCR primer SEQ ID NO:105.

XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
PCR primer; hybridisation; probe; ss.

XX OS Homo sapiens.

XX PN WO200012708-A2.

XX PD 09-MAR-2000.

XX PF 01-SEP-1999; 99WO-US020111.

XX PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0098536P.

PR 09-SEP-1998; 98US-0098598P.

PR 09-SEP-1998; 98US-0098598P.

PR 09-SEP-1998; 98US-0098602P.

PR 10-SEP-1998; 98US-0098642P.

PR 10-SEP-1998; 98US-0098741P.

PR 10-SEP-1998; 98US-0098754P.

PR 10-SEP-1998; 98US-0098763P.

PR 15-SEP-1998; 98US-0100390P.

PR 16-SEP-1998; 98US-0100584P.

PR 16-SEP-1998; 98US-0100627P.

PR 16-SEP-1998; 98US-0100661P.

PR 16-SEP-1998; 98US-0100662P.

PR 16-SEP-1998; 98US-0100664P.

PR 17-SEP-1998; 98US-0100683P.

PR 17-SEP-1998; 98US-0100684P.

PR 17-SEP-1998; 98US-0100710P.

PR 17-SEP-1998; 98US-0100711P.

PR 17-SEP-1998; 98US-0100919P.

PR 17-SEP-1998; 98US-0100930P.

PR 18-SEP-1998; 98US-0100848P.

PR 18-SEP-1998; 98US-0100849P.

PR 18-SEP-1998; 98US-0101014P.

PR 18-SEP-1998; 98US-0101068P.

PR 18-SEP-1998; 98US-0101071P.

PR 22-SEP-1998; 98US-0101279P.

PR 23-SEP-1998; 98US-0101471P.

PR 23-SEP-1998; 98US-0101472P.

PR 23-SEP-1998; 98US-0101474P.

PR 23-SEP-1998; 98US-0101475P.

PR 23-SEP-1998; 98US-0101476P.

PR 23-SEP-1998; 98US-0101477P.

PR 23-SEP-1998; 98US-0101479P.

PR 24-SEP-1998; 98US-0101738P.

PR 24-SEP-1998; 98US-0101741P.

PR 24-SEP-1998; 98US-0101743P.

PR 24-SEP-1998; 98US-0101915P.

PR 24-SEP-1998; 98US-0101916P.

PR 29-SEP-1998; 98US-0102207P.

PR 29-SEP-1998; 98US-0102240P.

PR 29-SEP-1998; 98US-0102307P.

PR 29-SEP-1998; 98US-0102330P.

PR 29-SEP-1998; 98US-0102331P.

PR 30-SEP-1998; 98US-0102484P.

PR 30-SEP-1998; 98US-0102487P.

PR 30-SEP-1998; 98US-0102570P.

PR 30-SEP-1998; 98US-0102571P.

PR 01-OCT-1998; 98US-0102684P.

PR 01-OCT-1998; 98US-0102687P.

PR 02-OCT-1998; 98US-0102965P.

PR 06-OCT-1998; 98US-0103258P.

PR 06-OCT-1998; 98US-0103449P.

PR 07-OCT-1998; 98US-0103314P.

PR 07-OCT-1998; 98US-0103315P.

PR 07-OCT-1998; 98US-0103328P.

PR 07-OCT-1998; 98US-0103395P.

PR 07-OCT-1998; 98US-0103396P.

PR 08-OCT-1998; 98US-0103401P.

PR 08-OCT-1998; 98US-0103678P.

PR 08-OCT-1998; 98US-0103679P.

PR 08-OCT-1998; 98US-0103711P.

PR 14-OCT-1998; 98US-0104257P.

PR 20-OCT-1998; 98US-0104987P.

PR 20-OCT-1998; 98US-0105000P.

PR 20-OCT-1998; 98US-0105002P.

PR 21-OCT-1998; 98US-0105104P.

PR 22-OCT-1998; 98US-0105169P.

PR 22-OCT-1998; 98US-0105266P.

PR 26-OCT-1998; 98US-0105693P.

PR 26-OCT-1998; 98US-0105694P.

PR 27-OCT-1998; 98US-0105807P.

PR 27-OCT-1998; 98US-0105881P.

PR 27-OCT-1998; 98US-0105882P.

PR 27-OCT-1998; 98US-0106082P.

PR 28-OCT-1998; 98US-0106023P.

PR 28-OCT-1998; 98US-0106029P.

PR 28-OCT-1998; 98US-0106030P.

PR 28-OCT-1998; 98US-0106032P.

PR 28-OCT-1998; 98US-0106033P.

PR 28-OCT-1998; 98US-0106178P.


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PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
XX
XX (GETH ) GENENTECH INC.
PA
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
PI
XX WPI; 2000-237871/20.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.
XX
XX Example 34; Page 402; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding them have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention
XX
SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 106
AAC73260
ID AAC73260 standard; DNA; 21 BP.
XX
XX AAC73260;
XX
XX 02-FEB-2001 (first entry)
XX
XX SNP flanking sequence #48 used in multiplexing PCR/SBE assay.
XX
XX Oligonucleotide array; genotyping; single base extension reaction; SBE;

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KW polymorphic locus; single nucleotide polymorphism; ss.
XX Unidentified.
XX WO2000058516-A2.
XX
XX 05-OCT-2000.
XX
XX 27-MAR-2000; 2000WO-US008069.
XX
XX 26-MAR-1999; 99US-0126473P.
XX 23-JUN-1999; 99US-0140359P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (AFFY-) AFFYMETRIX INC.
XX
XX Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
XX Ryder T, Sklar P;
XX
XX WPI; 2000-656171/63.
XX
XX Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
XX Example 7; Page 52; 70pp; English.
XX
XX The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one such polymorphic locus
CC used in the present invention. The amplified nucleic acid product is then
CC used as a template in a SBE reaction with an extension primer. Note: This
CC reaction products are used to form the oligonucleotide array. This
CC sequence includes a SNP represented by the degenerate codon in the
XX sequence
XX
SQ Sequence 21 BP; 8 A; 5 C; 7 G; 0 T; 0 U; 1 Other;

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1404 AGCAACAGCAGCAGCAGCAGC 1424
Db 1 AGGACAGCAGCAGCAGCAGC 21

RESULT 107
AAF54275/c
ID AAF54275 standard; DNA; 21 BP.
XX
XX AAF54275;
XX
XX 02-APR-2001 (first entry)
XX
XX Primer #26 used in the identification of proteins.
XX
XX Secreted; transmembrane; gene therapy; ss.
XX Unidentified.
XX
XX WO2000078961-A1.
XX
XX 28-DEC-2000.
XX
XX 18-FEB-2000; 2000WO-US004342.
XX
XX 23-JUN-1999; 99US-0141037P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.

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PR 01-SEP-1999; 99WO-US020111. 98US-0098723P.
PR 29-OCT-1999; 99US-0162508P. 98US-0098749P.
PR 30-NOV-1999; 99WO-US028313. 98US-0098750P.
PR 02-DEC-1999; 99WO-US028551. 98US-0098803P.
PR 16-DEC-1999; 99WO-US030095. 98US-0098821P.
PR 05-JAN-2000; 2000WO-US000219. 98US-0098843P.
PR 06-JAN-2000; 2000WO-US000376. 98US-0099536P.
XX (GETH ) GENENTECH INC. 98US-0099596P.
PA 98US-0099598P.
XX 98US-0099602P.
XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S; 98US-0099642P.
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; 98US-0099741P.
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK; 98US-0099754P.
PI Williams PW, Wood WI; 98US-0099763P.
XX WPI; 2001-071395/08. 98US-0099792P.
DR 98US-0099808P.
XX 98US-0099812P.
XX 98US-0099815P.
PT Secreted and transmembrane proteins and nucleic acids designated PRO, 98US-0099816P.
PT useful as hybridization probes, in chromosome and gene mapping and gene 98US-0100388P.
PT therapy. 98US-0100389P.
XX Example 34; Page 416; 787bp; English. 98US-0100584P.
XX The present invention relates to secreted and transmembrane proteins. 98US-0100627P.
CC These proteins and the DNA encoding them may be used as hybridization 98US-0100661P.
CC probes, in chromosome and gene mapping and in the generation of anti- 98US-0100662P.
CC sense RNA and DNA. They may also be used to generate either 98US-0100664P.
CC transgenic animals or knockout animals which are in turn useful for 98US-0100683P.
CC development and screening of therapeutically useful reagents. The nucleic 98US-0100684P.
CC acids may also be used in gene therapy 98US-0100710P.
XX Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other; 98US-0100711P.
SQ 98US-0100919P.
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGCAGCAACAGCAGCAGC 2
RESULT 108
ACD68312/C
ID ACD68312 standard; DNA; 21 BP.
XX
XX
AC ACD68312;
XX
DT 17-SEP-2003 (first entry)
XX
DE
DE Novel human secreted and transmembrane protein related primer #23.
XX
XX Human; secreted and transmembrane protein; PRO; angiogenesis;
KW endothelial cell proliferation; wound healing; immune response;
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
KW cardiac insufficiency disorder; calcium flux; inflammation;
KW vascular endothelial growth factor-stimulated proliferation;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
KW pancreatic beta-cell precursor cell differentiation; thalassemias;
KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
KW cartilage disorder; sports injury; arthritis; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX US2003073130-A1.
PN
XX
XX 17-APR-2003.
PD
XX
XX 11-DEC-2001; 2001US-00015869.
PF
XX
XX 01-SEP-1998; 98US-0098716P.
PR

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PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106454P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US004520.
PR 01-MAR-2001; 2001WO-US008666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-585293/55.
XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
PT muscle cells, and are useful for treating diabetes, hyper- or hypo-
PT insulinemia.
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCACAGCAGCAGC 2
|||||
|||||

RESULT 109
ACH04114/c
ID ACH04414 standard; DNA; 21 BP.
XX
AC ACH04414;
XX
DT 01-OCT-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX Human; ss; PCR: secreted protein; transmembrane protein; PRO; vulnery;
KW cardiant; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
KW adrenal cortical capillary; endothelial cell growth; wound healing;
KW stimulated T-lymphocyte proliferation; immune response suppression;
KW neonatal heart hypertrophy; cardiac insufficiency disorder;
KW vascular endothelial growth factor; inflammation; mononuclear cell;
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
KW sports injury; arthritis; primer.
XX
OS Homo sapiens.
XX
XX US2003044841-A1.
PN
XX
PD 06-MAR-2003.
XX
XX 06-DEC-2001; 2001US-00006856.
XX
XX 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
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PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
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PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
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PR 10-SEP-1998; 98US-0099816P.
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PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
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XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2003-492259/46.
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CC medicament for treating a condition responsive to a PRO polypeptide. The
CC polypeptides are useful in a number of functional biological assays, as
CC molecular weight markers for protein electrophoresis and as therapeutic
CC agents. The polynucleotides are useful as hybridisation probes for a cDNA

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KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.

XX OS Homo sapiens.

XX US2003099625-A1.

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PR 23-SEP-1998; 98US-0101477P.
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PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
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PR 26-OCT-1998; 98US-0105693P.
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PR 27-OCT-1998; 98US-0105807P.
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PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
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PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
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PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.

PT hypo-insulinemia, sports injuries and arthritis.
XX Example 34; SEQ ID NO 105; 557pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
transmembrane protein) having at least 80% amino acid sequence identity
to an amino acid sequence chosen from 123 fully defined sequences as
given in the specification (including their extracellular domains either
with or without their associated signal peptides. Also include are the
nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
host cell comprising the vector, producing PRO, a chimaeric molecule
comprising PRO fused to a heterologous amino acid sequence, and an anti-
PRO antibody. PRO is useful as molecular weight markers for protein
electrophoresis and also for chromosome identification. PRO is also
useful for tissue typing. PRO and PRO NA are useful as hybridisation
probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
useful for generating transgenic animals or knock-out animals which are
useful in development and screening useful reagents. PRO NA is also
useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
polypeptides are useful for suppressing immune response. PRO1246
polypeptide is useful for treating cardiac insufficiency disorders.
PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
PRO1561 polypeptide are useful for stimulating calcium flux in human
umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
polypeptides are useful for treating bone and/or cartilage disorders
(e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
polypeptides are useful for treating diabetes in skeletal muscle cells
and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
treating Berger disease or other nephropathies associated with Schönlain-
Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
PRO1410 and PRO1575 are useful in treating thalassaemias. The present
sequence is a PCR primer used to isolate a cDNA encoding a PRO protein of
the invention.

XX SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1400 CAGCAGCAACGACGACG 1418
Db 20 CAGGAGCAACGACGACG 2
RESULT 114
ADD70143/c
ID ADD70143 standard; DNA; 21 BP.
XX AC ADD70143;
XX DT 15-JAN-2004 (first entry)
XX XX Human secreted/transmembrane protein PRO1315 PCR primer #1.
KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schönlain-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
XX OS Homo sapiens.
XX XX US2003054406-A1.
XX PN 20-MAR-2003.
XX PD 06-DEC-2001; 2001US-00006818.
XX PF 01-SEP-1998; 98US-0099716P.
XX PR

PR 01-SEP-1998; 98US-0098723P.
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PR 01-SEP-1998; 98US-0098750P.
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PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 03-SEP-1998; 98US-0099536P.
PR 03-SEP-1998; 98US-0099596P.
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PR 03-SEP-1998; 98US-0099602P.
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PR 10-SEP-1998; 98US-0099808P.
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PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
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PR 07-OCT-1998; 98US-0103396P.
PR 08-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.

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PR 03-NOV-1998; 98US-0106933P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
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PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
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PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028133.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US008520.
PR 01-MAR-2001; 2001WO-US008666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
XX Pan J, Paoni NP, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
XX Williams PM, Wood WI;
XX WPI; 2003-708344/67.
XX Novel isolated PRO polypeptide useful for tissue typing, modulating
XX biological activity of cell, as molecular weight markers in protein
XX electrophoresis, for treating arthritis, tumor.
XX Example 34; SEQ ID NO 105; 549pp; English.
XX The invention relates to an isolated PRO polypeptide (secreted or
XX transmembrane protein) having at least 80% amino acid sequence identity
XX Query Match 0.5%; Score 17.4; DB 1; Length 21;
XX Best Local Similarity 94.7%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1400 CAGCAGCACAGCAGCAGC 1418
DB 20 CAGGAGCACAGCAGCAGC 2
RESULT 115
ADD38264/C
ID ADD38264 standard; DNA; 21 BP.
XX AC ADD38264;
XX DT 15-JAN-2004 (first entry)
XX DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
XX Homo sapiens.
XX US2003096955-A1.
XX 22-MAY-2003.
XX 07-DEC-2001; 2001US-00012755.
XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
XX 09-SEP-1998; 98US-0099536P.
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PR	15-SEP-1998;	98US-01000390P.	PR	29-OCT-1998;	98US-0106384P.
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PR	16-SEP-1998;	98US-0100662P.	PR	03-NOV-1998;	98US-0106902P.
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PR	18-SEP-1998;	98US-0101068P.	PR	17-NOV-1998;	98US-0108802P.
PR	22-SEP-1998;	98US-0101071P.	PR	17-NOV-1998;	98US-0108806P.
PR	23-SEP-1998;	98US-0101279P.	PR	17-NOV-1998;	98US-0108807P.
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PR	23-SEP-1998;	98US-0101474P.	PR	18-NOV-1998;	98US-0108848P.
PR	23-SEP-1998;	98US-0101475P.	PR	18-NOV-1998;	98US-0108849P.
PR	23-SEP-1998;	98US-0101476P.	PR	18-NOV-1998;	98US-0108850P.
PR	23-SEP-1998;	98US-0101477P.	PR	18-NOV-1998;	98US-0108851P.
PR	23-SEP-1998;	98US-0101479P.	PR	18-NOV-1998;	98US-0108852P.
PR	24-SEP-1998;	98US-0101738P.	PR	18-NOV-1998;	98US-0108858P.
PR	24-SEP-1998;	98US-0101741P.	PR	18-NOV-1998;	98US-0108904P.
PR	24-SEP-1998;	98US-0101915P.	PR	22-DEC-1998;	98US-0113296P.
PR	24-SEP-1998;	98US-0102191P.	PR	30-DEC-1998;	98US-0114223P.
PR	29-SEP-1998;	98US-0102207P.	PR	05-JAN-1999;	98US-0114223P.
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PR	30-SEP-1998;	98US-0102331P.	PR	26-JUL-1999;	98US-0145698P.
PR	30-SEP-1998;	98US-0102484P.	PR	01-SEP-1999;	98US-0145698P.
PR	30-SEP-1998;	98US-0102487P.	PR	15-SEP-1999;	98US-0145698P.
PR	30-SEP-1998;	98US-0102570P.	PR	29-OCT-1999;	98US-0162506P.
PR	30-SEP-1998;	98US-0102571P.	PR	30-NOV-1999;	98US-0162506P.
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PR 20-JUN-2001; 2001WO-US019592.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX (GETH ) GENENTECH INC.
XX
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WFI; 2003-787000/74.
XX
XX Novel isolated PRO polypeptide, useful for treating cancerous tumors,
PT cardiac insufficiency disorders, wound healing, diabetes mellitus,
PT thalassemias.
XX
XX Example 34; SEQ ID NO 105; 556pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2
RESULT 116
ADD39220/C
ID ADD39220 standard; DNA; 21 BP.
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XX AC ADD39220;
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XX DT 15-JAN-2004 (first entry)
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XX DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
XX
XX OS Homo sapiens.
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XX PN US2003096954-A1.
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XX PD 22-MAY-2003.
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XX PF 07-DEC-2001; 2001US-00011671.
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XX PR 01-SEP-1998; 98US-0098716P.
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(GETH) GENENTECH INC.

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PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
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DR WPI; 2003-765477/72.

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XX (GETH ) GENENTECH INC.
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XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX
XX WPI; 2003-755104/71.
XX
XX New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
XX PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
XX insufficiency disorders.
XX
XX Example 34; SEQ ID NO 105; 550pp; English.
XX
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CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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XX
DT 29-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
XX
OS Homo sapiens.
XX
XX US2003069179-A1.
XX
PD 10-APR-2003.
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XX 11-DEC-2001; 2001US-00015393.
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RESULT 120
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AC ADE20007;
XX
XX
DT 29-JAN-2004 (first entry)
XX
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XX
KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
XX
OS Homo sapiens.
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PD 15-MAY-2003.
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PF 10-DEC-2001; 2001US-00013430.
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PR 30-DEC-1998; 98US-0114223P.
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PR 15-SEP-1999; 99WO-US021194.
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PI Gao W, Goddard A, Godowski RJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PW, Wood WI;
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DR WPI; 2003-765493/72.
XX
XX New isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis and tumors.
XX
PS Example 34; SEQ ID NO 105; 555pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. NO. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schönlain-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
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XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-765413/72.
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DR
XX
PT Novel isolated PRO polypeptides useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis and tumors.
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Query Match 0.5%; Score 17.4; DB 1; Length 21;
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Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpetiformis; Crohn's disease; thalassaemia; ss.
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PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-755105/71.
XX
XX Novel secreted and transmembrane PRO polypeptides useful for treating
PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
PT hypo-insulinemia, sports injuries and arthritis.
XX
XX Example 34; SEQ ID NO 105; 548bp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2
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DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
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XX
XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2003-900674/82.
XX
XX New PRO nucleic acid, useful for the manufacture of a medicament for
XX diagnosing or treating tumor or for tissue typing.
XX
XX Example 34; SEQ ID NO 105; 558bp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
XX transmembrane protein) having at least 80% amino acid sequence identity
XX to an amino acid sequence chosen from 123 fully defined sequences as
XX given in the specification (including their extracellular domains either
XX or without their associated signal peptides. Also include are the
XX
XX Query Match 0.5%; Score 17.4; DB 1; Length 21;
XX Best Local Similarity 94.7%; Pred. No. 1.4e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1400 CAGCAGCAACAGCAGCAGC 1418
XX Db 20 CAGCAGCAACAGCAGCAGC 2
XX
XX RESULT 124
XX ADF55794/c
XX ID ADF55794 standard; DNA; 21 BP.
XX
XX AC ADF55794;
XX
XX DT 12-FEB-2004 (first entry)
XX
XX DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
XX
XX OS Homo sapiens.
XX
XX US2003204054-A1.
XX
XX 30-OCT-2003.
XX
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 XX 17-NOV-1998; 98US-0108787P.
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 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2003-900675/82.
 DR New PRO nucleic acid, useful for the manufacture of a medicament for
 PT diagnosing or treating tumor or for tissue typing.
 XX Example 34; SEQ ID NO 105; 558pp; English.
 PS The invention relates to an isolated PRO polypeptide (secreted or
 CC transmembrane protein) having at least 80% amino acid sequence identity
 CC to an amino acid sequence chosen from 123 fully defined sequences as
 CC given in the specification (including their extracellular domains either
 CC or without their associated signal peptides. Also include are the
 CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
 CC host cell comprising the vector, producing PRO, a chimeric molecule
 CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
 CC PRO antibody. PRO is useful as molecular weight markers for protein
 CC electrophoresis and also for chromosome identification. PRO is also
 CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
 CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
 CC useful for generating transgenic animals or knock-out animals which are
 CC useful in development and screening useful reagents. PRO NA is also
 CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
 CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
 CC polypeptides are useful for suppressing immune response. PRO1246
 CC polypeptide is useful for treating cardiac insufficiency disorders.
 CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
 CC PRO1561 polypeptide are useful for stimulating calcium flux in human
 CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
 CC polypeptides are useful for treating bone and/or cartilage disorders
 CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
 CC polypeptides are useful for treating diabetes in skeletal muscle cells
 CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
 CC treating Berger disease or other nephropathies associated with Schonlein-
 CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
 CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
 CC sequence is a PCR primer used to isolate a cDNA encoding a PRO protein of
 CC the invention.
 XX Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Beat Local Similarity 94.7%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 XX AC ADH99298;
 XX 15-APR-2004 (first entry)
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DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
 XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
 XX Homo sapiens.
 XX US2003065142-A1.
 XX 03-APR-2003.
 XX 11-DEC-2001; 2001US-00015499.
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KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
XX Homo sapiens.
XX US2003195347-A1.
XX 16-OCT-2003.
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PR	15-MAR-2000; 2000WO-US006884.	PR	01-SEP-1998; 98US-0098749P.	PR
PR	17-MAY-2000; 2000WO-US013705.	PR	02-SEP-1998; 98US-0098750P.	PR
PR	22-MAY-2000; 2000WO-US014042.	PR	02-SEP-1998; 98US-0098803P.	PR
PR	30-MAY-2000; 2000WO-US014941.	PR	02-SEP-1998; 98US-0098821P.	PR
PR	02-JUN-2000; 2000WO-US015264.	PR	02-SEP-1998; 98US-0098843P.	PR
PR	23-AUG-2000; 2000WO-US023522.	PR	09-SEP-1998; 98US-0099536P.	PR
PR	24-AUG-2000; 2000WO-US023328.	PR	09-SEP-1998; 98US-0099596P.	PR
PR	08-NOV-2000; 2000WO-US030952.	PR	09-SEP-1998; 98US-0099598P.	PR
PR	10-NOV-2000; 2000WO-US030873.	PR	09-SEP-1998; 98US-0099602P.	PR
PR	01-DEC-2000; 2000WO-US032678.	PR	09-SEP-1998; 98US-0099642P.	PR
PR	28-FEB-2001; 2001WO-US006520.	PR	10-SEP-1998; 98US-0099741P.	PR
PR	01-MAR-2001; 2001WO-US006666.	PR	10-SEP-1998; 98US-0099754P.	PR
PR	01-JUN-2001; 2001WO-US017800.	PR	10-SEP-1998; 98US-0099763P.	PR
PR	20-JUN-2001; 2001WO-US019692.	PR	10-SEP-1998; 98US-0099812P.	PR
PR	29-JUN-2001; 2001WO-US021066.	PR	10-SEP-1998; 98US-0099815P.	PR
PR	09-JUL-2001; 2001WO-US021735.	PR	10-SEP-1998; 98US-0099816P.	PR
PR	04-SEP-2001; 2001US-00946374.	PR	15-SEP-1998; 98US-0100385P.	PR
XX	(GETH) GENENTECH INC.	PR	15-SEP-1998; 98US-0100388P.	PR
XX		PR	15-SEP-1998; 98US-0100390P.	PR
PI	Baker KP, Botstein D, Deanoyers L, Eaton DL, Ferrara N, Fong S;	PR	16-SEP-1998; 98US-0100584P.	PR
PI	Gao W, Goddard A, Godowski RJ, Grimaldi JC, Gurney AL, Hillan KJ;	PR	16-SEP-1998; 98US-0100627P.	PR
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;	PR	16-SEP-1998; 98US-0100661P.	PR
PI	Williams PM, Wood WI;	PR	16-SEP-1998; 98US-0100662P.	PR
XX		PR	16-SEP-1998; 98US-0100664P.	PR
DR	WPI; 2004-021098/02.	PR	17-SEP-1998; 98US-0100683P.	PR
XX		PR	17-SEP-1998; 98US-0100684P.	PR
XX	New secreted and transmembrane PRO nucleic acid, for use in molecular	PR	17-SEP-1998; 98US-0100710P.	PR
PT	biology, chromosome and gene mapping, in generating antisense RNA and	PR	17-SEP-1998; 98US-0100711P.	PR
PT	DNA, in various diagnostic assays and in gene therapy.	PR	17-SEP-1998; 98US-0100819P.	PR
XX		PR	17-SEP-1998; 98US-0100830P.	PR
PS	Example 34; SEQ ID NO 105; 552pp; English.	PR	18-SEP-1998; 98US-0100848P.	PR
XX		PR	18-SEP-1998; 98US-0100849P.	PR
CC	The invention relates to an isolated PRO polypeptide (secreted or	PR	18-SEP-1998; 98US-0101014P.	PR
CC	transmembrane protein) having at least 80% amino acid sequence identity	PR	18-SEP-1998; 98US-0101068P.	PR
CC	to an amino acid sequence chosen from 123 fully defined sequences as	PR	18-SEP-1998; 98US-0101071P.	PR
CC	given in the specification (including their extracellular domains either	PR	22-SEP-1998; 98US-0101279P.	PR
	Query Match 0.5%; Score 17.4; DB 1; Length 21;	PR	23-SEP-1998; 98US-0101471P.	PR
	Best Local Similarity 94.7%; Pred. No. 1.4e+02;	PR	23-SEP-1998; 98US-0101472P.	PR
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	PR	23-SEP-1998; 98US-0101474P.	PR
		PR	23-SEP-1998; 98US-0101475P.	PR
		PR	23-SEP-1998; 98US-0101476P.	PR
		PR	23-SEP-1998; 98US-0101477P.	PR
		PR	23-SEP-1998; 98US-0101479P.	PR
QY	1400 CAGCAGCAACAGCAGCAGC 1418	PR	24-SEP-1998; 98US-0101738P.	PR
		PR	24-SEP-1998; 98US-0101741P.	PR
Db	20 CAGGAGCAACAGCAGCAGC 2	PR	24-SEP-1998; 98US-0101743P.	PR
		PR	24-SEP-1998; 98US-0101915P.	PR
RESULT 127		PR	24-SEP-1998; 98US-0101916P.	PR
ADF25789/c		PR	29-SEP-1998; 98US-0102207P.	PR
ID ADF25789 standard; DNA; 21 BP.		PR	29-SEP-1998; 98US-0102240P.	PR
XX		PR	29-SEP-1998; 98US-0102307P.	PR
AC	ADF25789;	PR	29-SEP-1998; 98US-0102330P.	PR
XX		PR	29-SEP-1998; 98US-0102331P.	PR
DT	12-FEB-2004 (first entry)	PR	29-SEP-1998; 98US-0102484P.	PR
XX		PR	30-SEP-1998; 98US-0102487P.	PR
DE	Human secreted/transmembrane protein PRO1315 PCR primer #1.	PR	30-SEP-1998; 98US-0102570P.	PR
XX		PR	30-SEP-1998; 98US-0102571P.	PR
KW	Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;	PR	30-SEP-1998; 98US-0102684P.	PR
KW	immune response; cardiac insufficiency disorder; calcium flux;	PR	01-OCT-1998; 98US-0102687P.	PR
KW	umbilical vein endothelial cell; bone disorder; cartilage disorder;	PR	02-OCT-1998; 98US-0102965P.	PR
KW	arthritis; wound healing; diabetes; skeletal muscle cells; obesity;	PR	06-OCT-1998; 98US-0103258P.	PR
KW	Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;	PR	06-OCT-1998; 98US-0103449P.	PR
KW	dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.	PR	07-OCT-1998; 98US-0103314P.	PR
XX		PR	07-OCT-1998; 98US-0103315P.	PR
OS	Homo sapiens.	PR	07-OCT-1998; 98US-0103328P.	PR
XX		PR	07-OCT-1998; 98US-0103395P.	PR
PN	US2003199675-A1.			
XX				
XX	23-OCT-2003.			
PD				

PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 15-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
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PR 17-SEP-1998; 98US-0100711P.
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PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101273P.
PR 23-SEP-1998; 98US-0101471P.
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PR 23-SEP-1998; 98US-0101474P.
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PR 23-SEP-1998; 98US-0101476P.
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PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
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PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
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PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
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PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
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PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
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PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
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PR 18-NOV-1998; 98US-0108849P.
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PR 18-NOV-1998; 98US-0108851P.
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PR 18-NOV-1998; 98US-0108858P.
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PR 30-DEC-1998; 98US-0114223P.
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PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005804.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
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PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.

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PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019892.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2004-041347/04.
XX
XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
XX
XX Example 34; SEQ ID NO 105; 553pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1400 CAGCGACCAACAGCAGCAGC 1418
Db 20 CAGCGACCAACAGCAGCAGC 2
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AC ADF29424;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
XX
OS Homo sapiens.
XX
XX US2003203401-A1.
XX
XX 30-OCT-2003.
XX
XX 11-DEC-2001; 2001US-00015519.
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XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
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XX 02-SEP-1998; 98US-0098821P.
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XX 09-SEP-1998; 98US-0099536P.
XX 09-SEP-1998; 98US-0099596P.
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XX 09-SEP-1998; 98US-0099642P.
XX 10-SEP-1998; 98US-0099741P.
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PR 18-NOV-1998; 98US-0108849P.
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PR 20-JUL-1999; 98US-0144750P.
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PR 02-DEC-1999; 98US-0162506P.
PR 16-DEC-1999; 98US-0162506P.
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PR 06-JAN-2000; 98US-0162506P.
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PR 18-FEB-2000; 98US-0162506P.
PR 24-FEB-2000; 98US-0162506P.
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PR 15-MAR-2000; 98US-0162506P.
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PR 22-MAY-2000; 98US-0162506P.
PR 30-MAY-2000; 98US-0162506P.
PR 02-JUN-2000; 98US-0162506P.
PR 23-AUG-2000; 98US-0162506P.
PR 24-AUG-2000; 98US-0162506P.
PR 08-NOV-2000; 98US-0162506P.
PR 10-NOV-2000; 98US-0162506P.
PR 01-DEC-2000; 98US-0162506P.
PR 28-FEB-2001; 98US-0162506P.
PR 01-MAR-2001; 98US-0162506P.
PR 01-JUN-2001; 98US-0162506P.
PR 20-JUN-2001; 98US-0162506P.
PR 29-JUN-2001; 98US-0162506P.

PR C9-JUL-2001; 2001WO-US021735.
PR C4-SEP-2001; 2001US-00946374.
PR (GETH ) GENENTECH INC.
PR Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,
PI Williams PM, Wood WJ;
XX WPI; 2004-041478/04.
XX New isolated PRO polypeptide useful for tissue typing, modulating the
PT biological activity of a cell, as molecular weight markers in protein
PT electrophoresis, and for treating e.g. arthritis, or tumor.
XX Example 34; SEQ ID NO 105; 551pp; English.
XX the invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC transmembrane protein) having at least 80% amino acid sequence identity

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCACAGCAGCAGC 1418
DB 20 CAGCAGCACAGCAGCAGC 2

RESULT 130
ADE96955/c
ID ADE96955 standard; DNA; 21 BP.
AC ADE96955;
XX ADE96955;
XX ADE96955;
DT 12-FEB-2004 (first entry)
DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX dermatitis; herpeticiformis; Crohn's disease; thalassemia; es.
XX Homo sapiens.
XX US2003195334-A1.
XX 16-OCT-2003.
XX 07-DEC-2001; 2001US-00012753.
XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
XX 02-SEP-1998; 98US-0098953P.
XX 09-SEP-1998; 98US-0099596P.
XX 09-SEP-1998; 98US-0099598P.
XX 09-SEP-1998; 98US-0099602P.
XX 09-SEP-1998; 98US-0099642P.
XX 10-SEP-1998; 98US-0099741P.
XX 10-SEP-1998; 98US-0099754P.
XX 10-SEP-1998; 98US-0099763P.
XX 10-SEP-1998; 98US-0099792P.
XX 10-SEP-1998; 98US-0099808P.
XX 10-SEP-1998; 98US-0099812P.
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XX WPI; 2004-041280/04.
XX
XX DR
XX PT New isolated PRO polypeptides useful for treating diseases such as cancer
XX and diabetes.
XX
XX Example 34; SEQ ID NO 105; 551pp; English.
XX
XX PS
XX CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1400 CAGCAGCAACGACGACG 1418
Db 20 CAGGAGCAACGACGACG 2
RESULT 131
ADH02993/c
ID ADH02993 standard; DNA; 21 BP.
XX
XX AC ADH02993;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
XX KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX dermatitis; herpetiformis; Crohn's disease; thalassaemia; ss.
XX
XX OS Homo sapiens.
XX
XX US2003216562-A1.
XX
XX PD 20-NOV-2003.
XX
XX PF 12-DEC-2001; 2001US-00015390.
XX
XX PR 01-SEP-1998; 98US-0098718P.
XX PR 01-SEP-1998; 98US-0098723P.
XX PR 01-SEP-1998; 98US-0098749P.
XX PR 01-SEP-1998; 98US-0098750P.
XX PR 02-SEP-1998; 98US-0098803P.
XX PR 02-SEP-1998; 98US-0098821P.
XX PR 02-SEP-1998; 98US-0098843P.
XX PR 02-SEP-1998; 98US-0099536P.
XX PR 09-SEP-1998; 98US-0099596P.
XX PR 09-SEP-1998; 98US-0099598P.
XX PR 09-SEP-1998; 98US-0099602P.
XX PR 09-SEP-1998; 98US-0099642P.
XX PR 10-SEP-1998; 98US-0099741P.
XX PR 10-SEP-1998; 98US-0099754P.
XX PR 10-SEP-1998; 98US-0099763P.
XX PR 10-SEP-1998; 98US-0099792P.
XX PR 10-SEP-1998; 98US-0099808P.
XX PR 10-SEP-1998; 98US-0099812P.
XX PR 10-SEP-1998; 98US-0099815P.
XX PR 10-SEP-1998; 98US-0099816P.
XX PR 15-SEP-1998; 98US-0100385P.
XX PR 15-SEP-1998; 98US-0100388P.
XX PR 15-SEP-1998; 98US-0100390P.
XX PR 16-SEP-1998; 98US-0100584P.
XX PR 16-SEP-1998; 98US-0100627P.
XX PR 16-SEP-1998; 98US-0100661P.
XX PR 16-SEP-1998; 98US-0100662P.
XX PR 16-SEP-1998; 98US-0100664P.
XX PR 17-SEP-1998; 98US-0100683P.
XX PR 17-SEP-1998; 98US-0100684P.
XX PR 17-SEP-1998; 98US-0100710P.
XX PR 17-SEP-1998; 98US-0100711P.
XX PR 17-SEP-1998; 98US-0100919P.
XX PR 17-SEP-1998; 98US-0100930P.
XX PR 18-SEP-1998; 98US-0100848P.
XX PR 18-SEP-1998; 98US-0100849P.
XX PR 18-SEP-1998; 98US-0101014P.
XX PR 18-SEP-1998; 98US-0101068P.
XX PR 18-SEP-1998; 98US-0101071P.
XX PR 18-SEP-1998; 98US-0101279P.
XX PR 22-SEP-1998; 98US-0101471P.
XX PR 23-SEP-1998; 98US-0101472P.
XX PR 23-SEP-1998; 98US-0101474P.
XX PR 23-SEP-1998; 98US-0101475P.
XX PR 23-SEP-1998; 98US-0101476P.
XX PR 23-SEP-1998; 98US-0101479P.
XX PR 24-SEP-1998; 98US-0101738P.
XX PR 24-SEP-1998; 98US-0101741P.
XX PR 24-SEP-1998; 98US-0101743P.
XX PR 24-SEP-1998; 98US-0101915P.
XX PR 24-SEP-1998; 98US-0101916P.
XX PR 29-SEP-1998; 98US-010207P.
XX PR 29-SEP-1998; 98US-0102240P.
XX PR 29-SEP-1998; 98US-0102307P.
XX PR 29-SEP-1998; 98US-0102330P.
XX PR 29-SEP-1998; 98US-0102331P.
XX PR 30-SEP-1998; 98US-0102484P.
XX PR 30-SEP-1998; 98US-0102487P.
XX PR 30-SEP-1998; 98US-0102570P.
XX PR 30-SEP-1998; 98US-0102571P.
XX PR 01-OCT-1998; 98US-0102684P.
XX PR 01-OCT-1998; 98US-0102687P.
XX PR 06-OCT-1998; 98US-0102965P.
XX PR 06-OCT-1998; 98US-0103258P.
XX PR 06-OCT-1998; 98US-0103449P.
XX PR 07-OCT-1998; 98US-0103314P.
XX PR 07-OCT-1998; 98US-0103315P.
XX PR 07-OCT-1998; 98US-0103328P.
XX PR 07-OCT-1998; 98US-0103395P.
XX PR 07-OCT-1998; 98US-0103396P.
XX PR 07-OCT-1998; 98US-0103401P.
XX PR 08-OCT-1998; 98US-0103633P.
XX PR 08-OCT-1998; 98US-0103678P.
XX PR 08-OCT-1998; 98US-0103679P.
XX PR 08-OCT-1998; 98US-0103711P.
XX PR 14-OCT-1998; 98US-0104257P.
XX PR 20-OCT-1998; 98US-0104987P.
XX PR 20-OCT-1998; 98US-0105000P.
XX PR 20-OCT-1998; 98US-0105002P.
XX PR 22-OCT-1998; 98US-0105104P.
XX PR 22-OCT-1998; 98US-0105169P.
XX PR 26-OCT-1998; 98US-0105266P.
XX PR 26-OCT-1998; 98US-0105693P.
XX PR 26-OCT-1998; 98US-0105694P.
XX PR 27-OCT-1998; 98US-0105807P.
XX PR 27-OCT-1998; 98US-0105881P.
XX PR 27-OCT-1998; 98US-0105882P.
XX PR 27-OCT-1998; 98US-0106062P.
XX PR 28-OCT-1998; 98US-0106023P.
XX PR 28-OCT-1998; 98US-0106029P.
XX PR 28-OCT-1998; 98US-0106030P.
XX PR 28-OCT-1998; 98US-0106032P.
XX PR 28-OCT-1998; 98US-0106033P.
XX PR 29-OCT-1998; 98US-0106178P.
XX PR 29-OCT-1998; 98US-0106248P.
XX PR 29-OCT-1998; 98US-0106384P.
XX PR 29-OCT-1998; 98US-0108500P.
XX PR 30-OCT-1998; 98US-0106464P.
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PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113286P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 28-JUL-1999; 99US-0145021P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
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PR 03-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030973.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH ) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2004-021867/02.
XX Novel isolated PRO polypeptide useful for treating tumor, kidney
XX disorders, diabetes mellitus, thalassemias.
XX Example 34; SEQ ID NO 105; 552pp; English.
PS
```

XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 132
ADH03947/c
ID ADH03947 standard; DNA; 21 BP.
XX AC ADH03947;
XX 11-MAR-2004 (first entry)
XX Human secreted/transmembrane protein PRO1315 PCR primer #1.
DE Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; neuropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
XX Homo sapiens.
XX OS
XX US2003220471-A1.
XX 27-NOV-2003.
XX 06-DEC-2001; 2001US-00006746.
XX 04-SEP-2001; 2001US-00946374.
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2004-010888/01.
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
XX in gene therapy, chromosome identification, tissue typing, or as
XX hybridization probes in chromosome and gene mapping.
XX Example 34; SEQ ID NO 105; 554pp; English.
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimeric molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. Pro is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful for generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are

CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
 CC polypeptides are useful for suppressing immune response. PRO1246
 CC polypeptide is useful for treating cardiac insufficiency disorders.
 CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
 CC PRO1561 polypeptide are useful for stimulating calcium flux in human
 CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
 CC polypeptides are useful for treating bone and/or cartilage disorders
 CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
 CC polypeptides are useful for treating diabetes in skeletal muscle cells
 CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
 CC treating Berger disease or other nephropathies associated with Schonlein-
 CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
 CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
 CC sequence is a PCR primer used to isolate a cDNA encoding a PRO protein of
 CC the invention.
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1400 CAGCAGCAACAGCAGCAGC 1418
 Db 20 CAGGAGCAACAGCAGCAGC 2
 RESULT 133
 ADH03470/C
 ID ADH03470 standard; DNA; 21 BP.
 XX
 AC ADH03470;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
 XX
 KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
 XX
 OS Homo sapiens.
 XX
 FN US2003224478-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 21-AUG-2002; 2002US-00226254.
 XX
 PR 29-OCT-1999; 99US-0162506P.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2004-022072/02.
 XX
 PT New secreted and transmembrane PRO polypeptides and nucleic acid
 PT molecules, useful in gene therapy, or preparing a medicament for treating
 PT a condition that is responsive to the PRO polypeptide or anti-PRO
 PT antibody, e.g. cancer.
 XX
 PS Example 34; SEQ ID NO 105; 557pp; English.
 XX

CC The invention relates to an isolated PRO polypeptide (secreted or
 CC transmembrane protein) having at least 80% amino acid sequence identity
 CC to an amino acid sequence chosen from 123 fully defined sequences as
 CC given in the specification (including their extracellular domains either
 CC or without their associated signal peptides. Also include are the
 CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
 CC host cell comprising the vector, producing PRO, a chimaeric molecule
 CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
 CC PRO antibody. PRO is useful as molecular weight markers for protein
 CC electrophoresis and also for chromosome identification. PRO is also
 CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
 CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
 CC useful for generating transgenic animals or knock-out animals which are
 CC useful in development and screening useful reagents. PRO NA is also
 CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
 CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
 CC polypeptides are useful for suppressing immune response. PRO1246
 CC polypeptide is useful for treating cardiac insufficiency disorders.
 CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
 CC PRO1561 polypeptide are useful for stimulating calcium flux in human
 CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
 CC polypeptides are useful for treating bone and/or cartilage disorders
 CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
 CC polypeptides are useful for treating diabetes in skeletal muscle cells
 CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
 CC treating Berger disease or other nephropathies associated with Schonlein-
 CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
 CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
 CC sequence is a PCR primer used to isolate a cDNA encoding a PRO protein of
 CC the invention.
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1400 CAGCAGCAACAGCAGCAGC 1418
 Db 20 CAGGAGCAACAGCAGCAGC 2
 RESULT 134
 ADH04424/C
 ID ADH04424 standard; DNA; 21 BP.
 XX
 AC ADH04424;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO1315 PCR primer #1.
 XX
 KW Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia; ss.
 XX
 OS Homo sapiens.
 XX
 FN US2004005626-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 07-DEC-2001; 2001US-00011795.
 XX
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
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PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
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PR 16-SEP-1998; 98US-0100627P.
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PR 16-SEP-1998; 98US-0100662P.
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PR 17-SEP-1998; 98US-0100711P.
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PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103385P.
PR 07-OCT-1998; 98US-0103396P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105893P.
PR 26-OCT-1998; 98US-0105894P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 28-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
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PR 03-NOV-1998; 98US-0106934P.
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PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 18-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 03-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-014758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 02-JAN-2000; 2000WO-US000219.
PR 08-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.

[illegible]

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PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108857P.
PR 17-NOV-1998; 98US-0108857P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145658P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 23-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

XX (GETH ) GENENTECH INC.
PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2004-108212/11.
XX
XX Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
XX Example 34; SEQ ID NO 105; 562pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 136
ADJ94624/c
ID ADL94624 standard; DNA; 21 BP.
XX
XX AC ADL94624;
XX
XX DT 01-JUL-2004 (first entry)
XX
XX Human secreted/transmembrane protein PRO1315 PCR primer #1.
XX
XX Human; PCR; primer; secreted protein; transmembrane protein; PRO; tumour;
XX immune response; cardiac insufficiency disorder; calcium flux;
XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX dermatitis; herpeticiformis; Crohn's disease; thalassemia; ss.
XX Homo sapiens.
XX
XX US2004073015-A1.
XX
XX 15-APR-2004.
XX
XX 12-DEC-2001; 2001US-00015395.
XX
XX 23-SEP-1998; 98US-0101477P.
XX 20-JUL-1999; 99US-0144758P.
XX 01-SEP-1999; 99WO-US020111.
XX 18-OCT-1999; 99US-00403297.
XX 18-FEB-2000; 2000WO-US004342.
XX 04-SEP-2001; 2001US-00946374.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2004-315422/29.
XX
XX New PRO polynucleotides and polypeptides, useful in promoting wound
PT healing and in diagnosing and treating cancer, neurodegenerative
PT diseases, stroke, hypertension or diabetes mellitus.
```

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XX
PS Example 34; SEQ ID NO 105; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimeric molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. PRO is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful for generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
CC polypeptides are useful for suppressing immune response. PRO1246
CC polypeptide is useful for treating cardiac insufficiency disorders.
CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
CC PRO1561 polypeptide are useful for stimulating calcium flux in human
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC polypeptides are useful for treating bone and/or cartilage disorders
CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
CC polypeptides are useful for treating diabetes in skeletal muscle cells
CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC treating Berger disease or other nephropathies associated with Schonlein-
CC Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's
CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1306, PRO1418,
CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
CC sequence is a PCR primer used to isolate a cDNA encoding a PRO protein of
CC the invention.
XX
SQ Sequence 21 BP; 0 A; 7 C; 7 G; 7 T; 0 U; 0 Other;
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1400 CAGCAGCAGCAACGAGCAGC 1418
Db 20 CAGGAGCAACGAGCAGCAGC 2
RESULT 137
ADO61397/c
ID ADO61397 standard; DNA; 21 BP.
AC ADO61397;
XX
XX 26-AUG-2004 (first entry)
XX
XX Human ATP1A2 DNA PCR primer #1.
XX
KW Human; Na/K pump alpha 2 subunit; Na/K human pump; ATPase; ATP1A2;
KW chromosome 1; migraine disorder; migraine;
KW alternating hemiplegia of childhood; hemiplegia; PCR; primer; ss;
KW antimigraine.
XX
XX Homo sapiens.
XX
XX WO2004046377-A2.
XX
XX 03-JUN-2004.
XX
XX 12-NOV-2003; 2003WO-EF012635.
XX
XX 15-NOV-2002; 2002IT-RM000576.
XX
XX (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
XX
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PI Casari G, De Fusco M, Marconi R;
XX WPI; 2004-420637/39.
XX
XX New alpha 2 subunit of the Na/K pump, useful in diagnosing and treating
XX PT pathologies associated with migraine or with alternating hemiplegia of
XX PT childhood.
XX
XX Claim 6; SEQ ID NO 1; 39pp; English.
XX
XX The invention relates to a nucleic acid comprising at least one segment
XX of the gene encoding a functional portion of the gene-regulating region
XX of the alpha 2 subunit of the Na/K pump (ATPase, ATP1A2), for use in the
XX CC diagnosis of or in genetic therapy of pathologies associated with
XX CC migraine or with alternating hemiplegia of childhood. The invention also
XX CC relates to a method for detecting in an individual at least one mutation
XX CC in the gene encoding the alpha 2 subunit of the Na/K human pump (ATPase,
XX CC ATP1A2) located on chromosome 1, associated with migraine disorders, at
XX CC least one pair of oligonucleotides for the exponential amplification
XX CC reaction of at least one segment of the gene encoding the alpha 2 subunit
XX CC of the Na/K human pump (ATPase, ATP1A2), in which the segment encodes a
XX CC functional portion or a gene-regulating portion of the subunit and a
XX CC method for identifying an agonist or antagonist agent of the Na/K human
XX CC pump (ATPase, ATP1A2) or its functional portion or a gene-regulating
XX CC portion of the subunit. The nucleic acids, proteins and methods are
XX CC useful in diagnosing and treating pathologies associated with migraine or
XX CC with alternating hemiplegia of childhood. This sequence represents a PCR
XX CC primer used to amplify human ATP1A2 DNA of the invention.
XX
SQ Sequence 21 BP; 0 A; 4 C; 5 G; 12 T; 0 U; 0 Other;
Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2296 ACAGAGAAACCCAAAGCAA 2314
Db 21 ACAGAGAAAGCCAAAGCAA 3
RESULT 138
ADC37823
ID ADC37823 standard; DNA; 17 BP.
XX
XX ADC37823;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:172.
XX
XX human; angiotensin-like protein 1; AMLP1; cytostatic; gene therapy;
XX KW AMLP1a; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO2003037931-A2.
XX
XX 08-MAY-2003.
XX
XX 01-NOV-2002; 2002WO-US035129.
XX
XX 01-NOV-2001; 2001US-0334773P.
XX
XX (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX Shannon M, Phan T;
XX
XX WPI; 2003-430501/40.
XX
XX New isolated nucleic acid molecule encoding a human angiotensin-like
XX PT protein, useful for treating or preventing a disorder associated with
XX PT decreased or increased expression or activity of AMLP1.
XX
```


KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
XX
XX
PD 08-MAY-2003.
XX
XX 01-NOV-2002; 2002WO-US035129.
XX
XX 01-NOV-2001; 2001US-0334773P.
XX
XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX Shannon M, Phan T;
XX
XX WPI; 2003-430501/40.
XX
XX New isolated nucleic acid molecule encoding a human angiomotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
XX Example 2; SEQ ID NO 168; 172pp; English.
XX
XX The present invention describes the human angiomotin-like protein 1
CC (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
CC therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLPI. The present sequence represents a scanning
CC oligonucleotide for human AMLPIa, which is used in an example from the
CC present invention.
XX
XX Sequence 17 BP; 7 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1430 CAGCAGCAGCAACAGCA 1446
DB 1 CAGCAGCAGCAACAGCA 17
RESULT 142
ADC37820
ID ADC37820 standard; DNA; 17 BP.
XX
XX ADC37820;
AC
XX 18-DEC-2003 (first entry)
DT
DE Human AMLPIa scanning 17-mer oligonucleotide SEQ ID NO:169.
XX
XX human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
XX
XX 08-MAY-2003.
PD
XX 01-NOV-2002; 2002WO-US035129.
XX
XX 01-NOV-2001; 2001US-0334773P.
XX
XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX Shannon M, Phan T;
XX

DR WPI; 2003-430501/40.
XX
XX New isolated nucleic acid molecule encoding a human angiomotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
XX Example 2; SEQ ID NO 169; 172pp; English.
XX
XX The present invention describes the human angiomotin-like protein 1
CC (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
CC therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLPIa, which is used in an example from the
CC present invention.
XX
XX Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1431 AGCAGCAGCAACAGCAG 1447
DB 1 AGCAGCAGCAACAGCAG 17
RESULT 143
ADC37822
ID ADC37822 standard; DNA; 17 BP.
XX
XX ADC37822;
AC
XX 18-DEC-2003 (first entry)
DT
XX
DE Human AMLPIa scanning 17-mer oligonucleotide SEQ ID NO:171.
XX
XX human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLP1a; ss.
XX Synthetic.
OS Homo sapiens.
XX WO2003037931-A2.
XX
XX 08-MAY-2003.
PD
XX 01-NOV-2002; 2002WO-US035129.
XX
XX 01-NOV-2001; 2001US-0334773P.
XX
XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX Shannon M, Phan T;
XX
XX WPI; 2003-430501/40.
XX
XX New isolated nucleic acid molecule encoding a human angiomotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
XX Example 2; SEQ ID NO 171; 172pp; English.
XX
XX The present invention describes the human angiomotin-like protein 1
CC (AMLPI). human AMLPI has cytostatic activity, and can be used in gene
CC therapy. The AMLPI protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLPIa, which is used in an example from the
CC present invention.
XX

SQ Sequence 17 BP; 7 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1400 CAGCAGCAACAGCAGCA 1416
 Db 1 CAGCAGCAACAGCAGCA 17

RESULT 144
 AAV30172
 ID AAV30172 standard; DNA; 18 BP.
 XX
 AC AAV30172;
 XX
 XX
 DT 14-SEP-1998 (first entry)
 XX
 DE Protein kinase catalytic subunit PCR primer 265.
 XX
 KW Severe combined immunodeficiency disease; SCID; horse; diagnosis;
 KW DNA-dependent protein kinase; PCR; primer; ds.
 XX
 XX Synthetic.
 OS Equus caballus.
 OS
 XX WO9821367-A1.
 PN
 XX
 PD 22-MAY-1998.
 XX
 XX 14-NOV-1997; 97WO-US021066.
 XX
 XX 15-NOV-1996; 96US-0031261P.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX
 XX Meeks K;
 PI
 XX
 XX WPI; 1998-297967/26.
 DR
 XX
 XX DNA-dependent protein kinase catalytic subunit - useful for determining
 PT equine severe combined immunodeficiency alleles.
 XX
 XX Example 3; Page 19; 98pp; English.
 PS
 XX Primer 265 was used in an RT-PCR strategy to clone and sequence equine
 CC DNA-dependent protein kinase catalytic subunit transcripts. Primer 265,
 CC and other primers used in the RT-PCR (see also AAV30171-93), are based on
 CC a published human DNA-dependent protein kinase catalytic subunit
 CC sequence. cDNA template was derived from 2 fibroblast cell lines, 0176
 CC (from a normal, non-Arabian horse) and 1821 (from a SCID foal). Sequence
 CC analysis showed that in SCID horses, a 5 bp deletion is present
 CC corresponding to nucleotide 9454 of the 12,381 nucleotide coding sequence
 CC of the human transcript. This results in premature termination of the
 CC catalytic subunit at amino acid 3160 (see AAW56642) of the polypeptide.
 CC Primers 405 and 392 (see AAV30192-93) can be used to screen for mutant
 CC SCID allele. Methods are provided for identifying carriers of the
 CC mutation and for differentiating SCID homozygotes, heterozygotes and
 CC normal horses
 XX
 SQ Sequence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 GGGAGATCTCTCTGCA 271
 Db 1 GGGAGATCTCTCTGCA 17

RESULT 145
 AAV30172
 ID AAV30172 standard; DNA; 18 BP.
 XX
 AC AAV30172;
 XX
 XX
 DT 14-SEP-1998 (first entry)
 XX
 DE Protein kinase catalytic subunit PCR primer 265.
 XX
 KW Severe combined immunodeficiency disease; SCID; horse; diagnosis;
 KW DNA-dependent protein kinase; PCR; primer; ds.
 XX
 XX Synthetic.
 OS Equus caballus.
 OS
 XX WO9821367-A1.
 PN
 XX
 PD 22-MAY-1998.
 XX
 XX 14-NOV-1997; 97WO-US021066.
 XX
 XX 15-NOV-1996; 96US-0031261P.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX
 XX Meeks K;
 PI
 XX
 XX WPI; 1998-297967/26.
 DR
 XX
 XX DNA-dependent protein kinase catalytic subunit - useful for determining
 PT equine severe combined immunodeficiency alleles.
 XX
 XX Example 3; Page 19; 98pp; English.
 PS
 XX Primer 265 was used in an RT-PCR strategy to clone and sequence equine
 CC DNA-dependent protein kinase catalytic subunit transcripts. Primer 265,
 CC and other primers used in the RT-PCR (see also AAV30171-93), are based on
 CC a published human DNA-dependent protein kinase catalytic subunit
 CC sequence. cDNA template was derived from 2 fibroblast cell lines, 0176
 CC (from a normal, non-Arabian horse) and 1821 (from a SCID foal). Sequence
 CC analysis showed that in SCID horses, a 5 bp deletion is present
 CC corresponding to nucleotide 9454 of the 12,381 nucleotide coding sequence
 CC of the human transcript. This results in premature termination of the
 CC catalytic subunit at amino acid 3160 (see AAW56642) of the polypeptide.
 CC Primers 405 and 392 (see AAV30192-93) can be used to screen for mutant
 CC SCID allele. Methods are provided for identifying carriers of the
 CC mutation and for differentiating SCID homozygotes, heterozygotes and
 CC normal horses
 XX
 SQ Sequence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1397 CAACAGCAGCAACAGCA 1413
 Db 1 CAACAGCAGCAACAGCA 17

RESULT 146
 AAV30172
 ID AAV30172 standard; DNA; 18 BP.
 XX
 AC AAV30172;
 XX
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Complementary oligo of sequence containing a mixture of CAG/CAA codons.
 XX

AAH19623
 ID AAH19623 standard; DNA; 18 BP.
 XX
 AC AAH19623;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Oligonucleotide containing a mixture of CAG/CAA codons.
 XX
 KW Polyglutamine region; polypeptide aggregation; aggregation disruption;
 KW Huntington's disease; Alzheimer's disease; Parkinson's disease;
 KW spinocerebellar ataxia; multiple myeloma; amyloidosis; anticonvulsant;
 KW spongiform encephalopathy; neuroprotective; nootropic; antiparkinsonian;
 KW ss.
 XX
 XX Synthetic.
 OS
 XX WO200123412-A2.
 PN
 XX
 PD 05-APR-2001.
 XX
 XX 27-SEP-2000; 2000WO-US041008.
 XX
 XX 27-SEP-1999; 99US-00405048.
 PR
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA
 XX Housman DE, Preisinger EA, Kazantsev AG;
 XX
 XX WPI; 2001-300097/31.
 DR
 XX
 XX Screening for agents which disrupt aggregation of polypeptides for
 PT treating aggregation-associated disorders e.g. Alzheimer's disease, by
 PT using aggregation-disposed polypeptides or cell expressing the
 PT polypeptides.
 XX
 XX Example 1; Page 25; 42pp; English.
 PS
 XX The present sequence was used to generate a polypeptide with extended
 CC polyglutamine regions. This was performed in an example illustrating a
 CC method for identifying a compound which disrupts polypeptide aggregation.
 CC The method is carried out using a cell which has been genetically
 CC modified to express aggregation-disposed polypeptides, or using purified
 CC aggregation-disposed polypeptides. The compounds identified by this
 CC method are useful for treating disorders associated with such polypeptide
 CC aggregation, including Huntington's disease, Alzheimer's disease,
 CC Parkinson's disease, spinocerebellar ataxia, multiple myeloma,
 CC amyloidosis, and spongiform encephalopathies like Creutzfeldt-Jakob
 CC disease and kuru in humans. The present sequence was annealed to its
 CC complement to generate double stranded duplex DNA with trinucleotide
 CC extensions
 XX
 SQ Sequence 18 BP; 9 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1397 CAACAGCAGCAACAGCA 1413
 Db 1 CAACAGCAGCAACAGCA 17

RESULT 146
 AAV30172
 ID AAV30172 standard; DNA; 18 BP.
 XX
 AC AAV30172;
 XX
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Complementary oligo of sequence containing a mixture of CAG/CAA codons.
 XX

KW Polyglutamine region; polypeptide aggregation; aggregation disruption;
KW Huntington's disease; Alzheimer's disease; Parkinson's disease;
KW spinocerebellar ataxia; multiple myeloma; amyloidosis; anticonvulsant;
KW spongiform encephalopathy; neuroprotective; neurotropic; antiparkinsonian;
KW ss.
XX
XX Synthetic.
OS
XX WO200123412-A2.
XX PN
XX 05-APR-2001.
XX PD
XX 27-SEP-2000; 2000WO-US041008.
XX PF
XX 27-SEP-1999; 99US-00405048.
XX PR
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX PA
XX Housman DE, Preisinger EA, Kazantsev AG;
XX FI
XX WPI; 2001-300097/31.
XX DR
XX Screening for agents which disrupt aggregation of polypeptides for
XX treating aggregation-associated disorders e.g. Alzheimer's disease, by
XX using aggregation-disposed polypeptides or cell expressing the
XX polypeptides.
XX
XX Example 1; Page 25; 42pp; English.
XX PS
XX The present sequence was used to generate a polypeptide with extended
XX polyglutamine regions. This was performed in an example illustrating a
XX method for identifying a compound which disrupts polypeptide aggregation.
XX The method is carried out using a cell which has been genetically
XX modified to express aggregation-disposed polypeptides, or using purified
XX aggregation-disposed polypeptides. The compounds identified by this
XX method are useful for treating disorders associated with such polypeptide
XX aggregation, including Huntington's disease, Alzheimer's disease,
XX Parkinson's disease, spinocerebellar ataxia, multiple myeloma,
XX amyloidosis, and spongiform encephalopathies like Creutzfeldt-Jakob
XX disease and kuru in humans. The present sequence was annealed to its
XX complement to generate double stranded DNA with trinucleotide
XX extensions
XX
XX Sequence 18 BP; 0 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1451 CAGCAGCAACGCAACA 1467
DB 18 CAGCAGCAACGCAACA 2
RESULT 147
ABK11198
ID ABK11198 standard; DNA; 18 BP.
XX
XX AC ABK11198;
XX
XX 05-JUN-2002 (first entry)
XX DT
XX Oligonucleotide #1 used to generate DNA with trinucleotide extensions.
XX DE
XX Inhibition of protein-protein interaction; Alzheimer's disease;
KW polyglutamine-containing transcription factor; hexamerisation of p53;
KW homodimerisation of Jun; expanded trinucleotide repeat; CAG repeat;
KW Huntington's disease; HD; Primal and bulbar muscular atrophy; SBMA;
KW dentatorubral-pallidoluysian atrophy; spinocerebellar ataxia type 1;
KW spinocerebellar ataxia type 2; spinocerebellar ataxia type 6;
KW spinocerebellar ataxia type 7; Machado-Joseph disease; MJD/SCA3;
KW neurotropic; anticonvulsant; cerebroprotective; neuroprotective; ss.
XX

OS Synthetic.
XX WO200216644-A1.
XX PN
XX 28-FEB-2002.
XX PD
XX 20-AUG-2001; 2001WO-US026097.
XX PF
XX 18-AUG-2000; 2000US-0226502P.
XX PR
XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX PA
XX Kazantsev A, Thompson L, Housman DE;
XX FI
XX WPI; 2002-280948/32.
XX DR
XX Novel agent for inhibiting protein-protein interaction useful to treat
XX Alzheimer's disease, has two domains which bind first, second proteins
XX with seven consecutive glutamine residues and a domain separating two
XX domains.
XX PS
XX Disclosure; Page 8; 40pp; English.
XX
XX The present invention relates to therapeutic agents comprising a first
XX domain (D1) that binds a protein having at least seven consecutive
XX glutamine (Glu) residues, a second domain (D2) that binds another protein
XX having at least 7 consecutive Glu residues, and a third domain (D3) that
XX separates D1 from D2. The therapeutic agents of the invention are useful
XX for inhibiting protein-protein interactions (e.g. aggregation,
XX dimerisation or other physiologically significant association), and can
XX be used for treating Alzheimer's disease, and disorders in which
XX polyglutamine-containing transcription factors or coactivators are
XX desirably active (e.g. disorders associated with homodimerisation of Jun
XX or hexamerisation of p53). The therapeutic agents can also be used to
XX treat various disorders, including those associated with expanded
XX trinucleotide (CAG) repeats. For example such disorders can include
XX Huntington's disease (HD), Primal and bulbar muscular atrophy (SBMA),
XX dentatorubral-pallidoluysian atrophy, spinocerebellar ataxia type 1, type
XX 2, type 6 or type 7, or Machado-Joseph disease (MJD/SCA3). The present
XX sequence represents an oligonucleotide used to generate double stranded
XX DNA with trinucleotide extensions
XX
XX Sequence 18 BP; 9 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1397 CAACAGCAGCAACAGCA 1413
DB 1 CAACAGCAGCAACAGCA 17
RESULT 148
ABK11199/C
ID ABK11199 standard; DNA; 18 BP.
XX
XX AC ABK11199;
XX
XX 05-JUN-2002 (first entry)
XX DT
XX Oligonucleotide #2 used to generate DNA with trinucleotide extensions.
XX DE
XX Inhibition of protein-protein interaction; Alzheimer's disease;
KW polyglutamine-containing transcription factor; hexamerisation of p53;
KW homodimerisation of Jun; expanded trinucleotide repeat; CAG repeat;
KW Huntington's disease; HD; Primal and bulbar muscular atrophy; SBMA;
KW dentatorubral-pallidoluysian atrophy; spinocerebellar ataxia type 1;
KW spinocerebellar ataxia type 2; spinocerebellar ataxia type 6;
KW spinocerebellar ataxia type 7; Machado-Joseph disease; MJD/SCA3;
KW neurotropic; anticonvulsant; cerebroprotective; neuroprotective; ss.
XX
XX Synthetic.
OS

XX WO200216644-A1.
 XX
 XX
 XX PD 28-FEB-2002.
 XX
 XX PF 20-AUG-2001; 2001WO-US026097.
 XX PR 18-AUG-2000; 2000US-0226502P.
 XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX PI Kazantsev A, Thompson L, Housman DE;
 XX WPI; 2002-280948/32.
 XX Novel agent for inhibiting protein-protein interaction useful to treat
 PT Alzheimer's disease, has two domains which bind first, second proteins
 PT with seven consecutive glutamine residues and a domain separating two
 PT domains.
 XX Disclosure; Page 8; 40pp; English.
 XX The present invention relates to therapeutic agents comprising a first
 CC domain (D1) that binds a protein having at least seven consecutive
 CC glutamine (Glu) residues, a second domain (D2) that binds another protein
 CC having at least 7 consecutive Glu residues, and a third domain (D3) that
 CC separates D1 from D2. The therapeutic agents of the invention are useful
 CC for inhibiting protein-protein interactions (e.g. aggregation, and can
 CC dimerisation or other physiologically significant association), and can
 CC be used for treating Alzheimer's disease, and disorders in which
 CC polyglutamine-containing transcription factors or coactivators are
 CC desirably active (e.g. disorders associated with homodimerisation of jun
 CC or hexamerisation of p53. The therapeutic agents can also be used to
 CC treat various disorders, including those associated with expanded
 CC trinucleotide (CAG) repeats. For example such disorders can include
 CC Huntington's disease (HD), primal and bulbar muscular atrophy (SMA),
 CC dentatorubral-pallidoluysian atrophy, spinocerebellar ataxia type 1, type
 CC 2, type 6 or type 7, or Machado-Joseph disease (MJD/SCA3). The present
 CC sequence represents an oligonucleotide used to generate double stranded
 CC DNA with trinucleotide extensions
 XX
 XX SQ Sequence 18 BP; 0 A; 3 C; 6 G; 9 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1451 CAGCAGCAACAGCA 1467
 DB 18 CAGCAGCAACAGCA 2
 RESULT 149
 ABZ81759
 ID ABZ81759 standard; DNA; 18 BP.
 AC
 AC ABZ81759;
 XX
 XX DT 11-JUN-2003 (first entry)
 XX
 XX DE Huntington's disease exon 1 triplet repeat sequence.
 XX
 XX KW Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
 KW gene therapy; ss.
 XX Homo sapiens.
 OS
 XX WO2003013437-A2.
 XX
 XX PD 20-FEB-2003.
 XX
 XX PF 07-AUG-2002; 2002WO-US025352.
 XX
 XX PT

PR 07-AUG-2001; 2001US-0310757P.
 PR 08-AUG-2001; 2001US-0310770P.
 PR 08-AUG-2001; 2001US-0310889P.
 PR 04-DEC-2001; 2001US-0337219P.
 XX
 XX PA (UYDE) UNIV DELAWARE.
 XX
 XX PI Kniec EB, Parekh-Olmedo H;
 XX WPI; 2003-256478/25.
 DR
 XX New single stranded oligonucleotides comprising a DNA domain having at
 PT least one mismatch with respect to the genetic sequence of the
 PT Huntington's disease gene to be altered, useful for treating or
 PT preventing Huntington's disease.
 XX
 XX PS Example 5; Page 72; 133pp; English.
 XX
 CC The present sequence is an example of a poly-glutamine triplet repeat
 CC region found in exon 1 of the Huntington's disease (HD) gene. In an
 CC example from the invention, neuronal PC12 cells were engineered to
 CC include an HD gene exon 1 containing this sequence. These cells were used
 CC to demonstrate the ability of single-stranded chemically-modified
 CC oligonucleotides (see ABZ81747-51) to decrease the formation of
 CC Huntington's protein (huntingtin) aggregates in cell culture. The
 CC invention provides chemically modified oligonucleotides that target
 CC sequence alterations to the triplet repeat region of the HD gene exon 1
 CC and/or which reduce the formation of huntingtin protein-containing
 CC aggregates. These are useful for the treatment or prevention of HD
 XX
 XX SQ Sequence 18 BP; 9 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 0.5%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1397 CAACAGCAGCAACAGCA 1413
 DB 1 CAACAGCAGCAACAGCA 17
 RESULT 150
 ADK67650
 ID ADK67650 standard; DNA; 18 BP.
 XX
 AC ADK67650;
 XX
 XX DT 06-MAY-2004 (first entry)
 XX
 XX DE Huntington's disease gene exon 1 DNA fragment.
 XX
 XX KW Huntington's disease; huntingtin; protein aggregation; gene therapy;
 KW human; ds.
 XX Homo sapiens.
 OS
 XX WO2004014306-A2.
 XX
 XX PD 19-FEB-2004.
 XX
 XX PF 07-AUG-2003; 2003WO-US024868.
 XX
 XX PR 07-AUG-2002; 2002US-0402198P.
 XX
 XX PA (UYDE) UNIV DELAWARE.
 XX
 XX PI Kniec EB, Parekh-Olmedo H;
 XX WPI; 2004-180536/17.
 DR
 XX Identifying the oligonucleotide species that disrupts aggregation of a
 PT protein aggregant in a cell by introducing the oligonucleotide species or
 PT composition separately into cells that have or are likely to develop

SQ Sequence 18 BP; 8 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1407 AACGAGCAGCAGCAG 1423
DB 2 AACGAGCAGCAGCAG 18
|||||

RESULT 153
ABZ85595/c
ID ABZ85595 standard; DNA; 20 BP.
XX
AC ABZ85595;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Claim 15; SEQ ID NO 837; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 20 BP; 0 A; 5 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 0.5%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1425
DB 20 CAGCAGCAGCAGCAGCA 4
|||||

RESULT 154
ABD21825/c
ID ABD21825 standard; DNA; 20 BP.
XX
AC ABD21825;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human stanniocalcin-derived oligo SEQ ID 837.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antisthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 837; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antisthmatic, is a
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung

CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 SQ Sequence 20 BP; 0 A; 5 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 0.5%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1425
 DB 20 CAGCAGCAGCAGCAGCA 4

RESULT 155
 AAT72522/C
 ID AAT72522 standard; DNA; 21 BP.

AC AAT72522;
 XX
 DT 17-OCT-1997 (first entry)
 XX
 DE 5-Cys-encoding oligonucleotide.
 XX
 KW Streptavidin; mutagenesis; stabilisation; Stv-43; ss.
 XX
 OS Synthetic.

XX WO9711183-A1.
 XX 27-MAR-1997.

PF 10-SEP-1996; 96WO-US005169.
 PR 11-APR-1995; 95US-00420010.
 XX (UYBO-) UNIV BOSTON.

XX Sano T, Cantor CR, Vajda S, Reznik GO, Smith CL, Pandori MW;
 XX WPI; 1997-202890/18.
 XX New streptavidin mutants - have increased stability or altered affinity
 XX for biotin.

PS Example 14; Page 33; 91pp; English.

XX Two 21-mer oligonucleotides (AAT72522 and AAT72523) were annealed and the
 CC resulting double-stranded DNA was ligated into the EcoRI and BamHI sites
 CC of the predigested DNA of a plasmid encoding residues 16 to 133 of
 CC streptavidin with Lys at position 127. The gene was cloned into a
 CC bacterial expression vector and the mutated streptavidin expressed and
 CC purified. The mutant streptavidin forms heterotetramers in solution and,
 CC with Phe at position 120, has a reduced biotin-binding affinity of less
 CC than about 10 power 8/M. It can be conjugated to other proteins and
 CC macromolecules, and also to solid supports through the sulphhydryl group
 CC on the cysteine residues

SQ Sequence 21 BP; 4 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 0.5%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCAA 1441
 DB 19 AGCAGCAGCAGCAGCAA 3

RESULT 156
 AAV17227
 ID AAV17227 standard; DNA; 20 BP.

XX AAV17227;
 AC AAV17227;
 XX 29-JUN-1998 (first entry)
 DT SCA2 gene CAG repeat unit fragment.

XX SCA2 gene; spinocerebellar ataxia type II; CAG repeat; PCR primer; ss.
 KW Synthetic.
 OS WO9803679-A1.

PN 29-JAN-1998.
 PD 18-JUL-1996; 96WO-JP001999.

XX 18-JUL-1996; 96WO-JP001999.
 PR (SRLS-) SRL INC.

XX Tsuji S, Sanpei K;
 PI WPI; 1998-120796/11.

XX Diagnosing spinocerebellar ataxia type II - by PCR and determining number
 XX of CAG repeat units.

PS Example 1; Page 12; 23pp; Japanese.

XX This sequence represents a fragment of the SCA2 gene. It can be used in
 CC the method of the invention for diagnosing spinocerebellar ataxia type
 CC II, by performing PCR on the test DNA using two primers hybridising to
 CC parts of the SCA2 gene sequence, and determining the number of CAG
 CC repeats in the amplified products. The method provides an easy means for
 CC the diagnosis of spinocerebellar ataxia type II

XX Sequence 20 BP; 9 A; 9 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1448 CAGCAGCAGCAGCAACA 1467
 DB 1 CACCACCAGCAGCAGCA 20

RESULT 157
 AAV30272
 ID AAV30272 standard; DNA; 20 BP.

AC AAV30272;

XX C2-OCT-1998 (first entry)

DT Spinocerebellar ataxia type 2 associated gene specific primer 1.

XX Spinocerebellar ataxia type 2; SCA2; gene therapy; antisense therapy;
 KW CAG repeat; neurodegenerative disease; PCR primer; ss.

XX Synthetic.
 OS Homo sapiens.
 XX WO9818920-A1.

XX 07-MAY-1998.
 XX 30-OCT-1997; 97WO-JP003946.
 XX 30-OCT-1996; 96JP-00304059.
 XX (SRLS-) SRL INC.
 XX Teuji S, Sanpei K;
 XX WPI; 1998-272215/24.
 XX Nucleic acid fragments associated with spinocerebellar ataxia type 2 -
 PT contain increased number of CAG repeat region compared to normal gene.
 XX Example 1; Page 7; 38pp; Japanese.
 XX This primer is used for the PCR amplification of a gene causative of
 CC spinocerebellar ataxia type 2 (SCA2), a neurodegenerative disease. The
 CC gene associated with SCA2, has a tri-nucleotide (CAG) repeat region which
 CC in the expression product produces a polyglutamine sequence from Gln-166
 CC to Gln-188. In the normal gene there are 15-25 CAG repeats but in SCA2
 CC patients this number is increased to 35-100. Peptides encoded by nucleic
 CC acid fragments (DNA or RNA) containing sequences from the SCA2 associated
 CC gene, antibodies recognising the peptides and antisense nucleic acids
 CC hybridising with the nucleic acid fragments can be used for the
 CC investigation and diagnosis of SCA2. They can also be used for the
 CC treatment of SCA2 by antisense therapy or gene therapy
 XX Sequence 20 BP; 9 A; 9 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1448 CAGCAGCAGCAACAGCAACA 1467
 DB 1 CACCACAGCAGCAACAGCAACA 20
 RESULT 158
 ID ADD68486 standard; DNA; 20 BP.
 AC ADD68486;
 DT 15-JAN-2004 (first entry)
 DE SNP typing-related PCR primer - SEQ ID 43.
 XX single nucleotide polymorphism; SNP; typing; PCR; primer; ss.
 XX Unidentified.
 XX JP2002300894-A.
 XX 15-OCT-2002.
 XX 29-JAN-2002; 2002JP-00019752.
 XX 01-FEB-2001; 2001JP-00025700.
 XX (RIKA) RIKAGAKU KENKYUSHO.
 XX WPI; 2003-397221/38.
 XX A typing method for single nucleotide polymorphism (SNP) of several
 PT hundred thousands of SNP sites with comparatively a small amount of
 PT genome DNA.
 XX Example 2; SEQ ID NO 43; 45pp; Japanese.

CC The invention relates to a novel method for typing a single nucleotide
 CC polymorphism (SNP) using a small amount of genomic DNA comprising
 CC simultaneous amplification of plural base sequences containing one or
 CC more SNP sites and differentiation of the bases within the SNP sites. The
 CC method of the invention may be useful for typing several hundred thousand
 CC SNP sites using only a comparatively small amount of genomic DNA. The
 CC current sequence is that of the SNP typing-related PCR primer of the
 CC invention.
 XX Sequence 20 BP; 8 A; 8 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1601 CAGCAGCAGCAACACATC 1620
 DB 1 CAGCAGCAGCAACACCGTC 20
 RESULT 159
 ID ABZ86069/c
 XX ABZ86069 standard; DNA; 20 BP.
 AC ABZ86069;
 DT 17-OCT-2003 (first entry)
 DE Human oligonucleotide sequence.
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ss.
 XX Homo sapiens.
 OS WO200285308-A2.
 PN 31-OCT-2002.
 PD 23-APR-2002; 2002WO-US013135.
 PF 24-APR-2001; 2001US-0286137P.
 PR (EPIG-) EPIGENESIS PHARM INC.
 XX Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX Claim 15; SEQ ID NO 1311; 872pp; English.
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CAGCGCGCGCAGCAGCAGCA 1
||||| ||||||| |||||||

RESULT 160
ABZ85597/c
ID ABZ85597 standard; DNA; 20 BP.
XX AC ABZ85597;
XX DT 17-OCT-2003 (first entry)
XX DE Human oligonucleotide sequence.
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX WO200285308-A2.
XX PN 31-OCT-2002.
XX PD 23-APR-2002; 2002WO-US013135.
XX PF 24-APR-2001; 2001US-0286137P.
XX PR (EPIG-) EPIGENESIS PHARM INC.
XX PA Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 839; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 977 CAGCAGCACCAGCAGCAGCA 996
Db 20 CAGCAGCACCAGCAGCAGCA 1
||||| ||||||| |||||||

RESULT 161
ABZ92556/c
ID ABZ92556 standard; DNA; 20 BP.
XX AC ABZ92556;
XX DT 17-OCT-2003 (first entry)
XX DE Human oligonucleotide sequence.
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX WO200285308-A2.
XX PN 31-OCT-2002.
XX PD 23-APR-2002; 2002WO-US013135.
XX PF 24-APR-2001; 2001US-0286137P.
XX PR (EPIG-) EPIGENESIS PHARM INC.
XX PA Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX DR WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 7798; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 2 A; 8 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 83 GAGGAGACGGCGCTTCGA 102
 DB 20 GAGGAGACGGCGCTTCGA 1

RESULT 162
 ABZ86062/c
 ID ABZ86062 standard; DNA; 20 BP.

XX AC ABZ86062;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX PS Claim 15; SEQ ID NO 1304; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 1 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1424 CAGCAGCAGCAGCAGCAACA 1443
 DB 20 CAGCAGCAGCAGCAGCAACA 1

RESULT 163

ABZ86061/c

ID ABZ86061 standard; DNA; 20 BP.

XX AC ABZ86061;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX PS Claim 15; SEQ ID NO 1303; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 1 A; 1 C; 8 G; 10 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1565 CAGCAGCAGCAACACACACA 1584
||| ||||| ||||| |||||
Db 20 CATCACCAGCAACACACACA 1

RESULT 164
ABZ98989/c
ID ABZ98989 standard; DNA; 20 BP.

XX AC ABZ98989;

XX 17-OCT-2003 (first entry)

XX Human PDE4A oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 14231; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 602 GAACTGGAGAACATGATCAA 621
||||| ||||| ||||| |||||
Db 20 GAACTGGAGAACCTGAACAA 1

RESULT 165

ABZ86070/c

ID ABZ86070 standard; DNA; 20 BP.

XX AC ABZ86070;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Claim 15; SEQ ID NO 1312; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCA 1428
|||||
DB 20 CAGCAGCAGCGCGCGCAGCA 1

RESULT 166
ABZ86077/c

ID ABZ86077 standard; DNA; 20 BP.

XX ABZ86077;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Claim 15; SEQ ID NO 1319; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 1 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1403 CAGCAACAGCAGCAGCAGCA 1422
|||||
DB 20 CAGCGACTGCAGCAGCAGCA 1

RESULT 167

ACC62133

ID ACC62133 standard; DNA; 20 BP.

XX ACC62133;

XX 20-JUN-2003 (first entry)

XX Human alipoprotein B antisense oligonucleotide SEQ ID NO: 22.

XX alipoprotein B; ApoB; antilipemic; antiarteriosclerotic; antidiabetic;
KW anorectic; cardiovascular; gene therapy; lipid metabolism;
KW cholesterol metabolism; atherosclerosis; hyperlipidaemia; diabetes;
KW type 2 diabetes; obesity; atherosclerosis; cardiovascular disease;
KW glucose; antisense oligonucleotide; ss.

XX Synthetic.

XX WO2003011887-A2.

XX 13-FEB-2003.

XX 30-JUL-2002; 2002WO-US024247.

XX 01-AUG-2001; 2001US-00920033.

XX 30-APR-2002; 2002US-00135985.

XX 15-MAY-2002; 2002US-00147196.

XX (ISIS-) ISIS PHARM INC.

XX Crooke RM, Graham MJ;

XX WPI; 2003-268105/26.

XX New antisense oligonucleotides for modulating apolipoprotein B,
PT especially for preventing or treating atherosclerosis, hyperlipidemia or
PT diabetes, or for modulating glucose, cholesterol, lipoprotein or
PT triglyceride levels.

XX Example 15; Page 96; 160pp; English.

XX The invention relates to a novel compound that is 8-50 nucleotides in
CC length that is targeted to a nucleic acid molecule encoding
CC apolipoprotein B (ApoB), and specifically hybridises with and inhibits
CC the expression of a nucleic acid molecule encoding ApoB, or which
CC specifically hybridises with at least an 8-nucleotide portion of an
CC active site on a nucleic acid molecule encoding ApoB. A compound of the
CC invention has antilipemic, antiarteriosclerotic, antidiabetic,
CC anorectic, and cardiovascular activity. The compound may have a use in
CC gene therapy. The antisense oligonucleotide is useful for treating an
CC animal having a disease or conditions associated with ApoB, e.g. a
CC condition involving abnormal lipid metabolism, a condition involving
CC abnormal cholesterol metabolism, atherosclerosis, or a condition

CC involving an abnormal metabolic condition (e.g. hyperlipidaemia, diabetes
 CC (specifically Type 2 diabetes), obesity, atherosclerosis or
 CC cardiovascular disease). The new compound or the antisense
 CC oligonucleotide is also useful for modulating glucose levels
 CC (particularly plasma or serum glucose levels) in a human or diabetic
 CC animal, or for modulating serum cholesterol levels, lipoprotein levels
 CC (specifically VLDL, HDL or LDL) or serum triglyceride levels,
 CC particularly in a human. The antisense compound is also useful for
 CC preventing or delaying the onset of a disease or condition associated
 CC with ApoB, or the onset of an increase in glucose levels in the animal or
 CC human. The present sequence is used in the exemplification of the
 CC invention

SQ Sequence 20 BP; 5 A; 9 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551

Db 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 168

ABZ84008/C

ID ABZ84008 standard; DNA; 20 BP.

XX AC ABZ84008;

DT 14-MAY-2003 (first entry)

DE Toxicologically relevant rat PCR primer #1167.

XX Toxicologically relevant gene; toxicological response; PCR primer; ss.

XX Rattus sp.

OS Synthetic.

XX WO2003016500-A2.

XX 27-FEB-2003.

XX 16-AUG-2002; 2002WO-US026514.

XX 16-AUG-2001; 2001US-0313080P.

XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX Neft RE, Dunn RT, Adkins K, Pickett OG, Kier LD, Schmeiser K;

PI Alen P;

XX WPI; 2003-268322/26.

XX Determining a toxicological response to an agent, useful for screening of
 PT drugs, comprises comparing the expression profile of one or more human
 PT toxic response genes to a reference gene expression profile indicative of
 PT toxicity.

XX Claim 1; Page 327; 455pp; English.

XX The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in ABZ82842
 CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
 CC; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)

CC exposing cells to an agent or isolating cells from a human subject who
 CC was exposed to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals

XX Sequence 20 BP; 0 A; 6 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1400 CAGCAGCAGCAGCAGCAGCA 1419

Db 20 CAGCAGGACAGCAGGAAGCA 1

RESULT 169

ABD22299/C

ID ABD22299 standard; DNA; 20 BP.

XX AC ABD22299;

DT 29-JUL-2004 (first entry)

XX Human stanniocalcin-derived oligo SEQ ID 1311.

DE Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX Homo sapiens.

XX WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 1311; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428

Db 20 CAGCGCGCGCAGCAGCAGCA 1

RESULT 170

ABD22300/C

ID ABD22300 standard; DNA; 20 BP.

XX AC ABD22300;

XX DT 29-JUL-2004 (first entry)

XX DE Human stanniocalcin-derived oligo SEQ ID 1312.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX OS Homo sapiens.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (BPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-093058/08.

XX PT Pharmaceutical composition for treating asthma, has antisense
 FT oligonucleotide containing less percentage of adenosine, targeted to
 FT nucleic acids associated with lung airway or lung dysfunction, and

PT bronchodilating agent.

XX Claim 15; SEQ ID NO 1312; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hyperextension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428

Db 20 CAGCAGCAGCAGCAGCAGCA 1

RESULT 171

ABD22291/C

ID ABD22291 standard; DNA; 20 BP.

XX AC ABD22291;

XX DT 29-JUL-2004 (first entry)

XX DE Human stanniocalcin-derived oligo SEQ ID 1303.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX OS Homo sapiens.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

```
PR 24-APR-2001; 2001US-0286036P.
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 1303; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has anti-allergic, anti-inflammatory, antiasthmatic, is a
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction, and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, respiratory
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 1 A; 1 C; 8 G; 10 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1565 CAGCAGCAGCAACACCAACA 1584
Db 20 CATCACCAGCAACCAACA 1
RESULT 172
ABD22307/c
ID ABD22307 standard; DNA; 20 BP.
XX
XX ABD22307;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human stannocalcin-derived oligo SEQ ID 1319.
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX
24-APR-2001; 2001US-0286036P.
KW (EPIG-) EPIGENESIS PHARM INC.
KW
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
KW Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 1319; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has anti-allergic, anti-inflammatory, antiasthmatic, is a
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction, and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX prevent any unwanted effects due to it
XX
XX Sequence 20 BP; 1 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1403 CAGCAACAGCAGCAGCAGCA 1422
Db 20 CAGCAGCTGCAGCAGCAGCA 1
RESULT 173
ABD32020/c
ID ABD32020 standard; DNA; 20 BP.
```


XX AC ABD32020;
XX DT 29-JUL-2004 (first entry)
XX DE Human PD84A-derived oligonucleotide SEQ ID 14231.
XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX OS Homo sapiens.
XX PN WO200285309-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013143.
XX PR 24-APR-2001; 2001US-0286036P.
XX PS (SPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX Claim 15; SEQ ID NO 14231; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX SQ Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 602 GAACGAGACATGATCAA 621
Db 20 GAACGAGACCTGAACAA 1
RESULT 174
ABD28786/C
ID ABD28786 standard; DNA; 20 BP.
XX AC ABD28786;
XX DT 29-JUL-2004 (first entry)
XX DE W81570-derived oligonucleotide SEQ ID 7798.
XX KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX OS Homo sapiens.
XX PN WO200285309-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013143.
XX PR 24-APR-2001; 2001US-0286036P.
XX PS (SPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX Claim 15; SEQ ID NO 7798; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 SQ Sequence 20 BP; 2 A; 8 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 83 GAGGAGACGGCGCTTCGA 102
 Db 20 GAGGAGACGGCGCTTCGA 1
 |||||

RESULT 175
 ABD21827/c
 ID ABD21827 standard; DNA; 20 BP.

XX AC ABD21827;

XX DT 29-JUL-2004 (first entry)

XX DE Human stannioalcin-derived oligo SEQ ID 839.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX OS Homo sapiens.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (EPITG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 839; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery

CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic, is a
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX

SQ Sequence 20 BP; 0 A; 5 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 977 GAGGAGACCGCAGCAGCA 996

Db 20 GAGGAGACCGCAGCAGCA 1
 |||||

RESULT 176

ABD22292/c

ID ABD22292 standard; DNA; 20 BP.

XX AC ABD22292;

XX DT 29-JUL-2004 (first entry)

XX DE Human stannioalcin-derived oligo SEQ ID 1304.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.

XX OS Homo sapiens.

XX PN WO200285309-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013143.

XX PR 24-APR-2001; 2001US-0286036P.

XX PA (EPITG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 1304; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,

CC comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and

CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,

CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating

CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC The invention also describes a kit, that comprises: (a) a delivery

CC device, in separate containers, (b) the oligonucleotides, (c)

CC instructions for adding a carrier and for use of the kit. The composition

CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,

CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a

CC beta-adrenergic agonist. The composition is useful for preventing or

CC treating a respiratory, lung or malignant disease. The administered

CC composition comprises oligo and is administered to reduce the production

CC or availability, or to increase the degradation of the target mRNA or to

CC reduce the amount of target polypeptide present in the lungs. The

CC pulmonary obstruction, and/or bronchoconstriction and/or lung

CC inflammation, allergies and/or surfactant hypoproduction are associated

CC with a disease or condition such as pulmonary vasoconstriction,

CC inflammation, allergies, asthma, impeded respiration, respiratory

CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary

CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary

CC transplantation rejection, pulmonary infections, bronchitis or cancer.

CC The reduced adenosine content of the anti-sense oligos corresponding to

CC thymidines present in the target RNA serves to prevent the breakdown of

CC the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to

CC prevent any unwanted effects due to it

XX

SQ Sequence 20 BP; 1 A; 3 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1424 CAGCAGCAGCAGCAGCA 1443

DB 20 CAGCAGCAGCAGCAGCA 1

RESULT 177

ADH18033

ID ADH18033 standard; DNA; 20 BP.

XX ADH18033;

AC

XX 11-MAR-2004 (first entry)

DT

XX 2'-MOE gapmer antisense oligo targeted to human ApoB DNA 1 - SEQ ID 22.

DE

XX apolipoprotein B; ApoB; antiarteriosclerotic; cardiant; antidiabetic;

XX anorectic; lipid; cholesterol metabolism; atherosclerosis;

XX diabetes Type 2; obesity; hyperlipidaemia; cardiovascular; gene therapy;

XX antisense; 2'-O-methoxyethyl gapmer; phosphorothioate backbone; 2'-MOE;

XX human; ss.

XX Homo sapiens.

OS

XX WO2003097662-A1.

PN

XX 27-NOV-2003.

PD

XX 15-MAY-2003; 2003WO-US015493.

XX

XX 15-MAY-2002; 2002US-00147196.

PR

XX 13-NOV-2002; 2002US-0426324P.

XX

XX (ISIS-) ISIS PHARM INC.

XX Crooke RM, Graham MJ;

PI WPI; 2004-022840/02.

DR

XX New antisense compound, useful for preparing a composition for treating

PT abnormal lipid or cholesterol metabolism, atherosclerosis, diabetes Type

PT 2, obesity, hyperlipidemia or cardiovascular disease.

PS

XX Example 15; SEQ ID NO 22; 405pp; English.

XX The invention relates to a novel antisense compound targeted to a nucleic

CC acid molecule encoding human apolipoprotein B (ApoB) which specifically

CC hybridises with and inhibits the expression of human apolipoprotein B.

CC The compound of the invention demonstrates antiarteriosclerotic,

CC cardiant, antidiabetic and anorectic activities and may be useful for

CC preparing a composition for treating abnormal lipid or cholesterol

CC metabolism, atherosclerosis, diabetes Type 2, obesity, hyperlipidemia or

CC cardiovascular disease. Furthermore, the compound has gene therapy

CC applications. The current sequence is that of the 2'-O-methoxyethyl (2'-

CC MOE) gapmer antisense oligo of the invention which has 2'-MOE 'wings', a

CC phosphorothioate backbone throughout and in which all cytidine residues

CC are 5-methylcytidines.

XX

SQ Sequence 20 BP; 5 A; 9 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551

DB 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 178

ADH65922/c

ID ADH65922 standard; DNA; 20 BP.

XX ADH65922;

AC

XX 25-MAR-2004 (first entry)

DT

XX Human glucocorticoid receptor-specific antisense oligonucleotide #2756.

DE

XX antisense oligonucleotide; glucocorticoid receptor; infection;

XX inflammation; tumour formation; diabetes; obesity;

XX cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;

XX phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

XX Homo sapiens.

OS

XX WO2003099215-A2.

PN

XX 04-DEC-2003.

PD

XX 20-MAY-2003; 2003WO-US016084.

XX

XX 20-MAY-2002; 2002US-0381857P.

PR

XX (PHAA) PHARMACIA CORP.

PA

XX Crosby SD, Nalaeeth AB;

PI

XX WPI; 2004-035034/03.

DR

XX New antisense compound targeted to a nucleic acid molecule encoding

PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,

PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.

XX

XX Claim 4; SEQ ID NO 2756; 985pp; English.

XX The invention comprises an antisense oligonucleotides that are targeted

CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 XX
 SQ Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 465 TGGATGGCCAAATGACCCAA 484
 DB 20 TGGATGACCAATGACCCCTA 1
 RESULT 179
 ADH64974/c
 ID ADH64974 standard; DNA; 20 BP.
 AC ADH64974;
 XX
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human glucocorticoid receptor-specific antisense oligonucleotide #1808.
 XX
 KW antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 XX
 OS Homo sapiens.
 XX
 PN WO2003099215-A2.
 XX
 PD 04-DEC-2003.
 XX
 PF 20-MAY-2003; 2003WO-US016084.
 XX
 PR 20-MAY-2002; 2002US-0381857P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Crosby SD, Nalseth AE;
 XX
 DR WPI; 2004-035034/03.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
 XX
 PS Claim 4; SEQ ID NO 1808; 985pp; English.
 XX
 CC The invention comprises an antisense oligonucleotides that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 XX
 SQ Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 465 TGGATGGCCAAATGACCCAA 484
 DB 20 TGGATGACCAATGACCCCTA 1
 RESULT 181
 ADH66562/c
 ID ADH66562 standard; DNA; 20 BP.
 AC ADH66562;
 XX
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human glucocorticoid receptor-specific antisense oligonucleotide #3396.
 XX

QY 463 CATGGATGGCCAAATGACCC 482
 DB 20 CCTGGATGACCAATGACCC 1
 RESULT 180
 ADH66495/c
 ID ADH66495 standard; DNA; 20 BP.
 XX
 AC ADH66495;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human glucocorticoid receptor-specific antisense oligonucleotide #3329.
 XX
 KW antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 XX
 OS Homo sapiens.
 XX
 PN WO2003099215-A2.
 XX
 PD 04-DEC-2003.
 XX
 PF 20-MAY-2003; 2003WO-US016084.
 XX
 PR 20-MAY-2002; 2002US-0381857P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Crosby SD, Nalseth AE;
 XX
 DR WPI; 2004-035034/03.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
 XX
 PS Claim 4; SEQ ID NO 3329; 985pp; English.
 XX
 CC The invention comprises an antisense oligonucleotides that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 XX
 SQ Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 462 ACATGGATGGCCAAATGACCC 481
 DB 20 ACCTGGATGACCAATGACCC 1
 RESULT 181
 ADH66562/c
 ID ADH66562 standard; DNA; 20 BP.
 AC ADH66562;
 XX
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human glucocorticoid receptor-specific antisense oligonucleotide #3396.
 XX

KW antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidaemia; Cushing's
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 XX Homo sapiens.
 PN W02003099215-A2.
 XX 04-DEC-2003.
 XX 20-MAY-2003; 2003WO-US016084.
 XX 20-MAY-2002; 2002US-0381857P.
 XX (PHAA) PHARMACIA CORP.
 XX Crosby SD, Nalseth AE;
 XX WPI; 2004-035034/03.
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
 XX Claim 4; SEQ ID NO 3396; 985pp; English.
 XX The invention comprises an antisense oligonucleotide that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 XX Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 461 CACATGGATGCCAAATGAC 480
 DB 20 CACCTGGATGACCAATGAC 1
 RESULT 182
 ADH64132/c
 ID ADH64132 standard; DNA; 20 BP.
 XX AC ADH64132;
 XX 25-MAR-2004 (first entry)
 XX Human glucocorticoid receptor-specific antisense oligonucleotide #966.
 DE antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.
 XX Homo sapiens.
 OS W02003099215-A2.
 PN 04-DEC-2003.
 XX 20-MAY-2003; 2003WO-US016084.
 XX 20-MAY-2002; 2002US-0381857P.
 XX

PA (PHAA) PHARMACIA CORP.
 XX Crosby SD, Nalseth AE;
 XX WPI; 2004-035034/03.
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidaemia or Cushing's syndrome.
 XX Claim 4; SEQ ID NO 966; 985pp; English.
 XX The invention comprises an antisense oligonucleotide that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity,
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.
 XX Sequence 20 BP; 0 A; 3 C; 7 G; 10 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1580 CAACAGCAACACAGCAGCA 1599
 DB 20 CAACAGCAACACAGCAGCA 1
 RESULT 183
 ADJ60872/c
 ID ADJ60872 standard; DNA; 20 BP.
 XX AC ADJ60872;
 XX 06-MAY-2004 (first entry)
 XX Oligonucleotide associated to PDE4A #155.
 DE interleukin; IL-4 receptor; IL-5 receptor; lung disease;
 KW airway inflammation; allergy; asthma; impeded respiration;
 KW cystic fibrosis; acute respiratory distress syndrome;
 KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
 KW ss.
 XX Homo sapiens.
 OS W02004011613-A2.
 PN 05-FEB-2004.
 XX 25-JUL-2003; 2003WO-US023509.
 XX 29-JUL-2002; 2002US-0399076P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX WPI; 2004-203534/19.
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codons and introns of respiratory disease-relevant genes e.g.,
 PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
 PT disease e.g., asthma.
 XX Claim 2; SEQ ID NO 1728; 85pp; English.
 XX

CC The present invention relates to an oligonucleotide anti-sense to e.g.,
 CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
 CC end of nucleic acid target comprising gene(s) chosen from e.g.
 CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
 CC oligonucleotide and optionally surfactant operatively linked to a
 CC oligonucleotide. The method is useful for preventing or treating a
 CC respiratory or lung disease, which involves administering to the airways
 CC of a subject an effective amount of an inhibitor. The oligonucleotide is
 CC useful for production of a medicament for the prevention and/or treatment
 CC of a respiratory or lung disease. The respiratory or lung disease is
 CC chosen from airway inflammation, allergy(ies), asthma, impeded
 CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
 CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
 CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
 CC obstruction. The present sequence represents an oligonucleotide of the
 CC invention.

XX
 SQ Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 602 GAACCTGGAGAACATGATCAA 621
 |||||
 DB 20 GAACCTGGAGAACCTGAACAA 1

RESULT 184
 ADJ53419/c
 ID ADJ53419 standard; DNA; 20 BP.
 AC ADJ53419;
 XX
 DT 06-MAY-2004 (first entry)
 DE Human G protein-coupled receptor 6 DNA antisense oligonucleotide #68.
 XX
 KW Human; G protein-coupled receptor 6; GPCR-6; ss;
 KW antisense oligonucleotide; phosphorothioate linkage;
 KW 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; metabolic disorder;
 KW aberrant signal transduction; brain tissue; neuronal disorder;
 KW motor disorder; sensory disorder; psychiatric disorder;
 KW behavioural disorder; drug addiction; chemical addiction; neuroleptic.
 XX
 OS Homo sapiens.
 XX
 PN US2004023380-A1.
 XX
 PD 05-FEB-2004.
 XX
 PF 31-JUL-2002; 2002US-00210479.
 XX
 PR 31-JUL-2002; 2002US-00210479.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Dobie KW;
 XX
 DR WPI; 2004-142661/14.
 XX
 XX Novel antisense compound targeted to nucleic acids encoding G protein-
 PT coupled receptor 6 (GPCR-6), useful for treating animal having disease
 PT associated with GPCR-6 e.g. metabolic, neuronal, motor, sensory or
 PT behavioral disorders.
 XX
 XX Example 15; SEQ ID NO 79; 54pp; English.
 XX
 CC The invention relates to an antisense oligonucleotide targeted to a
 CC nucleic acid encoding the human G protein-coupled receptor 6 (GPCR-6),
 CC which specifically hybridises with the nucleic acid encoding the GPCR-6
 CC and inhibits expression of the GPCR-6. The antisense oligonucleotide
 CC comprises at least one modified internucleoside linkage, i.e. a

CC phosphorothioate linkage, at least one modified sugar moiety, preferably
 CC a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase
 CC comprising a 5-methylcytosine. The antisense oligonucleotides are useful
 CC for inhibiting expression of the GPCR-6 and in preparation of a GPCR-6,
 CC composition for treating a disease or condition associated with GPCR-6,
 CC e.g., a metabolic disorder, aberrant signal transduction in brain tissue,
 CC a neuronal, motor, sensory, psychiatric or behavioural disorder or drug
 CC or chemical addiction. This sequence represents an antisense
 CC oligonucleotide of the invention.

XX
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1645 AGCCAGCCTTTCCTAAGGT 1664
 |||||
 DB 20 AAGCCAGCCTTTCGTAAGCT 1

RESULT 185
 ADO46361/c
 ID ADO46361 standard; DNA; 20 BP.
 XX
 AC ADO46361;
 XX
 DT 15-JUL-2004 (first entry)
 DE Human oligonucleotide #1727.
 XX
 KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
 KW CCR1; CCR3; Botaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
 KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
 KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
 KW asthma; lung allergy; inflammation; inflammatory disease; cystic fibrosis; CF;
 KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
 KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
 KW acute respiratory distress syndrome; pulmonary hypertension;
 KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
 XX
 OS Homo sapiens.
 XX
 PN US2004049022-A1.
 XX
 PD 11-MAR-2004.
 XX
 PF 25-JUL-2003; 2003US-00627930.
 XX
 PR 23-APR-2002; 2002WO-US013135.
 PR 23-APR-2002; 2002WO-US013143.
 XX
 PA (NYCE/) NYCE J W.
 PA (SAND/) SANDRASAGRA A.
 PA (TANG/) TANG L.
 PA (AGUI/) AGUILAR D.
 PA (MILL/) MILLER S.
 PA (SHAH/) SHAHABUDDIN S.
 PA (LUHH/) LU H.
 PA (CONG/) CONG H.
 XX
 XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
 PI Shahabuddin S, Lu H, Cong H;
 XX
 DR WPI; 2004-293804/27.
 XX
 XX Novel single or multiple target oligonucleotide anti-sense to e.g.
 PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
 PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
 PT asthma.
 XX
 PS Claim 2; SEQ ID NO 1728; 174pp; English.
 XX

CC The invention relates to oligonucleotides anti-sense to an initiation
CC codon, coding region, 5' or 3' intron-exon junction, intron or region
CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
CC -5 receptor, CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
CC also relates to a method of screening a candidate compound that binds to
CC one or more nucleic acid target(s) or expressed product(s), for the
CC prevention and/or treatment of a respiratory or lung disease. The
CC oligonucleotides are useful for reducing or inhibiting expression of a
CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
CC CCR1, CCR3, Botaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
CC useful for preventing or treating a respiratory or lung disease. The
CC respiratory or lung disease is associated with hyper-responsiveness to
CC and/or increased levels of, adenosine and/or levels of adenosine A
CC receptor(s), and/or asthma and/or lung allergies associated with
CC inflammation or an inflammatory disease. The respiratory or lung disease
CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
CC hypertension, lung inflammation, bronchitis, airway obstruction or
CC bronchoconstriction. This sequence represents an oligonucleotide of the
CC invention.

XX
SQ Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 602 GAACGGAGAACATGATCAA 621
|||||
Db 20 GAACGGAGAACCTGACAA 1

RESULT 186
AD032574
ID AD032574 standard; DNA; 20 BP.
AC
XX
AC AD032574;
XX
XX 12-AUG-2004 (first entry)
DT
XX
DE Antisense 2'-MOE gapmer oligo targeted to human ApoB RNA - SEQ 22.
XX
KW apolipoprotein B; ApoB; cardiovascular; antiarteriosclerotic;
KW antilipaeamic; antidiabetic; anorectic; cardiant; vasotropic; hypotensive;
KW anabolic; eating disorder; cytosstatic; endocrine; vasotropic;
KW neuroprotective; nototropic; lipid; cholesterol metabolism;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW Von Gierke's disease; lipodystrophy; Cushing's syndrome;
KW sexual ateliotic dwarfism; hyperthyroidism; hypertension;
KW anorexia nervosa; Werner's syndrome; hepatoma; multiple myeloma; uraemia;
KW impotence; obstructive liver disease; Alzheimer's; dementia; diabetes;
KW obesity; atherosclerosis; antisense; 2'-MOE gapmer; 2'-methoxyethyl wing;
KW phosphorothioate backbone; human; chromosome 2p23-2p24; ss.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER = Phosphorothioate backbone, bases 1-5 and
FT 16-20, 2'-MOE wing bases, all cytidine residues are 5-
FT methylcytidines"
XX
FN WO200404181-A2.
XX
XX 27-MAY-2004.
PD
XX
XX 13-NOV-2003; 2003WO-US036411.

XX
PR 13-NOV-2003; 2002US-0426234P.
PR 15-MAY-2003; 2003WO-US015493.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke R, Graham M, Lemonidis-Tarbet K, Dobie KW;
XX WPI; 2004-420321/39.
DR
XX
XX Antisense oligonucleotide compound that inhibits expression of mRNA
PT encoding human apolipoprotein B, useful for treating hyperlipidemia,
PT diabetes, obesity, von Gierke's disease, lipodystrophies, Cushing's
PT syndrome.
XX
PS Example 15; SEQ ID NO 22; 483pp; English.
XX
CC The invention relates to a novel antisense compound where the compound
CC hybridises to and inhibits expression of mRNA encoding human
CC apolipoprotein B (ApoB) after 16-24 hours by at least 30% in 80%
CC confluent HepG2 cells in culture at a concentration of 150 nM. The
CC compound of the invention demonstrates cardiovascular,
CC antiarteriosclerotic, antilipaeamic, antidiabetic, anorectic, cardiant,
CC vasotropic, hypotensive, anabolic, eating disorder-related, cytosstatic,
CC endocrine, vasotropic, neuroprotective and nototropic activities and may
CC be useful for inhibiting the expression of apolipoprotein B in cells or
CC tissues in vivo in order to address a condition associated with abnormal
CC lipid or cholesterol metabolism. The compound may be useful for
CC decreasing circulating lipoprotein levels, triglyceride levels,
CC cholesterol levels, lipid levels, fatty acid levels, acute phase
CC reactants and chylomicrons and thus may be utilised during treatment of
CC hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia,
CC cardiovascular disorders, Von Gierke's disease, lipodystrophy, Cushing's
CC syndrome, sexual ateliotic dwarfism, hyperthyroidism, hypertension,
CC anorexia nervosa, Werner's syndrome, hepatoma, multiple myeloma, uraemia,
CC impotence, obstructive liver disease, Alzheimer's disease, dementia,
CC diabetes, obesity and atherosclerosis. The current sequence is that of an
CC antisense 2'-MOE (2'-methoxyethyl) gapmer oligo of the invention which is
CC targeted to human ApoB RNA.
XX
SQ Sequence 20 BP; 5 A; 9 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1532 GCCACAGCAGCAGCAGCA 1551
|||||
Db 1 GCCCGCCAGCAGCAGCAGCA 20

RESULT 187
ADQ26559/C
ID ADQ26559 standard; DNA; 20 BP.
XX
AC ADQ26559;
XX
DT 23-SEP-2004 (first entry)
XX
XX
DE HOXB1 RT-PCR primer, SEQ ID 45.
XX
KW Cytostatic; Pre-B-cell transformation related gene; PBX; HOX; cancer;
KW HOX heptapeptide region; RT-PCR; primer; ss; HOXB1.
XX
OS Homo sapiens.
XX
XX WO2004055049-A1.
PN
XX
XX 01-JUL-2004.
XX
XX 12-DEC-2003; 2003WO-GB005425.
PF
XX 13-DEC-2002; 2002GB-00029151.
PR

XX PA (SGEO-) ST GEORGES ENTERPRISES LTD.
XX PI Morgan RGL, Pettengell R, Forraz NPB, Meguckin CP;
XX DR WPI; 2004-533662/51.
XX PS Use of peptide that impairs Pre-B-cell transformation related gene-
PT dependent regulation of gene transcription by affecting binding to Hox,
PT for treating or preventing disorders involving aberrant cell division,
PT especially cancer.
XX PS Example 4; SEQ ID NO 45; 113pp; English.
XX CC The present invention relates to peptides which impair Pre-B-cell
CC transformation related gene (PBX)-dependent regulation of gene
CC transcription, since they mimic the region of HOX to which PBX binds and
CC act as antagonists of that binding. The peptides are based on the
CC hexapeptide region of HOXB-4 but have been found to have cross-reactivity
CC and reduce the binding of PBX to all HOX proteins. The peptides are
CC useful for manufacturing a medicament for the treatment or prevention of
CC a disorder in which aberrant cell division occurs e.g. cancer. The
CC peptides also further comprise a cell penetration moiety that is linked
CC directly to the carboxy-terminal of the peptide. The peptides are also
CC useful for reducing the side effects of a cytotoxic or chemotherapeutic
CC agent, or for maintaining or expanding a stem cell population in vivo.
CC The stem cells, which are originally derived from the recipient
CC individual, may be used in manufacturing a medicament for the treatment
CC or prevention of a condition resulting in a decreased level of stem
CC cells, such as a condition resulting from chemotherapy or radiotherapy.
CC The present sequence is a RT-PCR which was used in an example from the
CC invention.
XX CC
XX Sequence 20 BP; 1 A; 8 C; 3 G; 8 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 67 CAATCAGAAGCGGCGGAGG 86
DB 20 CAATCAGAAGCGGCGGAGG 1
RESULT 188
AAV40968
ID AAV40968 standard; DNA; 21 BP.
XX AC AAV40968;
XX DT 25-SEP-1998 (first entry)
XX DE Primer HOX11:857121 for abnormality detection.
XX KW PCR primer; chromosomal abnormality; abnormality detection; leukaemia;
KW lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;
KW medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9824928-A2.
XX PD 11-JUN-1998.
XX PF 08-DEC-1997; 97WO-DK000556.
XX PR 06-DEC-1996; 96DK-00001401.
XX PA (PALL/) PALLISGAARD N.
XX PI Pallsigaard N, Hokland P;
XX

DR WPI; 1998-333344/29.
XX CC Detection of chromosomal abnormalities - by subjecting patient sample
PT nucleic acids to a multiplex molecular amplification procedure using
PT primers specific for characteristic nucleic acid sequence.
XX CC
XX Claim 73; Page 79; 126pp; English.
XX CC This sequence represents a primer used in the method of the invention for
CC the detection of the presence or absence of chromosomal abnormalities,
CC each abnormality being associated with a condition in a subject and each
CC being defined by at least one characteristic nucleic acid sequence. The
CC method comprises: (a) obtaining a sample of nucleic acids derived from a
CC subject which may harbour one of the chromosomal abnormalities; (b)
CC subjecting the sample to a multiplex molecular amplification (MMA)
CC procedure, where a number of the characteristic sequences, if present in
CC a sufficient amount, will be amplified; (c) retrieving the product(s)
CC from step (b), and detecting the presence and/or absence of an amplicon
CC characteristic of the abnormal sequences to detect the presence or
CC absence of corresponding chromosomal abnormalities; where the MMA
CC procedure comprises the use of at least 7 mutually distinct primers (MDP)
CC in one single reaction mixture, each of the primers defining an end of at
CC least one characteristic nucleic acid sequence, and where at least one of
CC the primers defines the first end of at least two characteristic nucleic
CC acid sequences, the characteristic nucleic acid sequences each being
CC determined in their opposite ends by MDP selected from the remainder of
CC the MDP. The methods can be used for detecting chromosomal abnormalities
CC associated with diseases including numerous leukaemia's, lymphoma's,
CC carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,
CC medullablastoma, malignant melanoma, and malignant neoplastic conditions
XX CC
XX Sequence 21 BP; 1 A; 8 C; 4 G; 8 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 815 TCTGCCCTCTCCACTTCGTC 834
DB 2 TCTGCCCTCTCCACTTCGTC 21
RESULT 189
AAF95430/C
ID AAF95430 standard; DNA; 21 BP.
XX AC AAF95430;
XX DT 18-NOV-2004 (revised)
DT 06-JUN-2001 (first entry)
XX DE Human gene single nucleotide polymorphism #191.
XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX OS Homo sapiens.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT variation 11
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
XX WO200118250-A2.
XX PD 15-MAR-2001.
XX PF 07-SEP-2000; 2000WO-US024503.
XX PR 10-SEP-1999; 99US-0153357P.
XX


```
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX WPI; 2001-226749/23.
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
XX applications such as forensics, paternity testing, medicine, genetic
XX analysis and phenotype correlations to diseases such as diabetes and
XX atherosclerosis.
XX Example; Page 61; 242pp; English.
XX The present invention provides a method of diagnosing a vascular disease
XX in an individual, involving determining the sequence at various
XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX genes. The sequences at a number of polymorphic sites are also provided
XX in the specification. In particular, the method can be used in the
XX diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX useful in forensics, paternity testing, genetic analysis and phenotype
XX correlations to diseases. The present sequence is an example of one of
XX the human gene SNPs shown in the specification
XX Revised record issued on 18-NOV-2004 : The variation feature was
XX incorrectly given a capital V
XX Sequence 21 BP; 0 A; 7 C; 4 G; 10 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1554 AACACAGCAGCAGCAGCAG 1573
DB 20 AACACAGCAGCAGCAGCAG 1
RESULT 190
AAH89072
ID AAH89072 standard; DNA; 21 BP.
XX AAH89072;
XX 09-SEP-2004 (revised)
XX 27-FEB-2002 (first entry)
XX Human polymorphic oligonucleotide L21952 fragment.
XX Human; single nucleotide polymorphic; SNP; forensic science;
XX paternity testing; phenotypic trait; genetic mapping; animal breeding;
XX plant breeding; ds.
XX Homo sapiens.
XX Unidentified.
XX Key Location/Qualifiers
XX variation 11 /*tag= a
XX /standard_name= "single nucleotide polymorphism"
XX WO200134840-A2.
XX 17-MAY-2001.
XX 10-NOV-2000; 2000WO-US030766.
XX 10-NOV-1999; 99US-0164596P.
XX
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XX (GLAX ) GLAXO GROUP LTD.
PA (AFFY-) AFFYMETRIX INC.
XX Au K, Chen J, Patil N, Thomas D;
XX WPI; 2001-335945/35.
XX New polymorphic sites derived from the human genome are useful to
XX determine sites correlating with phenotypic traits, particularly disease,
XX and also in forensics and paternity testing.
XX Claim 82; Page 13; 43pp; English.
XX The present invention relates to human oligonucleotides comprising a
XX single nucleotide polymorphic site (SNP: AAH8797-AAH89219). The present
XX sequence is one such oligonucleotide. The oligonucleotides can be used in
XX forensics, paternity testing, correlation of polymorphisms with
XX phenotypic traits, genetic mapping of phenotypic traits and marker
XX assisted breeding of animals and crop plants
XX Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX Sequence 21 BP; 7 A; 7 C; 6 G; 1 T; 0 U; 0 Other;
XX Query Match 0.4%; Score 16.8; DB 1; Length 21;
XX Best Local Similarity 90.0%; Pred. No. 1.7e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1440 AACAGCAGCAGCAGCAGCAA 1459
DB 2 AACAGCAGCAGCAGCAGCCA 21
RESULT 191
ABK70314
ID ABK70314 standard; DNA; 21 BP.
XX ABK70314;
XX 15-JUL-2002 (first entry)
XX Synthetic antisense IGFBP-2-oligodeoxynucleotide (ODN) #2.
XX Hormone-regulated cancer; antisense oligonucleotide; IGFBP-2;
XX insulin-like growth factor binding protein-2; hormone-regulated tumour;
XX breast cancer; prostate cancer; IGF-1-sensitive cancer; apoptosis;
XX hormone-responsive cancer; hormonal withdrawal; oligodeoxynucleotide;
XX ODN; endocrine tumour therapy; ss.
XX Synthetic.
XX WO200222642-A1.
XX 21-MAR-2002.
XX 13-SEP-2001; 2001WO-US028748.
XX 14-SEP-2000; 2000US-0232641P.
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX Gleave M, Satoshi K, Nelson C, Rennie PS;
XX WPI; 2002-339861/37.
XX Composition for treating hormone-regulated cancer, particularly of
XX prostate or breast, comprises oligonucleotide antisense to insulin-like
XX growth factor binding protein-2.
XX Claim 3; Page 12; 36pp; English.
XX The present invention relates to a new composition for treating hormone-
```

CC regulated cancer. The composition comprises an antisense oligonucleotide
CC that inhibits expression of IGFBP-2 (insulin-like growth factor binding
CC protein-2). The molecules of the invention are used to delay progression
CC of hormone-regulated tumours, particularly of breast or prostate, to the
CC of hormone-independent state, to delay metastatic progression to the bone of
CC IGF-1-sensitive cancers and to treat hormone-responsive cancers by
CC inducing apoptosis, after hormonal withdrawal. The present nucleic acid
CC sequence represents one of a collection (ABK70313-ABK70375) of antisense
CC IGFBP-2-oligodeoxynucleotides (ODN) that were used in the invention for
CC prostate and other endocrine tumour therapy

XX
SQ Sequence 21 BP; 6 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
||||| |||||||
Db 2 GCCCAGTAGCAGCAGCAGCA 21

RESULT 192
ABK70358
ID ABK70358 standard; DNA; 21 BP.
XX
AC ABK70358;
XX
DT 15-JUL-2002 (first entry)
XX
DE Synthetic antisense IGFBP-2-oligodeoxynucleotide (ODN) #46.
XX
KW Hormone-regulated cancer; antisense oligonucleotide; IGFBP-2;
KW insulin-like growth factor binding protein-2; hormone-regulated tumour;
KW breast cancer; prostate cancer; IGF-1-sensitive cancer; apoptosis;
KW hormone-responsive cancer; hormonal withdrawal; oligodeoxynucleotide;
KW ODN; endocrine tumour therapy; ss.
XX
OS Synthetic.
XX
FN WO200222642-A1.
XX
PD 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-US028748.
XX
PR 14-SEP-2000; 2000US-0232641P.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Gleave M, Satoshi K, Nelson C, Rennie PS;
XX
XX WPI; 2002-339861/37.
XX
PT Composition for treating hormone-regulated cancer, particularly of
PT prostate or breast, comprises oligonucleotide antisense to insulin-like
PT growth factor binding protein-2.
XX
PS Claim 3; Page 13; 36pp; English.
XX

The present invention relates to a new composition for treating hormone-regulated cancer. The composition comprises an antisense oligonucleotide that inhibits expression of IGFBP-2 (insulin-like growth factor binding protein-2). The molecules of the invention are used to delay progression of hormone-regulated tumours, particularly of breast or prostate, to the bone of hormone-independent state, to delay metastatic progression to the bone of IGF-1-sensitive cancers and to treat hormone-responsive cancers by inducing apoptosis, after hormonal withdrawal. The present nucleic acid sequence represents one of a collection (ABK70313-ABK70375) of antisense IGFBP-2-oligodeoxynucleotides (ODN) that were used in the invention for prostate and other endocrine tumour therapy

XX
SQ Sequence 21 BP; 6 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1532 GCCCAACAGCAGCAGCAGCA 1551
||||| |||||||
Db 2 GCCCAGTAGCAGCAGCAGCA 21

RESULT 193
ADL23446
ID PDL23446 standard; DNA; 21 BP.
XX
AC ADL23446;
XX
DT 20-MAY-2004 (first entry)
XX
DE Plant AMP-binding protein PCR primer #7.
XX
KW plant; acyl-coenzyme A synthetase; acyl-CoA synthetase; enzyme;
KW transgenic plant; PCR; ss; primer; AMP-binding protein.
XX
OS Unidentified.
XX
FN WO200209295-A2.
XX
PD 31-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US022774.
XX
PR 21-JUL-2000; 2000US-0220474P.
XX
PR 16-JUL-2001; 2001US-00906419.
XX
PA (SHOC/) SHOCKEY J M.
PA (SCHW/) SCHNURR J.
PA (BROW/) BROWSE J A.
XX
XX Shockey JM, Schnurr J, Browse JA;
XX WPI; 2002-241594/29.
XX
PT Novel acyl coenzyme A synthetases gene useful for altering a phenotype of
PT a plant, making a transgenic plant and for producing variants of acyl-CoA
PT synthetases.
XX
PS Example 3; SEQ ID NO 91; 155pp; English.
XX

The invention comprises the amino acid and coding sequences of plant acyl coenzyme A synthetase (acyl-CoA synthetase) enzymes. The DNA and protein sequences of the invention are useful for altering a phenotype of a plant (transgenic plant). The DNA and protein sequences of the invention are also useful for producing variants of acyl-CoA synthetases. The present DNA sequence represents a PCR primer that was used in an example of the invention.

XX
SQ Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2902 CAGGCTTTTCAAGAACTG 2921
||||| |||||||
Db 2 CAGGCTTTTCAAGAAATG 21

RESULT 194
ADL72332
ID ADL72332 standard; DNA; 21 BP.
XX
AC ADL72332;
XX

DT 20-MAY-2004 (first entry)
 XX Arabidopsis thaliana acyl-CoA synthetase gene primer #40.
 DE plant; acyl-CoA synthetase; soybean; sunflower; cotton; maize; castor;
 KW transgenic plant; triacylglycerol biosynthesis; fatty acid; seedling;
 KW beta-oxidation cycle substrate; jasmonic acid; plant defence; primer; ss.
 XX OS Arabidopsis thaliana.
 XX PN WO2003087321-A2.
 XX PD 23-OCT-2003.
 XX 09-APR-2003; 2003WO-US010754.
 XX 09-APR-2002; 2002US-00119136.
 PR 08-APR-2003; 2003US-00119136.
 XX (UYWA-) UNIV WASHINGTON STATE RES FOUND.
 PA Shockey JM, Schnurr J, Browse JA;
 PI WPI; 2003-853948/79.
 DR New plant acyl-CoA synthetase protein derived from soybean, sunflower,
 PT cotton, maize, and castor, useful in cuticle was synthesis, and in the
 PT synthesis of jasmonic acid which is involved in reproduction and plant
 PT defense.
 XX Disclosure; SEQ ID NO 91; 226pp; English.
 PS The invention relates to a new purified plant acyl-CoA synthetase protein
 CC comprising at least one of the motifs selected from 9 fully defined
 CC motifs given in the specification, and derived from a crop plant selected
 CC from soybean, sunflower, cotton, maize, and castor. The purified plant
 CC acyl-CoA synthetase protein comprises at least one motif selected from: V
 CC -P/T-L-I-Y-D/A/S-T-L-G; I-M/C-Y/F/K-T-S-G-T/S-T-S-G-XI-P-K-G-V; S/A-
 CC -Y/M/F-L-P-L-S-A/W-H; L/Q-K/R-P-T/P/S; S/G/V/-G-A/G/S-A/L/S-P-L/I/M; G-Y-G
 CC -L/M-T-E-T/S; P/S/A-R/K-G/A-E/I-V-C/K/V-I/V/L-R/G-G; IIDRKK; and L-
 CC L/V/M/L-P/A-T/S-F/L/M/Y-X-K-XI-K/R-R. The nucleic acid is useful in
 CC producing a transgenic plant (claimed). The plant acyl-CoA synthetase is
 CC useful in TAG biosynthesis, for activating fatty acids released from oil
 CC bodies in newly germinated seedlings, as substrates for the beta-
 CC oxidation cycle which supplies the plant with cellular energy until it
 CC becomes photosynthetically competent, in cuticle was synthesis, and in
 CC the synthesis of jasmonic acid, a fatty acid-derived signaling compound
 CC involved in reproduction, plant defence, and other response reactions.
 CC This sequence corresponds to a PCR primer to amplify the ACS genes of the
 CC invention.
 XX SQ Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. No. 1.7e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2502 CAGGGCTTTTCAAGGAACTG 2921
 Db 2 CAGGGCTTCTCAGGAATG 21
 RESULT 195
 ADP75370
 ID ADP75370 standard; DNA; 21 BP.
 AC ADP75370;
 XX 12-AUG-2004 (first entry)
 DT Human ADAM19 gene exon K reverse sequencing primer.
 DE Human; ss; primer; ADAM19; Endophilin 1; Endophilin 2; NRG2; ADAMTS2;
 KW

KW a disintegrin and metalloprotease; neuroregulin 2; SNP;
 KW single nucleotide polymorphism;
 KW a disintegrin and metalloprotease with thrombospondin type motif 2;
 KW asthma; atopy; obesity; inflammatory bowel disease; respiratory disorder.
 XX Homo sapiens.
 OS WO2003031594-A2.
 PN 17-APR-2003.
 XX 11-OCT-2002; 2002WO-US032700.
 XX 11-OCT-2001; 2001US-0328424P.
 PR (GENO-) GENOME THERAPEUTICS CORP.
 PA Keith T, Little RD, Van Eerdewegh P, Dupuis J, Del Mastro RG;
 PI Allen K;
 XX WPI; 2003-381712/36.
 DR New isolated nucleic acid or alternate splice variant, useful for
 XX diagnosing and treating a disintegrin and metalloprotease (ADAM) or
 PT interactor gene-associated disorder, e.g. asthma, atopy, obesity or
 PT inflammatory bowel disease.
 XX Claim 2; Page 128; 338pp; English.
 PS The invention relates to an isolated nucleic acid or alternate splice
 CC variant comprising a nucleotide sequence containing at least one of the
 CC single nucleotide polymorphisms given in the specification, a nucleotide
 CC sequence having at least 15 contiguous nucleotides of them, or
 CC complements of them. The genes are ADAM19 (a disintegrin and
 CC metalloprotease 19, also known as gene 845), NRG2 (neuroregulin 2, also
 CC known as gene 847), endophilin 1 (also known as gene 874), endophilin 2
 CC (also known as gene 803) and ADAMTS2 (a disintegrin and metalloprotease
 CC with thrombospondin type motif 2, also known as gene 962). Also included
 CC are a vector comprising the isolated nucleic acid (or alternate splice
 CC variant), a host cell containing the vector, an isolated polypeptide
 CC encoded by the novel nucleic acid (or alternate splice variant), an
 CC antibody or antibody fragment that binds to the polypeptide,
 CC pharmaceutical compositions (comprising the nucleic acid or alternate
 CC splice variant, vector, polypeptide or antibody, and a carrier,
 CC excipient or diluent), a kit for detecting a disintegrin and
 CC metalloprotease (ADAM) gene nucleotide sequence (comprising the isolated
 CC nucleic acid or alternate splice variant, antibody or antibody fragment,
 CC and at least one component to detect the hybridisation of the variant or
 CC the binding of the antibody to an ADAM gene amino acid sequence), a kit
 CC for detecting an interactor gene amino acid sequence (comprising the
 CC antibody or antibody fragment, and at least one component to detect the
 CC binding of the antibody to the interactor gene amino acid sequence),
 CC diagnosing an ADAM or interactor gene-associated disorder or a
 CC respiratory disorder in a human subject, determining an ADAM or
 CC interactor gene pharmacogenetic profile in a human subject, identifying
 CC an orthologue of a human ADAM or interactor gene, treating an ADAM or
 CC interactor gene-associated disorder (or a respiratory disorder) by
 CC administering the pharmaceutical composition, a transgenic mouse (whose
 CC genome comprises an introduced null mutation in an endogenous gene that
 CC is orthologous to a human ADAM gene), making a homozygous transgenic
 CC knockout mouse, forming a crystal of the isolated polypeptide, a cell
 CC line comprising the isolated nucleic acid or alternate splice variant, a
 CC biochip comprising the isolated nucleic acid or alternate splice variant,
 CC an isolated nucleic acid probe or primer comprising at least 8 contiguous
 CC nucleotides of the nucleic acid, an isolated antisense nucleic acid,
 CC identifying an ADAM or interactor gene ligand and an isolated nucleic
 CC acid variant of Gene 803, 845, 847, 874 or 962. The nucleic acid or
 CC alternate splice variants, methods, kits and antibody/antibody fragment
 CC are useful for diagnosing and treating an ADAM or interactor gene-
 CC associated disorder, e.g. asthma, atopy, obesity or inflammatory bowel
 CC disease. The present sequence is a primer used to sequence the regions
 CC surrounding polymorphisms in the above genes.
 XX

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SQ Sequence 21 BP; 6 A; 0 C; 9 G; 6 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2210 GTTCAGATATGGGATGTA 2229
||| ||||| ||||| ||||| |||||
DB 2 GTTCAGATATGGGATGGA 21

RESULT 196
ADP45615/C
ID ADP45615 standard; DNA; 21 BP.
XX
AC ADP45615;
XX
XX
DT 26-AUG-2004 (first entry)
XX
DE PCR primer 2 used to genotype human MAP kinase MAPK10 polymorphism.
XX
KW breast cancer; cytostatic; gene therapy; human; ss; primer; PCR; SNP;
KW single nucleotide polymorphism; MAP kinase; MAPK10; JNK3; JNK3A; P493F12;
KW P54BSAPK MAP kinase; c-Jun kinase 3; JNK3 alpha protein kinase;
KW c-Jun N-terminal kinase 3; stress activated protein kinase beta;
KW chromosome 4q22.1-q23.
XX
XX Homo sapiens.
OS
XX WO2004047623-A2.
PN
XX 10-JUN-2004.
PD
XX
XX 25-NOV-2003; 2003WO-US037948.
PF
XX 25-NOV-2002; 2002US-0429136P.
PR
XX 24-JUL-2003; 2003US-0490234P.
PR
XX (SEQU-) SEQUENOM INC.
PA
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
PI WPI; 2004-441051/41.
XX
DR Identifying a subject at risk of breast cancer by detecting the presence
PT of polymorphic variations in the ICAM, MAPK10, KIAA0861, NUWA1 or GALE
PT regions which are associated with breast cancer in a nucleic acid sample
PT from a subject.
XX
PS Example 2; Page 74; 289pp; English.
XX
CC The invention relates to a novel method for identifying a subject at risk
CC of breast cancer comprising detecting the presence or absence of one or
CC more polymorphic variations associated with breast cancer in a nucleic
CC acid sample from a subject. The method of the invention has cytostatic
CC applications and may be useful for identifying a subject at risk of
CC breast cancer, for early diagnosis, prevention and treatment of breast
CC cancer, possibly via gene therapy, as well as to analyse and predict a
CC response to a breast cancer treatment and in clinical drug trials. The
CC current sequence is that of a PCR primer of the invention which was used
CC to genotype human MAP kinase MAPK10 (JNK3;JNK3A;p493F12;p54BSAPK MAP
CC kinase;c-Jun kinase 3;JNK3 alpha protein kinase;c-Jun N-terminal kinase 3
CC ;stress activated protein kinase beta) gDNA which has been mapped to
CC chromosomal position 4q22.1-q23.
XX
SQ Sequence 21 BP; 4 A; 6 C; 2 G; 9 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2958 AACAAATGATACATGGGC 2977
||| ||||| ||||| ||||| |||||
DB 2 GTTCAGATATGGGATGGA 21

SQ Sequence 21 BP; 6 A; 0 C; 9 G; 6 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2958 AACAAATGATACATGGGC 2977
||| ||||| ||||| ||||| |||||
DB 2 GTTCAGATATGGGATGGA 21

RESULT 197
AAC73261
ID AAC73261 standard; DNA; 18 BP.
XX
AC AAC73261;
XX
XX
DT 02-FEB-2001 (first entry)
XX
DE Forward primer #48 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
XX WO200058516-A2.
PN
XX 05-OCT-2000.
PD
XX 27-MAR-2000; 2000WO-US008069.
XX
XX 26-MAR-1999; 99US-0126473P.
PR
XX 23-JUN-1999; 99US-0140359P.
PR
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
XX Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX WPI; 2000-656171/63.
XX
XX Universal array of oligonucleotides tags attached to a solid substrate
XX along with locus-specific tagged oligonucleotides useful in genotyping
XX using single base extension reactions.
XX
XX Example 7; Page 52; 70pp; English.
XX
CC The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one of the primers used in
CC the method of the present invention to amplify a polymorphic sample. The
CC amplified nucleic acid product is then used as a template in a SBE
CC reaction with an extension primer. The SBE reaction products are used to
CC form the oligonucleotide array
XX
SQ Sequence 18 BP; 8 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1395 AGCAACAGCAGCAACAGC 1412
||||| ||||| ||||| |||||
DB 1 AGCAACAGCAGCAACAGC 18

RESULT 198
AAF26668
ID AAF26668 standard; DNA; 18 BP.
XX
AC AAF26668;
XX
XX 09-SEP-2004 (revised)
DT 02-APR-2001 (first entry)
XX
XX Human Smad7 phosphorothioate antisense oligonucleotide SEQ ID NO:11.
DE
```

XX Human; Smad7; antisense oligonucleotide; phosphorothioate; inhibition;
 KW antiinflammatory; cytostatic; infection; inflammation; tumour formation;
 KW ss.
 XX Homo sapiens.
 OS Unidentified.
 OS
 XX Key Location/Qualifiers
 FH modified_base 1..18
 FT /*tag= a
 FT /mod_base
 FT /note= "phosphorothioate linkages"
 FT
 XX US6159697-A.
 PN
 XX 12-DEC-2000.
 PD
 XX 09-JAN-2000; 2000US-00487444.
 PF
 XX 09-JAN-2000; 2000US-00487444.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Monia BP, Cowsett LM;
 PI
 XX WPI; 2001-070108/08.
 DR
 XX
 XX Antisense compound capable of inhibiting the expression of human Smad7,
 PT useful for preventing or delaying infection, inflammation or tumor
 PT formation.
 PT
 XX Claim 1; Col 40; 33pp; English.
 PS
 XX The present invention describes an antisense compound (I) of up to 30
 CC nucleobases in length capable of inhibiting the expression of human
 CC Smad7. (I) has antiinflammatory and cytostatic, and is a modulator of
 CC Smad7 expression. (I) can be useful for inhibiting the expression of
 CC human Smad7 in human cells or tissues, in vitro. (I) is commonly used as
 CC a research reagent and in diagnostics for example, to elucidate the
 CC function of particular genes. (I) is also useful for distinguishing
 CC between functions of various members of a biological pathway and for
 CC research use. (I) is also utilised for diagnostics, therapeutics,
 CC prophylaxis and in kits. (I) is also useful prophylactically, e.g. to
 CC prevent or delay infection, inflammation or tumour formation. AAP26667 to
 CC AAP26706 represent human Smad7 antisense oligonucleotides from the
 CC present invention
 CC
 CC Revised record issued on 09-SEP-2004 : Correction to feature table key
 CC
 XX Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1406 CACAGCAGCAGCAGCAG 1423
 DB 1 CGACAGCAGCAGCAGCAG 18
 RESULT 199
 AAS13708
 ID AAS13708 standard; DNA; 18 BP.
 XX
 AC AAS13708;
 XX
 XX 08-MAY-2002 (first entry)
 DT
 XX Simple sequence repeat, SSR, #5.
 DE
 XX Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
 KW gamma-amino-butyric acid B receptor; epileps; pain syndrome;
 KW cereal profiling; grass profiling; seed batch purity testing.

XX Poae.
 OS
 XX NZ509193-A.
 PN
 XX 25-MAY-2001.
 PD
 XX 03-JAN-2001; 2001NZ-00509193.
 PF
 XX 24-DEC-1999; 99AU-00004906.
 PR
 XX 04-MAY-2000; 2000AU-00007310.
 PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
 PA (UYSC-) UNIV SOUTHERN CROSS.
 PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
 PA (UYAD-) UNIV ADELAIDE.
 PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
 XX Forster JW, Jones ES;
 PI WPI; 2001-512563/56.
 DR
 XX New simple sequence repeats having 2 or more tandemly repeated nucleotide
 PT core elements isolated from ryegrass and fescue, useful for selecting of
 PT genes in grass or cereal breeding or profiling grass or cereal species
 PT varieties.
 PT
 XX Claim 6; Page 51; 72pp; English.
 PS
 XX The invention relates to a substantially purified or isolated nucleic
 CC acid (I) from ryegrass or fescue species including a simple sequence
 CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
 CC 2-6 nucleotides in length. Also included are a nucleic acid primer
 CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
 CC library of ryegrass or fescue genomic DNA enriched for SSRs and
 CC identifying clones in the library containing SSRs, a library of ryegrass
 CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
 CC a gene in grass or cereal breeding by identifying an SSR that is closely
 CC associated with the gene such that the SSR and the gene are
 CC preferentially co-inherited, and selecting for the SSR in the breeding, a
 CC method for DNA profiling grass or cereal species varieties by assessing
 CC variation between SSR varieties and testing the purity of grass or cereal
 CC seed batches by assessing variation within seed batch of an SSR. The SSRs
 CC may be used in the selection of genes in grass or cereal breeding, for
 CC profiling grass or cereal species varieties, for testing the purity of
 CC grass or cereal seed batches, and for DNA profiling to establish the
 CC distinct identity, uniformity and/or stability of a cultivar. The present
 CC sequence is a ryegrass or fescue SSR
 XX
 XX Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1574 CAACAACAACAGCAGCAACA 1591
 DB 1 CAACAACAACAGCAGCAACA 18
 RESULT 200.
 ABA93493
 ID ABA93493 standard; DNA; 18 BP.
 XX
 AC ABA93493;
 XX
 XX 25-APR-2002 (first entry)
 DT
 XX GAGA-B receptor 1a (gbl a) antisense oligonucleotide.
 DE
 XX Identification; gamma-amino-butyric acid; GABA; GABA-B receptor;
 KW gamma-amino-butyric acid B receptor; epileps; pain syndrome;
 KW antisense oligonucleotide; ss.

PT New single stranded oligonucleotides comprising a DNA domain having at
PT least one mismatch with respect to the genetic sequence of the
PT Huntington's disease gene to be altered, useful for treating or
PT preventing Huntington's disease.
XX
PS Example 7; Fig 20; 133pp; English.
XX
CC The present sequence is that of a portion of a mutated glutamine (CAG)
CC triplet repeat region of exon 1 of the human Huntington's disease (HD)
CC gene (see also AB281760). The triplet repeat region is mutated following
CC treatment with single-stranded phosphorothioate-containing HD gene-
CC targeted oligonucleotide HD35/52 (see AB281756). The second glutamine
CC (CAG) repeat triplet is converted to CTG, creating a restriction fragment
CC length polymorphism site that enables cleavage by PvuII. HD35/25 is an
CC example of oligonucleotides of the invention for targeted alteration of
CC the HD gene. Such oligonucleotides can be used for the treatment or
CC prevention of HD
XX
SQ Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAG 1426
Db 1 CAGCTGCAGCAGCAGCAG 18
|||||

RESULT 203
AB281779
ID AB281779 standard; DNA; 18 BP.
XX
AC AB281779;
XX
DT 11-JUN-2003 (first entry)
XX
XX Huntington's disease gene mutated exon 1 region.
DE
KW Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
KW gene therapy; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH mutation replace(5,A)
FT /*tag= a
XX
XX WO2003013437-A2.
XX
XX 20-FEB-2003.
XX
XX 07-AUG-2002; 2002WO-US025352.
XX
XX 07-AUG-2001; 2001US-0310757P.
XX 08-AUG-2001; 2001US-0310770P.
XX 08-AUG-2001; 2001US-0310889P.
XX 04-DEC-2001; 2001US-0337219P.
XX
XX (UYDE) UNIV DELAWARE.
XX
XX Kmiec EB, Parekh-Olmedo H;
XX
XX WPI; 2003-256478/25.
XX
XX New single stranded oligonucleotides comprising a DNA domain having at
XX least one mismatch with respect to the genetic sequence of the
XX Huntington's disease gene to be altered, useful for treating or
XX preventing Huntington's disease.
XX
XX Example 7; Fig 20; 133pp; English.
XX

CC The present sequence is that of a portion of a mutated glutamine (CAG)
CC triplet repeat region of exon 1 of the human Huntington's disease (HD)
CC gene (see also AB281760). The triplet repeat region is mutated following
CC treatment with single-stranded phosphorothioate-containing HD gene-
CC targeted oligonucleotide HD35/25 (see AB281755). The second glutamine
CC (CAG) repeat triplet is converted to CTG, creating a restriction fragment
CC length polymorphism site that enables cleavage by PvuII. HD35/25 is an
CC example of oligonucleotides of the invention for targeted alteration of
CC the HD gene. Such oligonucleotides can be used for the treatment or
CC prevention of HD
XX
SQ Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAG 1426
Db 1 CAGCTGCAGCAGCAGCAG 18
|||||

RESULT 204
ADP75262
ID ADP75262 standard; DNA; 18 BP.
XX
AC ADP75262;
XX
DT 12-AUG-2004 (first entry)
XX
XX Human ADAM19 gene exon X SSCP reverse primer.
DE
KW Human; SSCP; ss; primer; ADAM19; Endophilin 1; Endophilin 2; NRG2;
KW ADAMTS2; a disintegrin and metalloprotease; neuroregulin 2; SNP;
KW single nucleotide polymorphism;
KW a disintegrin and metalloprotease with thrombospondin type 1 motif 2;
KW asthma; atopy; obesity; inflammatory bowel disease; respiratory disorder;
KW single-strand conformation polymorphism.
XX
XX Homo sapiens.
XX
XX WO2003031594-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032700.
XX
XX 11-OCT-2001; 2001US-0328424P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Keith T, Little RD, Van Eerdewegh P, Dupuis J, Del Mastro RG;
XX Allen K;
XX
XX WPI; 2003-381712/36.
XX
XX New isolated nucleic acid or alternate splice variant, useful for
XX diagnosing and treating a disintegrin and metalloprotease (ADAM) or
XX interactor gene-associated disorder, e.g. asthma, atopy, obesity or
XX inflammatory bowel disease.
XX
XX Claim 2; Page 124; 338pp; English.
XX
XX The invention relates to an isolated nucleic acid or alternate splice
XX variant comprising a nucleotide sequence containing at least one of the
XX single nucleotide polymorphisms given in the specification, a nucleotide
XX sequence having at least 15 contiguous nucleotides of them, or
XX complements of them. The genes are ADAM19 (a disintegrin and
XX metalloprotease 19, also known as gene 845), NRG2 (neuroregulin 2, also
XX known as gene 847), endophilin 1 (also known as gene 874), endophilin 2
XX (also known as gene 803) and ADAMTS2 (a disintegrin and metalloprotease
XX with thrombospondin type 1 motif 2, also known as gene 962). Also included
XX are a vector comprising the isolated nucleic acid (or alternate splice

variant), a host cell containing the vector, an isolated polypeptide encoded by the novel nucleic acid (or alternate splice variant), an antibody or antibody fragment that binds to the polypeptide, an pharmaceutical compositions (comprising the nucleic acid or alternate splice variant, vector, polypeptide or antibody, and a carrier, excipient or diluent), a kit for detecting a disintegrin and metalloprotease (ADAM) gene nucleotide sequence (comprising the isolated nucleic acid or alternate splice variant, antibody or antibody fragment, and at least one component to detect the hybridisation of the variant or the binding of the antibody to an ADAM gene amino acid sequence), a kit for detecting an interactor gene amino acid sequence (comprising the antibody or antibody fragment, and at least one component to detect the binding of the antibody to the interactor gene amino acid sequence), diagnosing an ADAM or interactor gene-associated disorder or a respiratory disorder in a human subject, determining an ADAM or interactor gene pharmacogenetic profile in a human subject, identifying an orthologue of a human ADAM or interactor gene, treating an ADAM or interactor gene-associated disorder (or a respiratory disorder) by administering the pharmaceutical composition, a transgenic mouse (whose genome comprises an introduced null mutation in an endogenous gene that is orthologous to a human ADAM gene), making a homozygous transgenic knockout mouse, forming a crystal of the isolated polypeptide, a cell line comprising the isolated nucleic acid or alternate splice variant, a biochip comprising the isolated nucleic acid or alternate splice variant, an isolated nucleic acid probe or primer comprising at least 8 contiguous nucleotides of the nucleic acid, an isolated antisense nucleic acid, identifying an ADAM or interactor gene ligand and an isolated nucleic acid variant of Gene 803, 845, 847, 874 or 962. The nucleic acid or alternate splice variants, methods, kits and antibody/antibody fragment are useful for diagnosing and treating an ADAM or interactor gene-associated disorder, e.g. asthma, atopy, obesity or inflammatory bowel disease. The present sequence is an SSCP (single-strand conformation polymorphism) primer used to analyse the above genes for the presence of polymorphisms.

Seq Sequence 18 BP; 8 A; 5 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1541 CAGCAGCAGCAGCAACAA 1558
||| ||||| ||||| |||||
Db 1 CAGGAGCAGCAGCAACAA 18

RESULT 205

ADN97298
ID ADN97298 standard; DNA; 18 BP.

AC ADN97298;

DT 01-JUL-2004 (first entry)

DE Primer of the invention #88.

KW DNA fingerprinting; Cannabis sativa; short tandem repeat marker;
KW forensic identification; marijuana; primer; ss.

XX Synthetic.

OS WO2004008841-A2.

PN 29-JAN-2004.

PD 21-JUL-2003; 2003WO-US022887.

PR 19-JUL-2002; 2002US-0397179P.

PA (UVAR-) UNIV ARIZONA.

PA (KEIM/) KEIM P S

PA (ZINN/) ZINNAMON K.

XX

PI Keim PS, Zinnamon K;
XX WPI; 2004-143139/14.

XX New isolated nucleic acid for amplification of a short tandem repeat
PT located in DNA isolated from Cannabis sativa L species, useful for
PT forensic identification of marijuana or for linking a marijuana sample to
PT its plant source.

XX Disclosure; SEQ ID NO 165; 79pp; English.

XX The present invention relates to DNA fingerprinting for Cannabis Sativa
CC using short tandem repeat markers. The nucleic acid is useful for
CC forensic identification of marijuana or for linking a marijuana sample to
CC its plant source. The present sequence represents a primer of the
CC invention.

XX Sequence 18 BP; 6 A; 7 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 984 ACCAGCAGCAGCACCAGC 1001
||| ||||| ||||| |||||
Db 1 AGCAGCAGCAGCACCAGC 18

RESULT 206

ADO26670/c
ID ADO26670 standard; DNA; 18 BP.

AC ADO26670;

DT 12-AUG-2004 (first entry)

DE Synthetic leader sequence encoding DNA SEQ ID NO:63.

XX phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

OS WO2004042059-A1.

PN 21-MAY-2004.

PF 10-NOV-2003; 2003WO-AU001487.

XX 08-NOV-2002; 2002US-0425163P.

PA (UVQU) UNIV QUEENSLAND.

PI Frazer IH;

XX WPI; 2004-411519/38.

DR P-PSDB; ADO26671.

XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprises replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 63; 86pp; English.

XX The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism

of interest and organisms that are related to the organisms of interest;
 and (b) replacing the first codon with the synonymous codon to construct
 the synthetic polynucleotide. Also described: (1) a method for
 determining the phenotypic preference of a first codon in an organism of
 interest or its parts; (2) a synthetic polynucleotide constructed from
 the method above; (3) an organism of interest or part containing a
 synthetic polynucleotide constructed from the method above; (4) an
 organism of interest or part containing a synthetic construct that
 comprises a regulatory polynucleotide operably linked to a tandem repeat
 of a first codon fused in frame with a reporter polynucleotide that
 encodes a reporter protein, which produces, or is predicted to produce a
 selected phenotype or a phenotype of the same class as the selected
 phenotype in the organism or part; (5) a method of modulating the quality
 of a selected phenotype that is displayed by an organism of interest or
 part and that results from the expression of a parent polynucleotide that
 encodes the polypeptide; (6) a method of enhancing the quality of a
 selected phenotype that is displayed by an organism of interest or part
 and that results from the expression of a parent polynucleotide that
 encodes the polypeptide; and (7) a method of reducing the quality of a
 selected phenotype that is displayed by an organism of interest or part
 and that results from the expression of a parent polynucleotide that
 encodes the polypeptide. The method is useful for constructing a
 synthetic polynucleotide from which a polypeptide is producible to confer
 a selected phenotype to an organism of interest or part in a different
 quality than that conferred by a parent polynucleotide that encodes the
 same polypeptide. It is useful for modulating the quality of a selected
 phenotype displayed by an organism or part. The present sequence encodes
 a synthetic leader sequence, which is used in an example from the present
 invention.

XX Sequence 18 BP; 0 A; 0 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACAACACAGCAACAA 1591

Db 18 CAACAACACACAAACAA 1

RESULT 207

ADO26722/c

ID ADO26722 standard; DNA; 18 BP.

XX ADO26722;

DT 12-AUG-2004 (first entry)

XX Synthetic leader sequence encoding DNA SEQ ID NO:115.

DE phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

PN WO2004042059-A1.

XX 21-MAY-2004.

XX 10-NOV-2003; 2003WO-AU001487.

PR 08-NOV-2002; 2002US-0425163P.

PA (UYQU) UNIV QUEENSLAND.

PI Frazer IH;

XX WPI; 2004-411519/38.

DR P-PSDB; ADO26723.

XX Constructing synthetic polynucleotide for modulating the quality of a
 PT selected phenotype displayed by an organism comprises replacing a first
 PT codon with a synonymous codon to construct the synthetic polynucleotide.

XX Example 1; SEQ ID NO 115; 86pp; English.

XX The present invention describes a method for constructing a synthetic
 CC polynucleotide from which a polypeptide is producible to confer a
 CC selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. The method comprises: (a) selecting a first codon of
 CC the parent polynucleotide for replacement with a synonymous codon, where
 CC the synonymous codon is selected on the basis that it exhibits a
 CC different phenotypic preference than the first codon in a comparison of
 CC phenotypic preferences in test organisms or parts, where the test
 CC organism are selected from organisms of the same species as the organism
 CC of interest and organisms that are related to the organisms of interest;
 CC and (b) replacing the first codon with the synonymous codon to construct;
 CC the synthetic polynucleotide. Also described: (1) a method for
 CC determining the phenotypic preference of a first codon in an organism of
 CC interest or its parts; (2) a synthetic polynucleotide constructed from
 CC the method above; (3) an organism of interest or part containing a
 CC synthetic polynucleotide constructed from the method above; (4) an
 CC organism of interest or part containing a synthetic construct that
 CC comprises a regulatory polynucleotide operably linked to a tandem repeat
 CC of a first codon fused in frame with a reporter polynucleotide that
 CC encodes a reporter protein, which produces, or is predicted to produce a
 CC selected phenotype or a phenotype of the same class as the selected
 CC phenotype in the organism or part; (5) a method of modulating the quality
 CC of a selected phenotype that is displayed by an organism of interest or
 CC part and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; (6) a method of enhancing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide; and (7) a method of reducing the quality of a
 CC selected phenotype that is displayed by an organism of interest or part
 CC and that results from the expression of a parent polynucleotide that
 CC encodes the polypeptide. The method is useful for constructing a
 CC synthetic polynucleotide from which a polypeptide is producible to confer
 CC a selected phenotype to an organism of interest or part in a different
 CC quality than that conferred by a parent polynucleotide that encodes the
 CC same polypeptide. It is useful for modulating the quality of a selected
 CC phenotype displayed by an organism or part. The present sequence encodes
 CC a synthetic leader sequence, which is used in an example from the present
 CC invention.

XX Sequence 18 BP; 0 A; 0 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1575 AACAAACACAGCAACAA 1592

Db 18 AACAAACACAAACAAAC 1

RESULT 208

ADO26640/c

ID ADO26640 standard; DNA; 18 BP.

XX ADO26640;

DT 12-AUG-2004 (first entry)

XX Synthetic leader sequence encoding DNA SEQ ID NO:33.

DE phenotype; phenotypic preference; phenotype modulation; leader; ds.

XX Synthetic.

XX WO2004042059-A1.

XX 21-MAY-2004.

XX 10-NOV-2003; 2003WO-AU001487.

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XX 08-NOV-2002; 2002US-0425163P.
XX (UYQU ) UNIV QUEENSLAND.
XX Frazer IH;
XX WPI; 2004-411519/38.
XX P-PSDB; ADO26641.
XX Constructing synthetic polynucleotide for modulating the quality of a
XX selected phenotype displayed by an organism comprises replacing a first
XX codon with a synonymous codon to construct the synthetic polynucleotide.
XX Example 1; SEQ ID NO 33; 86pp; English.
XX The present invention describes a method for constructing a synthetic
XX polynucleotide from which a polypeptide is producible to confer a
XX selected phenotype to an organism of interest or part in a different
XX quality than that conferred by a parent polynucleotide that encodes the
XX same polypeptide. The method comprises: (a) selecting a first codon of
XX the parent polynucleotide for replacement with a synonymous codon, where
XX the synonymous codon is selected on the basis that it exhibits a
XX different phenotypic preference than the first codon in a comparison of
XX phenotypic preferences in test organisms or parts, where the test
XX organism are selected from organisms of the same species as the organism
XX of interest and organisms that are related to the organisms of interest;
XX and (b) replacing the first codon with the synonymous codon to construct
XX the synthetic polynucleotide. Also described: (1) a method for
XX determining the phenotypic preference of a first codon in an organism of
XX interest or its parts; (2) a synthetic polynucleotide constructed from
XX the method above; (3) an organism or interest or part containing a
XX synthetic polynucleotide constructed from the method above; (4) an
XX organism or interest or part containing a synthetic construct that
XX comprises a regulatory polynucleotide operably linked to a tandem repeat
XX of a first codon fused in frame with a reporter polynucleotide that
XX encodes a reporter protein, which produces, or is predicted to produce a
XX selected phenotype or a phenotype of the same class as the selected
XX phenotype in the organism or part; (5) a method of modulating the quality
XX of a selected phenotype that is displayed by an organism of interest or
XX part and that results from the expression of a parent polynucleotide that
XX encodes the polypeptide; (6) a method of enhancing the quality of a
XX synthetic polynucleotide from which a polypeptide is producible to confer
XX a selected phenotype to an organism of interest or part in a different
XX quality than that conferred by a parent polynucleotide that encodes the
XX same polypeptide. It is useful for modulating the quality of a selected
XX phenotype displayed by an organism or part. The present sequence encodes
XX a synthetic leader sequence, which is used in an example from the present
XX invention.
XX Sequence 18 BP; 0 A; 0 C; 6 G; 12 T; 0 U; 0 Other;
XX Query Match 0.4%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.2e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1576 ACAACACAGCAACACACA 1593
XX ||||||| |||||||
XX 18 ACAACACACACACACACA 1
XX
XX RESULT 209
XX ADO26708
XX ID ADO26708 standard; DNA; 18 BP.
XX AC
XX ADO26708;
XX

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DT 12-AUG-2004 (first entry)
XX Synthetic leader sequence encoding DNA SEQ ID NO:101.
XX phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX Synthetic.
XX WO2004042059-A1.
XX PN
XX 21-MAY-2004.
XX PD
XX 10-NOV-2003; 2003WO-AU001487.
XX PF
XX 08-NOV-2002; 2002US-0425163P.
XX PR
XX (UYQU ) UNIV QUEENSLAND.
XX PA
XX Frazer IH;
XX PI
XX WPI; 2004-411519/38.
XX DR
XX F-PSDB; ADO26709.
XX DR
XX Constructing synthetic polynucleotide for modulating the quality of a
XX selected phenotype displayed by an organism comprises replacing a first
XX codon with a synonymous codon to construct the synthetic polynucleotide.
XX Example 1; SEQ ID NO 101; 86pp; English.
XX The present invention describes a method for constructing a synthetic
XX polynucleotide from which a polypeptide is producible to confer a
XX selected phenotype to an organism of interest or part in a different
XX quality than that conferred by a parent polynucleotide that encodes the
XX same polypeptide. The method comprises: (a) selecting a first codon of
XX the parent polynucleotide for replacement with a synonymous codon, where
XX the synonymous codon is selected on the basis that it exhibits a
XX different phenotypic preference than the first codon in a comparison of
XX phenotypic preferences in test organisms or parts, where the test
XX organism are selected from organisms of the same species as the organism
XX of interest and organisms that are related to the organisms of interest;
XX and (b) replacing the first codon with the synonymous codon to construct
XX the synthetic polynucleotide. Also described: (1) a method for
XX determining the phenotypic preference of a first codon in an organism of
XX interest or its parts; (2) a synthetic polynucleotide constructed from
XX the method above; (3) an organism or interest or part containing a
XX synthetic polynucleotide constructed from the method above; (4) an
XX organism or interest or part containing a synthetic construct that
XX comprises a regulatory polynucleotide operably linked to a tandem repeat
XX of a first codon fused in frame with a reporter polynucleotide that
XX encodes a reporter protein, which produces, or is predicted to produce a
XX selected phenotype or a phenotype of the same class as the selected
XX phenotype in the organism or part; (5) a method of modulating the quality
XX of a selected phenotype that is displayed by an organism of interest or
XX part and that results from the expression of a parent polynucleotide that
XX encodes the polypeptide; (6) a method of enhancing the quality of a
XX synthetic polynucleotide from which a polypeptide is producible to confer
XX a selected phenotype to an organism of interest or part in a different
XX quality than that conferred by a parent polynucleotide that encodes the
XX same polypeptide. It is useful for modulating the quality of a selected
XX phenotype displayed by an organism or part. The present sequence encodes
XX a synthetic leader sequence, which is used in an example from the present
XX invention.
XX Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
XX Query Match 0.4%; Score 16.4; DB 1; Length 18;
XX Best Local Similarity 94.4%; Pred. No. 1.2e+02;

```

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1576 ACAACACAGCAACAA 1593
||||||| |||||

Db 1 ACAACACACACAA 18

RESULT 210
ADO26630
ID ADO26630 standard; DNA; 18 BP.
AC ADO26630;
XX
XX
XX 12-AUG-2004 (first entry)
XX
XX
XX Synthetic leader sequence encoding DNA SEQ ID NO:23.
XX phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
XX Synthetic.
XX
XX WO2004042059-A1.
XX
XX 21-MAY-2004.
XX
XX 10-NOV-2003; 2003WO-AU001487.
XX
XX 08-NOV-2002; 2002US-0425163P.
XX
XX (UYQU) UNIV QUEENSLAND.
XX
XX Frazer IH;
XX
XX WPI; 2004-411519/38.
XX P-PSDB; ADO26631.
XX
XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprising replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
XX Example 1; SEQ ID NO 23; 86pp; English.
XX
XX The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism or interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism or interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; and (7) a method of reducing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that

CC encodes the polypeptide. The method is useful for constructing a
CC synthetic polynucleotide from which a polypeptide is producible to confer
CC a selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. It is useful for modulating the quality of a selected
CC phenotype displayed by an organism or part. The present sequence encodes
CC a synthetic leader sequence, which is used in an example from the present
XX invention.

SQ Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1575 AACACACAGCAACAA 1592
||||||| |||||

Db 1 AACACACACACAA 18

RESULT 211
ADO26642
ID ADO26642 standard; DNA; 18 BP.
XX
XX ADO26642;
AC
XX
XX 12-AUG-2004 (first entry)
XX
XX Synthetic leader sequence encoding DNA SEQ ID NO:35.
XX phenotype; phenotypic preference; phenotype modulation; leader; ds.
XX
XX Synthetic.
XX
XX WO2004042059-A1.
XX
XX 21-MAY-2004.
XX
XX 10-NOV-2003; 2003WO-AU001487.
XX
XX 08-NOV-2002; 2002US-0425163P.
XX
XX (UYQU) UNIV QUEENSLAND.
XX
XX Frazer IH;
XX
XX WPI; 2004-411519/38.
XX P-PSDB; ADO26643.
XX
XX Constructing synthetic polynucleotide for modulating the quality of a
PT selected phenotype displayed by an organism comprising replacing a first
PT codon with a synonymous codon to construct the synthetic polynucleotide.
XX
XX Example 1; SEQ ID NO 35; 86pp; English.
XX
XX The present invention describes a method for constructing a synthetic
CC polynucleotide from which a polypeptide is producible to confer a
CC selected phenotype to an organism of interest or part in a different
CC quality than that conferred by a parent polynucleotide that encodes the
CC same polypeptide. The method comprises: (a) selecting a first codon of
CC the parent polynucleotide for replacement with a synonymous codon, where
CC the synonymous codon is selected on the basis that it exhibits a
CC different phenotypic preference than the first codon in a comparison of
CC phenotypic preferences in test organisms or parts, where the test
CC organism are selected from organisms of the same species as the organism
CC of interest and organisms that are related to the organisms of interest;
CC and (b) replacing the first codon with the synonymous codon to construct
CC the synthetic polynucleotide. Also described: (1) a method for
CC determining the phenotypic preference of a first codon in an organism of
CC interest or its parts; (2) a synthetic polynucleotide constructed from
CC the method above; (3) an organism or interest or part containing a
CC synthetic polynucleotide constructed from the method above; (4) an
CC organism or interest or part containing a synthetic construct that
CC comprises a regulatory polynucleotide operably linked to a tandem repeat
CC of a first codon fused in frame with a reporter polynucleotide that
CC encodes a reporter protein, which produces, or is predicted to produce a
CC selected phenotype or a phenotype of the same class as the selected
CC phenotype in the organism or part; (5) a method of modulating the quality
CC of a selected phenotype that is displayed by an organism of interest or
CC part and that results from the expression of a parent polynucleotide that
CC encodes the polypeptide; (6) a method of enhancing the quality of a
CC selected phenotype that is displayed by an organism of interest or part
CC and that results from the expression of a parent polynucleotide that

comprises a regulatory polynucleotide operably linked to a tandem repeat of a first codon fused in frame with a reporter polynucleotide that encodes a reporter protein, which produces, or is predicted to produce a selected phenotype or a phenotype of the same class as the selected phenotype in the organism or part; (5) a method of modulating the quality of a selected phenotype that is displayed by an organism of interest or part and that results from the expression of a parent polynucleotide that encodes the polypeptide; (6) a method of enhancing the quality of a selected phenotype that is displayed by an organism of interest or part and that results from the expression of a parent polynucleotide that encodes the polypeptide; and (7) a method of reducing the quality of a selected phenotype that is displayed by an organism of interest or part and that results from the expression of a parent polynucleotide that encodes the polypeptide. The method is useful for constructing a synthetic polynucleotide from which a polypeptide is producible to confer a selected phenotype to an organism of interest or part in a different quality than that conferred by a parent polynucleotide that encodes the same polypeptide. It is useful for modulating the quality of a selected phenotype displayed by an organism or part. The present sequence encodes a synthetic leader sequence, which is used in an example from the present invention.

Sequence 18 BP; 12 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACACACACACACACAA 1591
DB 1 CAACACACACACACACAA 18
|||||

RESULT 212
AAAX77030/C

ID AAAX77030 standard; DNA; 20 BP.

AC AAAX77030;

DT 10-AUG-1999 (first entry)

DE PCR primer for the Rad23 (HHR23B) gene.

OS PCR primer; proto-oncogene; oncogene; nucleic acid synthesis; ultrasound;
KW stress protein; repair protein; phenylketonuria; p53 tumour suppressor;
KW phenylalanine hydroxylase; IL-2 production; cancer; AIDS; haemophilia;
KW autoimmune disease; chronic viral infection; cystic fibrosis; therapy;
KW ss.

OS Synthetic.

OS Homo sapiens.

PN WO925385-A1.

PD 27-MAY-1999.

PF 11-NOV-1998; 98WO-US023843.

PR 17-NOV-1997; 97US-00971540.

PA (IMAR-) IMARX PHARM CORP.

PI Unger EC, McCreery T, Sadewasser D;

DR WPI; 1999-370731/31.

XX Increasing nucleic acid synthesis by ultrasonic treatment of cells.

PS Example 1; Page 108; 124pp; English.

XX This sequence represents a PCR primer for a proto-oncogene/oncogene, and
CC was used to test the method of the invention. The method is for
CC increasing synthesis of nucleic acid (I) in a cell by exposing it to

CC ultrasound, where (I) is: (a) an endogenous sequence (Ia) encoding a
CC stress or repair protein; or (b) an introduced exogenous sequence (Ib).
CC The method is specifically used therapeutically: (i) to treat
CC phenylketonuria (following introduction of (Ib) for phenylalanine
CC hydroxylase); (ii) to increase expression of the p53 tumour suppressor;
CC (iii) to increase production of IL-2, particularly associated with
CC natural killer cells; and (iv) for treating cancer by administering a
CC sequence antisense to initiation factor 3 and/or tRNA synthase. More
CC generally, (Ib) may include one or more genes or fragments, or even
CC complete chromosomes, for delivery (in vivo, in vitro or ex vivo) to
CC animal or plant cells for treating a very wide range of conditions, e.g.
CC acquired immune deficiency syndrome, autoimmune diseases, chronic viral
CC infections, haemophilia, cystic fibrosis, and cancer. Ultrasonic
CC treatment increases expression of (I) and increases uptake of (Ib),
XX particularly of 4-6 kb

SQ Sequence 20 BP; 3 A; 3 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2000 TTGTCAAGGCCACCTCCA 2017
DB 18 TTGTCAAGGCCACCTCCA 1
|||||

RESULT 213

AAA66287

ID AAA66287 standard; DNA; 20 BP.

AC AAA66287;

DT 09-OCT-2000 (first entry)

DE Dog genomic marker oligonucleotide sequence SEQ ID NO:149.

OS Dog; genome; genomic marker; radiation hybrid map; identification;
KW chromosome location; gene marker; polymorphic microsatellite marker;
KW phenotype; behaviour; pedigree; ss.

OS Canis familiaris.

PN WO200029615-A2.

PD 25-MAY-2000.

PF 15-NOV-1999; 99WO-IB001907.

PR 13-NOV-1998; 98US-0108193P.

PA (CNRS) CNRS CENT NAT RECH SCI.

PI Galibert F, Andre C;

DR WPI; 2000-387821/33.

XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
PT for e.g. identifying genes implicated in phenotypic and behavioral traits
PT or in genetic diseases and for studying dog pedigrees.

PS Claim 1; Page 59; 87pp; English.

XX The present invention describes a radiation hybrid map of the dog (Canine
CC familiaris) genome comprising the genome location of a marker selected
CC from AAA66139 to AAA66942. The radiation hybrid map is useful for
CC identifying and localising dog genes, since it covers approximately 80 %
CC of the dog genome and provides a dense map integrating different types
CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
CC (or complementary sequences) are especially useful to identify genes
CC responsible for phenotypic and behavioural traits in dogs, to identify
CC morbid genes, to analyse diseases and identify implicated genes in such
CC diseases and their alleles, and to study dog pedigrees. They may also be

CC useful for isolating corresponding human gene sequences e.g. genes
 CC involved in genetic diseases
 CC
 SQ Sequence 20 BP; 7 A; 6 C; 7 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCAG 1426
 |||||
 Db 1 CAGCAGCAGCAGCAGCAG 18

RESULT 214
 AAH56692/C
 ID AAH56692 standard; DNA; 20 BP.
 XX
 AC AAH56692;
 XX
 06-SEP-2001 (first entry)
 XX
 Streptococcus pyogenes groEL antisense oligonucleotide SEQ ID NO:340.
 XX
 Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;
 KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;
 KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;
 KW antibacterial; antiviral; antiproliferative; antisense therapy;
 KW microbial infection; ss.
 XX
 Streptococcus pyogenes.
 OS
 XX WO200136625-A2.
 XX
 25-MAY-2001.
 XX
 20-NOV-2000; 2000WO-CA001347.
 PF
 18-NOV-1999; 99US-0166249P.
 XX
 (GENE-) GENESENSE TECHNOLOGIES INC.
 PA
 Wright JA, Young AH, Dugourd D;
 XX
 WPI; 2001-355633/37.
 XX
 Novel antisense compounds targeting nucleic acid encoding groEL or groES
 PT gene of microorganism, which hybridize with and inhibit expression of the
 PT genes, useful to inhibit growth of microorganism having the genes.
 XX
 Claim 3; Page 50; 110pp; English.
 PS
 XX The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or GS
 CC of a microorganism and specifically hybridises with and inhibits the
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral and
 CC antiproliferative activities, and can be used in antisense therapy and
 CC for inhibition of expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or a
 CC virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism, (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL or
 CC GS gene and administering (I) such that the growth of microorganism is
 CC inhibited. The antisense compounds are utilised for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to

CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention
 XX
 SQ Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1466 CAGCAGCAGCAGCAGCAG 1483
 |||||
 Db 20 CAGCAGCAGCAGCAGCAG 3

RESULT 215
 ABK30537/C
 ID ABK30537 standard; DNA; 20 BP.
 XX
 AC ABK30537;
 XX
 23-APR-2002 (first entry)
 DT
 XX Human glioma-associated oncogene-1 antisense oligonucleotide ISIS 124869.
 DE
 XX Human; glioma-associated oncogene-1 associated disease; infection;
 KW inflammation; tumour formation; cytostatic; antiinflammatory; antisense;
 KW phosphorothioate; ss.
 KW
 XX Homo sapiens.
 OS
 XX US6329203-B1.
 PN
 11-DEC-2001.
 PD
 08-SEP-2000; 2000US-00657042.
 PF
 08-SEP-2000; 2000US-00657042.
 XX
 (ISIS-) ISIS PHARM INC.
 PA
 Bennett CF, Wyatt J;
 XX
 WPI; 2002-138363/18.
 DR
 XX Novel antisense compounds targeted to nucleic acids encoding glioma-
 PT associated oncogene-1, for modulating the gene expression and treating
 PT diseases associated with expression of the oncogene in humans.
 PT
 XX Example 15; Col 45-46; 43pp; English.
 PS
 XX The present invention relates to antisense compounds and methods for
 CC modulating the expression of human glioma-associated oncogene-1. The
 CC antisense compounds, particularly antisense oligonucleotides, target and
 CC inhibit the expression of human glioma-associated oncogene-1. The
 CC antisense compounds are useful for inhibiting the expression of human
 CC glioma-associated oncogene-1 in human cells or tissues and for treating
 CC an animal, particularly a human suspected of having or being prone to a
 CC disease or condition associated with expression of glioma-associated
 CC oncogene-1. The compounds are useful for diagnostics, therapeutics and as
 CC research reagent, e.g. prophylactically to prevent or delay infection,
 CC inflammation or tumour formation. The antisense compounds are safely and
 CC effectively administered to humans. ABK30509-ABK30586 represent the
 CC antisense oligonucleotides of the invention which comprise a
 CC phosphorothioate backbone
 XX
 SQ Sequence 20 BP; 2 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 976 GCAGCAGCACCAGCAGCA 993
DB 19 GCAGCAGCTCCAGCAGCA 2

RESULT 216
ACC46964

ID ACC46964 standard; DNA; 20 BP.

XX AC ACC46964;

XX 05-JUN-2003 (first entry)

XX Human phospholipase A2 antisense oligonucleotide SEQ ID NO:61.

XX Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;

KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;

KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;

KW psoriasis; diabetes; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "phosphorothioate backbone"

FT modified_base 1..5

FT /*tag= b

FT /mod_base= OTHER

FT /*note= "2'-O-methoxyethyl (2'-MOE) gapmer"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /*note= "2'-O-methoxyethyl (2'-MOE) gapmer"

XX WO200297133-A1.

PN 05-DEC-2002.

PD 21-MAY-2002; 2002WO-US016135.

PF 25-MAY-2001; 2001US-00865866.

PR (ISIS-) ISIS PHARM INC.

PA Bennett CF, Wyatt JR;

PI WPI; 2003-140495/13.

DR

XX Example 15; Page 87; 135pp; English.

XX The present invention describes a compound (I) comprising 8-50

CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,

CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase

CC A2, group IIA (synovial), where the compound specifically hybridises with

CC and inhibits the expression of phospholipase A2, group IIA (synovial).

CC Also described: (1) a composition comprising the compound and a carrier

CC or diluent; (2) a method of inhibiting the expression of phospholipase

CC A2, group IIA in cells or tissues; and (3) a method of treating an animal

CC having a disease or condition associated with phospholipase A2, group IIA

CC (synovial). (1) has antiinflammatory, antidiabetic, cytostatic and

CC antipsoriatic activities, and can be used in vaccines and in gene

CC therapy. The compound (I) can be used for preparing a composition for

CC treating or preventing inflammation, cancer, psoriasis or diabetes. The

CC present sequence represents a human phospholipase A2 group IIA (synovial)

CC chimeric phosphorothioate antisense oligonucleotide, which is used in an

CC example from the present invention

XX SQ Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 1.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2556 TGACGTCTGCAGGAGTCC 2573

DB 3 TGACTTCTGCAGGAGTCC 20

RESULT 217

AAD56488/C

ID AAD56488 standard; DNA; 20 BP.

XX AC AAD56488;

XX 27-AUG-2003 (first entry)

XX Human ephrin-A2 cDNA amplifying RT-PCR primer, SEQ ID 11.

XX EphA7; ephrin-A5; ephrin-A2; borderline personality disorder; ischaemia;

KW epilepsy; trauma; infection; multiple sclerosis; autism; cerebral palsy;

KW Huntington's disease; Alzheimer's disease; schizophrenia; gene therapy;

KW memory disorder; Parkinson's disease; phobia; dementia; sleep disorder;

KW amyotrophic lateral sclerosis; attention deficit disorder; depression;

KW injury; human; RT; reverse transcription; PCR; primer; ss.

XX Homo sapiens.

OS WO2003040304-A2.

PN 15-MAY-2003.

PD 11-NOV-2002; 2002WO-IB004930.

PF C9-NOV-2001; 2001US-0345206P.

PR 02-JUL-2002; 2002US-0393272P.

XX (NEUR-) NEURONOVA AB.

PA Holmberg J, Frisen J;

PI WPI; 2003-441543/41.

DR

XX Alleviating a symptom of a disease or disorder of the nervous system by

PT administering a modulator of neural stem or neural progenitor cell

PT activity in vivo to a patient.

XX Example 6; Page 54; 93pp; English.

XX The invention relates to a method for alleviating a symptom of a disease

CC or disorder of nervous system which involves administering a modulator to

CC modulate an activity of a neural stem cell or a neural progenitor cell in

CC vivo to a patient suffering from the disease or disorder of the nervous

CC system (the modulator disrupts an interaction between EphA7 and ephrin-A5

CC or an interaction between EphA7 and ephrin-A2). The method is useful for

CC alleviating a symptom of a disease or disorder of the nervous system,

CC e.g., drug and alcohol abuse, neurological traumas, or neurodegenerative,

CC neural stem cell, neural progenitor, ischaemic, affective,

CC neuropsychiatric or learning and memory disorders, such as Parkinson's

CC disease, Huntington's disease, Alzheimer's disease, spinal ischaemia,

CC cancer-related brain/spinal cord injury, schizophrenia, psychoses,

CC depression, bipolar depression/disorder, anxiety syndromes/ disorders,

CC phobias, stress and related syndromes, cognitive function disorders,

CC aggression, obsessive compulsive behaviour syndromes, multi-infarct

CC dementia, seasonal mood disorder, Lewy body dementia, borderline

CC personality disorder, cerebral palsy, age related/geriatric dementia,

CC epilepsy and injury related to epilepsy, spinal cord injury, brain

CC injury, trauma related brain/spinal cord injury, anticancer treatment

CC related brain/spinal cord tissue injury, infection and inflammation
 CC related brain/spinal cord injury, environmental toxin related brain/
 CC spinal cord injury, multiple sclerosis, autism, attention deficit
 CC disorders, narcolepsy, retinal degenerative disorders, injury or trauma
 CC to the retina or sleep disorders. The invention is also used in gene
 CC therapy. The present sequence is a RT (reverse transcription)-PCR primer
 CC used for amplifying human ephrin-A2 cDNA. This sequence is used to
 CC illustrate the method of the invention
 XX
 SQ Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1407 AACAGCAGCAGCAGCAGC 1424
 DB 19 AACAGCAGGAGCAGCAGC 2
 RESULT 218
 AAD56486/C
 ID AAD56486 standard; DNA; 20 BP.
 AC AAD56486;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human ephrin-A2 cDNA amplifying RT-PCR primer, SEQ ID 9.
 XX
 KW EphA7; ephrin-A5; ephrin-A2; borderline personality disorder; ischaemia;
 KW epilepsy; trauma; infection; multiple sclerosis; autism; cerebral palsy;
 KW Huntington's disease; Alzheimer's disease; schizophrenia; gene therapy;
 KW memory disorder; Parkinson's disease; phobia; dementia; sleep disorder;
 KW amyotrophic lateral sclerosis; attention deficit disorder; depression;
 KW injury; human; RT; reverse transcription; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040304-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 11-NOV-2002; 2002WO-IB004930.
 XX
 PR 09-NOV-2001; 2001US-0345206P.
 PR 02-JUL-2002; 2002US-0393272P.
 XX
 PA (NEUR-) NEURNOVA AB.
 XX
 PI Holmberg J, Friese J;
 XX
 PI WPI; 2003-441543/41.
 DR
 XX
 PT Alleviating a symptom of a disease or disorder of the nervous system by
 PT administering a modulator of neural stem or neural progenitor cell
 PT activity in vivo to a patient.
 XX
 PS Example 6; Page 54; 93pp; English.
 XX
 CC The invention relates to a method for alleviating a symptom of a disease
 CC or disorder of nervous system which involves administering a modulator to
 CC modulate an activity of a neural stem cell or a neural progenitor cell in
 CC vivo to a patient suffering from the disease or disorder of the nervous
 CC system (the modulator disrupts an interaction between EphA7 and ephrin-A5
 CC or an interaction between EphA7 and ephrin-A2). The method is useful for
 CC alleviating a symptom of a disease or disorder of the nervous system,
 CC e.g., drug and alcohol abuse, neurological trauma, or neurodegenerative,
 CC neural stem cell, neural progenitor, ischaemic, affective,
 CC neuropsychiatric or learning and memory disorders, such as Parkinson's
 CC disease, Huntington's disease, Alzheimer's disease, spinal ischaemia,
 CC amyotrophic lateral sclerosis, ischaemic stroke, spinal cord injury or
 CC cancer-related brain/spinal cord injury, schizophrenia, psychoses,

CC depression, bipolar depression/disorder, anxiety syndromes/ disorders,
 CC phobias, stress and related syndromes, cognitive function disorders,
 CC aggression, obsessive compulsive behaviour syndromes, multi-infarct
 CC dementia, seasonal mood disorder, Lewy body dementia, borderline
 CC personality disorder, cerebral palsy, age related/geriatric dementia,
 CC epilepsy and injury related to epilepsy, spinal cord injury, brain
 CC injury, trauma related brain/spinal cord injury, anticancer treatment
 CC related brain/spinal cord tissue injury, infection and inflammation
 CC spinal cord injury, multiple sclerosis, autism, attention deficit
 CC disorders, narcolepsy, retinal degenerative disorders, injury or trauma
 CC to the retina or sleep disorders. The invention is also used in gene
 CC therapy. The present sequence is a RT (reverse transcription)-PCR primer
 CC used for amplifying human ephrin-A2 cDNA. This sequence is used to
 CC illustrate the method of the invention
 XX
 SQ Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1407 AACAGCAGCAGCAGCAGC 1424
 DB 19 AACAGCAGGAGCAGCAGC 2
 RESULT 219
 ADP75418
 ID ADP75418 standard; DNA; 20 BP.
 XX
 AC ADP75418;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human NRG2 gene exon 1 reverse sequencing primer #4.
 XX
 KW Human; ss; primer; ADAM19; Endophilin 1; Endophilin 2; NRG2; ADAMTS2;
 KW a disintegrin and metalloprotease; neuroregulin 2; SNP;
 KW single nucleotide polymorphism;
 KW a disintegrin and metalloprotease with thrombospondin type motif 2;
 KW asthma; atopy; obesity; inflammatory bowel disease; respiratory disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO2003031594-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032700.
 XX
 PR 11-OCT-2001; 2001US-0328424P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Keith T, Little RD, Van Eerdewegh P, Dupuis J, Del Mastro RG;
 PI Allen K;
 XX
 PI WPI; 2003-381712/36.
 DR
 XX
 PT New isolated nucleic acid or alternate splice variant, useful for
 PT diagnosing and treating a disintegrin and metalloprotease (ADAM) or
 PT interactor gene-associated disorder, e.g. asthma, atopy, obesity or
 PT inflammatory bowel disease.
 XX
 PS Claim 2; Page 129; 33pp; English.
 XX
 CC The invention relates to an isolated nucleic acid or alternate splice
 CC variant comprising a nucleotide sequence containing at least one of the
 CC single nucleotide polymorphisms given in the specification, a nucleotide
 CC sequence having at least 15 contiguous nucleotides of them, or
 CC complements of them. The genes are ADAM19 (a disintegrin and
 CC metalloprotease 19, also known as gene 845), NRG2 (neuroregulin 2, also

CC known as gene 847), endophilin 1 (also known as gene 874), endophilin 2
 CC (also known as gene 803) and ADAMTS2 (a disintegrin and metalloprotease
 CC with thrombospondin type1 motif 2, also known as gene 962). Also included
 CC are a vector comprising the isolated nucleic acid (or alternate splice
 CC variant), a host cell containing the vector, an isolated polypeptide
 CC encoded by the novel nucleic acid (or alternate splice variant), an
 CC antibody or antibody fragment that binds to the polypeptide,
 CC pharmaceutical compositions (comprising the nucleic acid or alternate
 CC splice variant, vector, polypeptide or antibody, and a carrier,
 CC excipient or diluent), a kit for detecting a disintegrin and
 CC metalloprotease (ADAM) gene nucleotide sequence (comprising the isolated
 CC nucleic acid or alternate splice variant, antibody or antibody fragment,
 CC and at least one component to detect the hybridisation of the variant or
 CC the binding of the antibody to an ADAM gene amino acid sequence), a kit
 CC for detecting an interactor gene amino acid sequence (comprising the
 CC antibody or antibody fragment, and at least one component to detect the
 CC binding of the antibody to the interactor gene amino acid sequence),
 CC diagnosing an ADAM or interactor gene-associated disorder or a
 CC respiratory disorder in a human subject, determining an ADAM or
 CC interactor gene pharmacogenetic profile in a human subject, identifying
 CC an orthologue of a human ADAM or interactor gene, treating an ADAM or
 CC interactor gene-associated disorder (or a respiratory disorder) by
 CC administering the pharmaceutical composition, a transgenic mouse (whose
 CC genome comprises an introduced null mutation in an endogenous gene that
 CC is orthologous to a human ADAM gene), making a homozygous transgenic
 CC knockout mouse, forming a crystal of the isolated polypeptide, a cell
 CC line comprising the isolated nucleic acid or alternate splice variant, a
 CC biochip comprising the isolated nucleic acid or alternate splice variant,
 CC an isolated nucleic acid probe or primer comprising at least 8 contiguous
 CC nucleotides of the nucleic acid, an isolated antisense nucleic acid,
 CC identifying an ADAM or interactor gene ligand and an isolated nucleic
 CC acid variant of Gene 803, 845, 847, 874 or 962. The nucleic acid or
 CC alternate splice variants, methods, kits and antibody/antibody fragment
 CC are useful for diagnosing and treating an ADAM or interactor gene-
 CC associated disorder, e.g. asthma, atopy, obesity or inflammatory bowel
 CC disease. The present sequence is a primer used to sequence the regions
 CC surrounding polymorphisms in the above genes.

XX Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 844 TTCAGTCCCTCAGAGCCA 861
 Db 1 TTCAGACCTCAGAGCCA 18

RESULT 220
 ADH65705/c
 ID ADH65705 standard; DNA; 20 BP.

XX AC ADH65705;

XX 25-MAR-2004 (first entry)

DE Human glucocorticoid receptor-specific antisense oligonucleotide #2539.

XX antisense oligonucleotide; glucocorticoid receptor; infection;
 KW inflammation; tumour formation; diabetes; obesity;
 KW cardiovascular disorder; hyperlipidaemia; Cushing's syndrome; human; ss;
 KW phosphorothioate backbone; 2'-methoxyethyl; 2'-MOE.

XX Homo sapiens.

XX WO2003099215-A2.

XX 04-DEC-2003.

XX 20-MAY-2003; 2003WO-US016084.

XX 20-MAY-2002; 2002US-0381857P.

XX (PHAA) PHARMACIA CORP.
 XX Crosby SD, Nalseth AE;
 XX WPI; 2004-035034/03.

XX New antisense compound targeted to a nucleic acid molecule encoding
 PT mammalian glucocorticoid receptor, useful for treating diabetes, obesity,
 PT cardiovascular disorder, hyperlipidemia or Cushing's syndrome.

XX Claim 4; SEQ ID NO 2539; 985pp; English.

XX The invention comprises an antisense oligonucleotides that are targeted
 CC to nucleic acids encoding a mammalian glucocorticoid receptor. The
 CC antisense oligonucleotides of the invention are useful for preventing or
 CC delaying infection, inflammation or tumour formation. The antisense
 CC oligonucleotides are also useful for treating diabetes, obesity. The
 CC cardiovascular disorders, hyperlipidaemia or Cushing's syndrome. The
 CC present DNA sequence represents an antisense oligonucleotide that targets
 CC the human glucocorticoid receptor gene. NOTE: The present sequence
 CC contains 2'-methoxyethyl (2'-MOE) wings and a phosphorothioate backbone.

XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 465 TGGATGGCCCAATGACCC 482
 Db 19 TGGATGACCAATGACCC 2

RESULT 221

ADN06173/c

ID ADN06173 standard; DNA; 20 BP.

XX AC ADN06173;

XX 17-JUN-2004 (first entry)

DE Human SPS2 specific antisense oligonucleotide, ISIS 138242.

XX Selenophosphate synthetase 2; SPS2; rheumatoid arthritis; infection;
 KW inflammation; tumour; antisense therapy; human; antisense;
 KW phosphorothioate backbone; ss.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 1..20

XX /*tag= b

XX /mod_base= OTHER

XX /note= "Phosphorothioate backbone in which all cytidines
 are 5-methylcytidines"

XX modified_base 1..5

XX /*tag= a

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl nucleotides"

XX modified_base 16..20

XX /*tag= c

XX /mod_base= OTHER

XX /note= "2'-methoxyethyl nucleotides"

XX US2004002151-A1.

XX 01-JAN-2004.

XX 28-JUN-2002; 2002US-00186157.

XX 28-JUN-2002; 2002US-00186157.

XX PA (ISIS-) ISIS PHARM INC.
 XX PI Watt AT, Freier SM;
 XX XX
 XX DR WPI; 2004-070740/07.
 XX XX
 XX PT New antisense oligonucleotides for modulating selenophosphate synthetase
 XX PT 2 (SPS2) expression, useful for diagnosing, preventing or treating
 XX PT conditions associated with SPS2, e.g. rheumatoid arthritis, inflammation
 XX PT or tumors.
 XX XX
 XX PS Example 15; SEQ ID NO 17; 47pp; English.
 XX XX
 XX CC The invention relates to antisense compounds, compositions and methods
 XX CC for modulating the expression of selenophosphate synthetase 2 (SPS2). The
 XX CC composition comprises antisense oligonucleotides targeted to SPS2 gene.
 XX CC The antisense oligonucleotide is useful for modulating the expression of
 XX CC SPS2 in cells or tissues to treat diseases associated with their
 XX CC expression, e.g. rheumatoid arthritis, infections, inflammation or
 XX CC tumours. It is also used for diagnostics, prophylaxis, or as research
 XX CC reagents or kits. The antisense oligonucleotide is useful in antisense
 XX CC therapy. The present sequence is an antisense oligonucleotide targeted to
 XX CC human SPS2 DNA. This sequence is used in the exemplification of the
 XX CC invention.
 XX CC
 XX SQ Sequence 20 BP; 4 A; 9 C; 6 G; 1 T; 0 U; 0 Other;
 XX
 XX Query Match 0.4%; Score 16.4; DB 1; Length 20;
 XX Best Local Similarity 94.4%; Pred. No. 1.7e+02;
 XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX QY 738 CGGCTTGACTCAGGCC 755
 XX DB 18 CGGCTTGACTCTGGCC 1
 XX
 XX RESULT 222
 XX ABL46975
 XX ID ABL46975 standard; RNA; 17 BP.
 XX AC ABL46975;
 XX XX
 XX DT 27-JUN-2003 (first entry)
 XX XX
 XX DE Human GRID zinzyme substrate oligonucleotide #59.
 XX XX
 XX KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 XX KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 XX KW leukaemia; cytostatic; ss.
 XX OS Homo sapiens.
 XX XX
 XX FN WO200162911-A2.
 XX XX
 XX PD 30-AUG-2001.
 XX XX
 XX PF 23-FEB-2001; 2001WO-US005957.
 XX XX
 XX PR 24-FEB-2000; 2000US-0184594P.
 XX XX
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (GLAX) GLAXO GROUP LTD.
 XX XX
 XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX DR WPI; 2001-550089/61.
 XX XX
 XX PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 XX PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 XX PT molecules such as hammerhead ribozymes.
 XX XX
 XX PS Claim 4; Page 72; 108pp; English.

XX CC The present invention relates to oligonucleotides that downregulate the
 XX CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 XX CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 XX CC for modulating the expression of GRID, to treat conditions such as
 XX CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 XX CC administered in conjunction with other therapies such as radiation,
 XX CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 XX CC used to illustrate the invention
 XX XX
 XX SQ Sequence 17 BP; 5 A; 7 C; 4 G; 0 T; 1 U; 0 Other;
 XX
 XX Query Match 0.4%; Score 16; DB 1; Length 17;
 XX Best Local Similarity 93.8%; Pred. No. 1.2e+02;
 XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 975 TGCAGCAGCAGCAGCA 990
 XX DB 2 UGCAGCAGCAGCAGCA 17
 XX
 XX RESULT 223
 XX ABZ81758
 XX ID ABZ81758 standard; DNA; 17 BP.
 XX AC ABZ81758;
 XX XX
 XX DT 11-JUN-2003 (first entry)
 XX XX
 XX DE Huntington's disease exon 1 triplet repeat sequence.
 XX XX
 XX KW Huntington's disease; nootropic; anticonvulsant; huntingtin; human;
 XX KW gene therapy; ss.
 XX OS Homo sapiens.
 XX XX
 XX FN WO2003013437-A2.
 XX XX
 XX PD 20-FEB-2003.
 XX XX
 XX PF 07-AUG-2002; 2002WO-US025352.
 XX XX
 XX PR 07-AUG-2001; 2001US-0310757P.
 XX PR 08-AUG-2001; 2001US-0310770P.
 XX PR 08-AUG-2001; 2001US-0310889P.
 XX PR 04-DEC-2001; 2001US-0337219P.
 XX XX
 XX PA (UYDE) UNIV DELAWARE.
 XX XX
 XX PI Kmiec EB, Parekh-Olmedo H;
 XX XX
 XX DR WPI; 2003-256478/25.
 XX XX
 XX PT New single stranded oligonucleotides comprising a DNA domain having at
 XX PT least one mismatch with respect to the genetic sequence of the
 XX PT Huntington's disease gene to be altered, useful for treating or
 XX PT preventing Huntington's disease.
 XX XX
 XX PS Example 2; Page 61; 133pp; English.
 XX XX
 XX CC The present sequence is an example of a poly-glutamine triplet repeat
 XX CC region found in exon 1 of the Huntington's disease (HD) gene. In an
 XX CC example from the invention, neuronal PC12 cells were engineered to
 XX CC include an HD gene exon 1 containing this sequence. These cells were used
 XX CC to demonstrate the ability of a single-stranded, phosphorothioate-
 XX CC modified oligonucleotide, HDA37/53 (see ABZ81736) having a mismatch with
 XX CC respect to the HD gene, to convert a CAG triplet to CTG in HD gene exon
 XX CC 1, and to reduce the formation of Huntington's protein (huntingtin)
 XX CC aggregates. HDA37/53 is an example of oligonucleotides of the invention
 XX CC that target sequence alterations to the triplet repeat region of the HD
 XX CC gene, and which can be used for the treatment or prevention of HD
 XX XX
 XX SQ Sequence 17 BP; 9 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

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Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1398 AACGACGACGACGACG 1413
Db 1 AACGACGACGACGACG 16

RESULT 224
ADC37824
ID ADC37824 standard; DNA; 17 BP.
XX AC ADC37824;
XX DT 18-DEC-2003 (first entry)
XX DE Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:173.
XX KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
XX KW AMLP1a; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003037931-A2.
XX PD 08-MAY-2003.
XX PF 01-NOV-2002; 2002WO-US035129.
XX PR 01-NOV-2001; 2001US-0334773P.
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX PI Shannon M, Phan T;
XX DR WPI; 2003-430501/40.
XX PT New isolated nucleic acid molecule encoding a human angiominotin-like
XX PT protein, useful for treating or preventing a disorder associated with
XX PT decreased or increased expression or activity of AMLP1.
XX PS Example 2; SEQ ID NO 173; 172pp; English.
XX CC The present invention describes the human angiominotin-like protein 1
XX CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
XX CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
XX CC compositions of the present invention can be used for treating or
XX CC preventing a disorder associated with decreased or increased expression
XX CC or activity of AMLP1. The present sequence represents a scanning
XX CC oligonucleotide for human AMLP1a, which is used in an example from the
XX CC present invention.
XX SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1402 GCAGCAACGACGACGACG 1417
Db 1 GCAGCAACGACGACGACG 16

RESULT 225
ADC37817
ID ADC37817 standard; DNA; 17 BP.
XX AC ADC37817;
XX DT 18-DEC-2003 (first entry)
```

```

XX DE Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:166.
XX KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
XX KW AMLP1a; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003037931-A2.
XX PD 08-MAY-2003.
XX PF 01-NOV-2002; 2002WO-US035129.
XX PR 01-NOV-2001; 2001US-0334773P.
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX PI Shannon M, Phan T;
XX DR WPI; 2003-430501/40.
XX PT New isolated nucleic acid molecule encoding a human angiominotin-like
XX PT protein, useful for treating or preventing a disorder associated with
XX PT decreased or increased expression or activity of AMLP1.
XX PS Example 2; SEQ ID NO 166; 172pp; English.
XX CC The present invention describes the human angiominotin-like protein 1
XX CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
XX CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
XX CC compositions of the present invention can be used for treating or
XX CC preventing a disorder associated with decreased or increased expression
XX CC or activity of AMLP1. The present sequence represents a scanning
XX CC oligonucleotide for human AMLP1a, which is used in an example from the
XX CC present invention.
XX SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1429 GCAGCAGCAGCAACAG 1444
Db 2 GCAGCAGCAGCAACAG 17

RESULT 226
ADM54298
ID ADM54298 standard; mRNA; 17 BP.
XX AC ADM54298;
XX DT 03-JUN-2004 (first entry)
XX DE Human GRID mRNA substrate sequence #608.
XX KW Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
XX KW NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNazyme; ambrzyme; Inozyme;
XX KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
XX OS Homo sapiens.
XX PN US2003134806-A1.
XX PD 17-JUL-2003.
XX PF 23-FEB-2001; 2001US-00792818.
XX PR 10-FEB-2000; 2000US-0181594P.
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PA (JARV/) JARVIS T.
 PA (CARL/) CARLOWITZ I V.
 PA (MCSW/) MCSWIGGEN J.
 PA (HAMB/) HAMBLIN P A.
 PA (ELLI/) ELLIS J H.
 XX
 XX Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
 PI
 XX WPI; 2003-829646/77.
 XX
 XX New nucleic acid molecule that down-regulates expression of Grb2-related
 PT with insert domain (GRID) gene, useful for treating a condition
 PT associated with the level of GRID, e.g. tissue/graft rejection and
 PT leukemia.
 XX
 XX Claim 4; SEQ ID NO 608; 74pp; English.
 PS
 XX The invention relates to a nucleic acid molecule that down-regulates
 CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
 CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNazyme,
 CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
 CC including the novel nucleic acid molecule, reducing GRID activity in a
 CC cell by contacting the cell with the novel nucleic acid molecule,
 CC treating a patient having a condition associated with the level of GRID
 CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
 CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
 CC contacting the cell with the novel nucleic acid molecule, an expression
 CC vector comprising a nucleic acid sequences (encoding at least the novel
 CC nucleic acid molecule in a manner that allows its expression), a
 CC mammalian cell including the expression vector and an enzymatic nucleic
 CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
 CC molecule is useful for treating a condition associated with the level of
 CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
 CC a target region for the enzymatic nucleic acids of the invention.
 XX
 XX Sequence 17 BP; 5 A; 7 C; 4 G; 0 T; 1 U; 0 Other;
 SQ
 Query Match 0.4%; Score 16; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 1.2e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 975 TGCAGCAGCACCAGCA 990
 Db :|||||||
 2 UGCAGCAGCACCAGCA 17
 RESULT 227
 ADS16441/C
 ID ADS16441 standard; DNA; 18 BP.
 AC
 AC ADS16441;
 XX
 XX 02-DEC-2004 (first entry)
 DT
 DE Allele A oligo #4, used in polynucleotide sequence detection.
 XX
 KW Single nucleotide polymorphism; SNP; genotyping; ss.
 XX
 OS Synthetic.
 XX
 XX US2004175704-A1.
 PN
 XX 09-SEP-2004.
 PD
 XX 12-MAY-2003; 2003US-00436231.
 PF
 XX 06-MAR-2003; 2003US-0452481P.
 PR
 XX (STRA-) STRATAGENE.
 PA
 XX Sorge JA, Firmin A;
 PI
 XX WPI; 2004-642120/62.
 DR
 XX
 XX Determining polynucleotide sequence differences by amplifying
 PT polynucleotide in presence of labeled nucleotide and detecting variation
 PT based on incorporation frequency of labeled nucleotide compared to known
 PT reference frequency.
 XX
 XX Disclosure; SEQ ID NO 5; 52pp; English.
 PS
 XX The invention relates to compositions, kits and methods for detecting
 CC polynucleotide sequence differences. The method involves amplifying the
 CC polynucleotide of interest in the presence of a labelled nucleotide and
 CC detecting variation based on incorporation frequency of labelled
 CC nucleotide compared to known reference frequency. The method is useful
 CC for determining a sequence difference such as a single nucleotide
 CC polymorphism (SNP) or a tandem repeat, between a region of interest in a
 CC polynucleotide and a reference sequence. It is useful for determining the
 CC presence of a mutation in a region of interest in a polynucleotide and is
 CC also useful for genotyping. The present sequence is an allelic
 CC oligonucleotide used in polynucleotide sequence detection.
 XX
 XX Sequence 18 BP; 0 A; 5 C; 8 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1409 CAGCAGCAGCAGCAGC 1424
 Db :|||||||
 18 CAGCAGCAGCAGCAGC 3
 RESULT 228
 ADS16440
 ID ADS16440 standard; DNA; 18 BP.
 AC
 AC ADS16440;
 XX
 XX 02-DEC-2004 (first entry)
 DT
 XX Allele A oligo #3, used in polynucleotide sequence detection.
 DE
 XX Single nucleotide polymorphism; SNP; genotyping; ss.
 KW
 OS Synthetic.
 XX
 XX US2004175704-A1.
 PN
 XX 09-SEP-2004.
 PD
 XX 12-MAY-2003; 2003US-00436231.
 PF
 XX 06-MAR-2003; 2003US-0452481P.
 PR
 XX (STRA-) STRATAGENE.
 PA
 XX Sorge JA, Firmin A;
 PI
 XX WPI; 2004-642120/62.
 DR
 XX
 XX Determining polynucleotide sequence differences by amplifying
 PT polynucleotide in presence of labeled nucleotide and detecting variation
 PT based on incorporation frequency of labeled nucleotide compared to known
 PT reference frequency.
 XX
 XX Disclosure; SEQ ID NO 6; 52pp; English.
 PS
 XX The invention relates to compositions, kits and methods for detecting
 CC polynucleotide sequence differences. The method involves amplifying the
 CC polynucleotide of interest in the presence of a labelled nucleotide and
 CC detecting variation based on incorporation frequency of labelled
 CC nucleotide compared to known reference frequency. The method is useful
 CC for determining a sequence difference such as a single nucleotide
 CC polymorphism (SNP) or a tandem repeat, between a region of interest in a
 CC polynucleotide and a reference sequence. It is useful for determining the
 CC presence of a mutation in a region of interest in a polynucleotide and is
 CC also useful for genotyping. The present sequence is an allelic
 CC oligonucleotide used in polynucleotide sequence detection.
 XX
 XX Sequence 18 BP; 0 A; 5 C; 8 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1409 CAGCAGCAGCAGCAGC 1424
 Db :|||||||
 18 CAGCAGCAGCAGCAGC 3

CC polynucleotide and a reference sequence. It is useful for determining the
CC presence of a mutation in a region of interest in a polynucleotide and is
CC also useful for genotyping. The present sequence is an allelic
CC oligonucleotide used in polynucleotide sequence detection.

XX
SQ Sequence 18 BP; 5 A; 8 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGC 1424
|||||
Db 1 CAGCAGCAGCAGCAGC 16

RESULT 229

AAH57033/C
ID AAH57033 standard; DNA; 20 BP.

XX
AC AAH57033;

DT 10-SEP-2001 (first entry)

XX Human oestrogen receptor alpha search PCR primer 58.

XX Ligand dependent transcriptional factor; oestrogen receptor; ER;
KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
KW MR; peroxisome proliferator-activated receptor protein; PPAR;
KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;
KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
KW transactivation; ERalpha; breast cancer; PCR primer; probe; ss.

XX Homo sapiens.

OS
XX WO200142307-A1.

XX
XX 14-JUN-2001.

XX
XX 01-DEC-2000; 2000WO-JP008553.

XX
XX 07-DEC-1999; 99JP-00348022.

XX
XX 27-DEC-1999; 99JP-00370667.

XX
XX 07-JUL-2000; 2000JP-00207011.

XX
XX 21-JUL-2000; 2000JP-00320508.

XX
XX 02-AUG-2000; 2000JP-00234053.

XX
XX 03-AUG-2000; 2000JP-00235460.

XX
XX 03-AUG-2000; 2000JP-00235461.

XX
XX 03-AUG-2000; 2000JP-00235463.

XX
XX (SUMO) SUMITOMO CHEM CO LTD.

XX
XX Saito K, Ohe N, Satoh H;

XX
XX WPI; 2001-367866/38.

XX
XX Example 9; Page 226; 276pp; English.

XX The present invention relates to ligand dependent transcriptional factors
CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
CC receptor protein (GR), mineralocorticoid receptor protein (MR),
CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic
CC acids encoding them and cells comprising them and a specified reporter
CC gene for the ligand dependent transcriptional factor. These proteins are
CC useful in the modulation of ligand dependent transcriptional factor
CC activity. The cells, mutant ERalpha and the polynucleotide encoding it
CC may be used in assays for qualitatively analysing an activity for

CC transactivation of a reporter gene by a test ERalpha, for screening
CC mutant ligand dependent transcriptional factors, for evaluating an
CC activity for transactivation of a reporter gene by a test ERalpha and/or
CC for screening a compound useful for treating a disorder of a mutant
CC ERalpha, especially breast cancer

XX
SQ Sequence 20 BP; 1 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 986 CAGCAGCAGCAGCAGC 1001
|||||
Db 18 CAGCAGCAGCAGCAGC 3

RESULT 230

ABS73433/C

ID ABS73433 standard; DNA; 20 BP.

XX
AC ABS73433;

XX
DT 03-DEC-2002 (first entry)

XX Chimeric phosphorotioate oligonucleotide #14.

XX Human; glioma-associated oncogene-2; antisense compound; infection;
KW inflammation; tumour formation; antiinflammatory; antitumour;
KW inhibitor of human glioma-associated oncogene-2 expression;
KW antisense gene therapy; phosphorothioate; ss.

XX Homo sapiens.

OS
XX Synthetic.

OS
XX Chimeric.

XX
XX US6440739-B1.

XX
XX 27-AUG-2002.

XX
XX 17-JUL-2001; 2001US-00907843.

XX
XX 17-JUL-2001; 2001US-00907843.

XX
XX (ISIS-) ISIS PHARM INC.

XX
XX Bennett CF, Freier SM;

XX
XX WPI; 2002-697096/75.

XX
XX Novel antisense compound that hybridizes and inhibits nucleic acid
XX encoding human glioma-associated oncogene-2, useful for treatment of
XX diseases associated with human glioma-associated oncogene-2.

XX
XX Example 15; Col 45; 43pp; English.

XX The present invention relates to a new antisense compound targeted to
CC human glioma-associated oncogene-2. The invention is useful for
CC inhibiting the expression of human glioma-associated oncogene-2 in cells
CC or tissues. The invention is also useful for treatment of diseases
CC associated with human glioma-associated oncogene-2. The invention is
CC further useful for diagnostics, therapeutics, prophylaxis, as research
CC reagents and kits, for distinguishing functions of various members of a
CC biological pathway, and in antisense gene therapy. The invention is also
CC useful prophylactically, e.g. to prevent or delay infection,
CC inflammation or tumour formation. The present nucleic acid sequence
CC represents an oligonucleotide that was used in the methods of the
CC invention to inhibit human glioma-associated oncogene-2

XX
SQ Sequence 20 BP; 2 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1427 CAGCAGCAGCAGCAAC 1442
 Db 17 CAGCAGCAGCAGCAAC 2
 |||||

RESULT 231
 AAH82617/c
 ID AAH82617 standard; DNA; 19 BP.
 AC AAA82617;
 XX
 XX 04-DEC-2000 (first entry)
 DT
 XX cdk2 ribozyme binding site #54.
 DE
 XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; reestenosis; ss.
 XX
 XX Mammalia.
 OS
 XX WO200032765-A2.
 PN
 XX 08-JUN-2000.
 PD
 XX 06-DEC-1999; 99WO-US028772.
 PF
 XX 04-DEC-1998; 98US-0110954P.
 PR
 XX (IMMU-) IMMUSOL INC.
 PA
 XX Tritz R, Welch PJ, Barber JR, Robbins JM;
 PI
 XX WPI; 2000-412314/35.
 DR
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 PT
 XX Disclosure; Page 49; 109pp; English.
 PS
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 CC
 XX Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAACAGATAGC 948
 Db 19 AGCAGCTGGAACAGATAGC 1
 |||||

RESULT 232
 AAH57779/c
 ID AAH57779 standard; DNA; 19 BP.
 AC AAH57779;
 XX
 XX 10-SEP-2001 (first entry)
 DT
 XX Cell-cycle dependent kinase cdk2 ribozyme binding site SEQ ID NO:203.
 DE
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 XX recognition site; target; ribozyme binding site; eye disease; vulnery;

KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 XX WO200130362-A2.
 PN
 XX 03-MAY-2001.
 PD
 XX 26-OCT-2000; 2000WO-US029500.
 PF
 XX 26-OCT-1999; 99US-0161532P.
 PR
 XX (IMMU-) IMMUSOL INC.
 PA
 XX Robbins JM, Tritz R;
 PI
 XX WPI; 2001-300427/31.
 DR
 XX Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 PT
 XX Example 1; Page 86; 408pp; English.
 PS
 XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
 CC ophthalmological, vulnery, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 CC
 XX Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAACAGATAGC 948
 Db 19 AGCAGCTGGAACAGATAGC 1
 |||||

RESULT 233
 ADQ62508
 ID ADQ62508 standard; RNA; 19 BP.
 XX
 XX ADQ62508;
 AC
 XX
 XX 09-SEP-2004 (first entry)
 DT
 XX Anti-TOP2A siRNA SEQ ID NO:2211.
 DE
 XX


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XX PD 29-OCT-2002.
XX PF 31-DEC-1999; 99US-00475947.
XX PR 31-DEC-1999; 99US-00475947.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX DR WPI; 2003-208818/20.
XX PT Identifying a candidate polymorphic repeat within a coding sequence, for
XX PT understanding or treating genetic disease, comprises detecting tandem
XX PT repeats in a target coding sequence and scoring the repeats for
XX PT polymorphic probability.
XX PS Example; Col 1089; 588pp; English.
XX CC The invention discloses a method for identifying a candidate polymorphic
XX CC repeat within a coding sequence (expressed sequence tag, EST), which
XX CC comprises detecting tandem repeats in a target coding sequence, scoring
XX CC the repeats for polymorphic probability and generating a dataset
XX CC correlating the repeats with polymorphic probability to identify a
XX CC candidate polymorphic repeat. The computational methods (polymorphic
XX CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
XX CC useful for identifying and detecting candidate polymorphic repeats in
XX CC human genes, which can be used to understand, treat or eliminate genetic
XX CC diseases, predispositions or adverse drug-treatment reactions. Examples
XX CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
XX CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
XX CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
XX CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
XX CC the polymorphic repeats identified for a search of human ESTs
XX SQ Sequence 33 BP; 11 A; 10 C; 11 G; 1 T; 0 U; 0 Other;
    Query Match 0.4%; Score 15.6; DB 1; Length 33;
    Best Local Similarity 70.0%; Pred. No. 5, 2e+02;
    Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Oy 1925 CAGCAACTTCTTCTCCAGCAGATGCTG 1954
    ||||| ||||| ||||| |||||
Db 30 CTGCTACTGCTGCTGCTGCTGCTGCTG 1

RESULT 236
AAAX72851/c
XX ID AAX72851 standard; RNA; 17 BP.
XX AC AAX72851;
XX DT 28-JUL-1999 (first entry)
XX DE Mouse flk-1 VEGF receptor hammerhead ribozyme substrate #284.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX OS Mus sp.
XX PN WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.

XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX XX WPI; 1997-259017/23.
XX DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 131; 218pp; English.
XX CC The present invention describes nucleic acid molecules which modulate the
XX CC synthesis, expression and/or stability of a mRNA encoding 1 or more
XX CC receptors of vascular endothelial growth factor (VEGF). A patient
XX CC (preferably human) having a condition associated with the level of the
XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX CC treated by administering the nucleic acid molecule or the expression
XX CC vector to the patient. AAX67275 to AAX75752 represent specific examples
XX CC of nucleic acid molecules from the present invention
XX SQ Sequence 17 BP; 4 A; 5 C; 5 G; 0 T; 3 U; 0 Other;
    Query Match 0.4%; Score 15.4; DB 1; Length 17;
    Best Local Similarity 94.1%; Pred. No. 1, 5e+02;
    Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 326 TTGCCTATGAGCCCAAGC 342
    ||||| ||||| |||||
Db 17 TTGCTGTGAGCCAAGC 1

RESULT 237
AAV97395
XX ID AAV97395 standard; RNA; 17 BP.
XX AC AAV97395;
XX DT 17-MAR-1999 (first entry)
XX DE Human EGF-R target sequence nucleotide position 1455.
XX KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
XX KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
XX KW cancer; genetic drift; detection; mutation; ss.
XX OS Homo sapiens.
XX PN WO9833893-A2.
XX PD 06-AUG-1998.
XX PF 14-JAN-1998; 98WO-US000730.
XX PR 31-JAN-1997; 97US-0036476P.
XX PR 04-DEC-1997; 97US-00985162.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (UYAS-) UNIV ASTON.
XX PI Akhtar S, Fell P, Mcswiggen JA;
XX XX WPI; 1998-437449/37.
XX PT Enzymatic nucleic acids - which cleave RNA derived from an epidermal
XX PT growth factor receptor, useful for inhibiting cell proliferation and for
XX PT treating cancers.
XX PS Claim 5; Page 71; 109pp; English.

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XX The present invention describes enzymatic nucleic acid molecules (NAMs)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMs can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell
 XX
 SQ Sequence 17 BP; 8 A; 3 C; 3 G; 0 T; 3 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1.5e+02;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3633 GAGAACCTAGAAAACAT 3649
 |||||:|||||:
 Db 1 GAGACCUGAAAUCAU 17
 RESULT 238
 ABL46976
 ID ABL46976 standard; RNA; 17 BP.
 XX
 AC ABL46976;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID zinzyme substrate oligonucleotide #60.
 XX
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX
 OS New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 XX (GRID) gene comprises using antiseense and enzymatic nucleic acid
 PN molecules such as hammerhead ribozymes.
 XX
 PD Claim 4; Page 72; 108pp; English.
 XX
 PF The present invention relates to oligonucleotides that downregulate the
 XX expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 XX a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 XX for modulating the expression of GRID, to treat conditions such as
 XX tissue/graft rejection and leukaemia. The oligonucleotides can also be
 XX administered in conjunction with other therapies such as radiation,
 XX chemotherapy and cyclosporin treatment. The present oligonucleotide was
 XX used to illustrate the invention
 XX
 SQ Sequence 17 BP; 5 A; 9 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1.5e+02;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3633 GAGAACCTAGAAAACAT 3649
 |||||:|||||:
 Db 1 GAGACCUGAAAUCAU 17
 RESULT 238
 ABL46976
 ID ABL46976 standard; RNA; 17 BP.
 XX
 AC ABL46976;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID zinzyme substrate oligonucleotide #60.
 XX
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX
 OS New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 XX (GRID) gene comprises using antiseense and enzymatic nucleic acid
 PN molecules such as hammerhead ribozymes.
 XX
 PD Claim 4; Page 72; 108pp; English.
 XX
 PF The present invention relates to oligonucleotides that downregulate the
 XX expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 XX a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 XX for modulating the expression of GRID, to treat conditions such as
 XX tissue/graft rejection and leukaemia. The oligonucleotides can also be
 XX administered in conjunction with other therapies such as radiation,
 XX chemotherapy and cyclosporin treatment. The present oligonucleotide was
 XX used to illustrate the invention
 XX
 SQ Sequence 17 BP; 5 A; 9 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 1.5e+02;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 94.1%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 986 CAGCAGCAGCAGCCAGCC 1002
 |||||:|||||:
 Db 1 CAGCACCAGCAGCCAGCC 17
 RESULT 239
 ABL46729
 ID ABL46729 standard; RNA; 17 BP.
 XX
 AC ABL46729;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID NCH ribozyme substrate oligonucleotide #183.
 XX
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX
 OS New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 XX (GRID) gene comprises using antiseense and enzymatic nucleic acid
 PN molecules such as hammerhead ribozymes.
 XX
 PD Claim 4; Page 66; 108pp; English.
 XX
 PF The present invention relates to oligonucleotides that downregulate the
 XX expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 XX a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 XX for modulating the expression of GRID, to treat conditions such as
 XX tissue/graft rejection and leukaemia. The oligonucleotides can also be
 XX administered in conjunction with other therapies such as radiation,
 XX chemotherapy and cyclosporin treatment. The present oligonucleotide was
 XX used to illustrate the invention
 XX
 SQ Sequence 17 BP; 6 A; 7 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 978 AGCAGCAGCAGCAGCCAG 994
 |||||:|||||:
 Db 1 AGCAGCAGCAGCAGCCAG 17
 RESULT 240
 ABL46727
 ID ABL46727 standard; RNA; 17 BP.
 XX
 AC ABL46727;
 XX
 DT 27-JUN-2003 (first entry)
 XX

DE Human GRID NCH ribozyme substrate oligonucleotide #181.
 XX Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytosstatic; ss.
 XX Homo sapiens.
 XX WO200162911-A2.
 XX 30-AUG-2001.
 XX 23-FEB-2001; 2001WO-US005957.
 XX 24-FEB-2000; 2000US-0184594P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX Claim 4; Page 66; 108pp; English.
 XX The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;
 SQ
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 985 CCAGCAGCAGCAGCAGC 1001
 DB 1 CCUGCAGCAGCAGCAGC 17
 RESULT 241
 ABL46728
 ID ABL46728 standard; RNA; 17 BP.
 XX ABL46728;
 AC ABL46728;
 XX 27-JUN-2003 (first entry)
 DT Human GRID NCH ribozyme substrate oligonucleotide #182.
 DE Human; Grb2-related with Insert Domain; GRID; T-cell;
 XX co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytosstatic; ss.
 XX Homo sapiens.
 XX WO200162911-A2.
 XX 30-AUG-2001.
 XX 23-FEB-2001; 2001WO-US005957.
 XX 24-FEB-2000; 2000US-0184594P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX Claim 4; Page 66; 108pp; English.
 XX The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;
 SQ
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 985 CCAGCAGCAGCAGCAGC 1001
 DB 1 CCUGCAGCAGCAGCAGC 17
 RESULT 241
 ABL46728
 ID ABL46728 standard; RNA; 17 BP.
 XX ABL46728;
 AC ABL46728;
 XX 27-JUN-2003 (first entry)
 DT Human GRID NCH ribozyme substrate oligonucleotide #182.
 DE Human; Grb2-related with Insert Domain; GRID; T-cell;
 XX co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytosstatic; ss.
 XX Homo sapiens.
 XX WO200162911-A2.
 XX 30-AUG-2001.
 XX 23-FEB-2001; 2001WO-US005957.
 XX 24-FEB-2000; 2000US-0184594P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX Claim 4; Page 66; 108pp; English.
 XX The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 0 U; 0 Other;
 SQ

PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX Claim 4; Page 66; 108pp; English.
 XX The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX Sequence 17 BP; 5 A; 8 C; 4 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 1.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 976 GCAGCAGCAGCAGCAGC 992
 DB 1 GCAGCAGCAGCAGCAGC 17
 RESULT 242
 ABL46730
 ID ABL46730 standard; RNA; 17 BP.
 XX ABL46730;
 AC ABL46730;
 XX 27-JUN-2003 (first entry)
 DT Human GRID NCH ribozyme substrate oligonucleotide #184.
 DE Human; Grb2-related with Insert Domain; GRID; T-cell;
 XX co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytosstatic; ss.
 XX Homo sapiens.
 XX WO200162911-A2.
 XX 30-AUG-2001.
 XX 23-FEB-2001; 2001WO-US005957.
 XX 24-FEB-2000; 2000US-0184594P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX Claim 4; Page 66; 108pp; English.
 XX The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX Sequence 17 BP; 5 A; 8 C; 4 G; 0 T; 0 U; 0 Other;
 SQ

CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention

XX
SQ Sequence 17 BP; 5 A; 8 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 979 GCAGCACCAGCAGCAGC 995
|||||
Db 1 GCAGCACCAGCAGCAGC 17

RESULT 243
ABT38591
ID ABT38591 standard; DNA; 17 BP.
XX
AC ABT38591;
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID No 4228.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
OS Homo sapiens.
XX
PN WO2003025175-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004208.
XX
PR 17-SEP-2001; 2001PR-00011978.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 528; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein

CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 7 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1909 GATCATGAGCAGCAAC 1925
|||||
Db 1 GATCATGTAGCAGCAAC 17

RESULT 244
ACC67653/C
ID ACC67653 standard; DNA; 17 BP.
XX
AC ACC67653;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4900.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001PR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-333167/31.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 603; 738pp; French.
XX
XX The present invention relates to murine oligonucleotides (ACC62754-
XX ACC68806), which are associated with tumour suppression, tumour
XX reversion, apoptosis and virus resistance. The oligonucleotides are
XX useful as (1) as probes and primers for detecting, identifying,
XX quantifying and/or amplifying nucleic acid, e.g. as one component of a
XX gene chip; in vitro as (anti)sense reagents; and (2) for production of
XX recombinant polypeptides. The oligonucleotides are useful for preparation
XX of pharmaceuticals for prevention and/or treatment of viral diseases that
XX are characterised by development of tumours or cell degeneration,
XX specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 4 A; 4 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 705 TGGAGAAATAGTGATC 721
|||||
Db 17 TAGAGAAATAGTGATC 1

```

RESULT 245
ADB40670/c
ID ADB40670 standard; DNA; 17 BP.
XX
XX
AC ADB40670;
XX
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX
DE Tumour suppression/reversion associated nucleotide #993.
XX
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003040369-A2.
XX
XX
PD 15-MAY-2003.
XX
XX
PP 17-SEP-2002; 2002WO-IB004219.
XX
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX
PI Telerman A, Anson R, Tuijnder M;
XX
XX
DR WPI; 2003-441574/41.
XX
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX
PS Disclosure; Page 148; 771pp; French.
XX
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 8% identity, after optimal alignment, with the
CC the nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX
SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1222 GCAAAAGCCTCAGGATC 1238
Db 17 GCCAAAGCCTCAGGATC 1
RESULT 246
ADC37825
ID ADC37825 standard; DNA; 17 BP.
XX
XX
AC ADC37825;
XX
XX
DT 18-DEC-2003 (first entry)
XX
XX
DE Human AMLPla scanning 17-mer oligonucleotide SEQ ID NO:174.
XX
XX
KW human; angiotomatin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLPla; ss.
XX
XX
OS Synthetic.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003037931-A2.
XX
XX
PD 08-MAY-2003.
XX
XX
PP 01-NOV-2002; 2002WO-US035129.
XX
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX
PI Shannon M, Phan T;
XX
XX
DR WPI; 2003-430501/40.
XX
XX
PT New isolated nucleic acid molecule encoding a human angiotomatin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
XX
XX
PS Example 2; SEQ ID NO 174; 172pp; English.
XX
XX
CC The present invention describes the human angiotomatin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLPla, which is used in an example from the
CC present invention.
XX
XX
SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1505 CAGCAACAGCAGCAGAG 1521
Db 1 CAGCAACAGCAGCAGAG 17
RESULT 247
ADB44769
ID ADB44769 standard; DNA; 17 BP.
XX
XX
AC ADB44769;
XX
XX
DT 18-DEC-2003 (first entry)
XX
XX
DE Tumour suppression/reversion associated nucleotide #5092.
XX
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003040369-A2.
XX

```


PA (MCSW//) MCSWIGGEN J.
PA (HAMB//) HAMBLIN P A.
PA (ELLI//) ELLIS J H.
XX
PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
XX
XX WPI; 2003-829646/77.
XX
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX
PS Claim 4; SEQ ID NO 360; 74pp; English.
XX
XX The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyne, DNazyme,
CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule,
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequences (encoding at least the novel
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX
SQ Sequence 17 BP; 4 A; 8 C; 4 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 985 CCAGCAGCAGCAGCAGC 1001
DB 1 CCUGCAGCAGCAGCAGC 17

RESULT 250
ADM54086
ID ADM54086 standard; mRNA; 17 BP.
XX
AC ADM54086;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human GRID mRNA substrate sequence #361.
XX
XX Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
KW NCH ribozyme; G-cleaver ribozyme; Zinzyne; DNazyme; amberzyme; Inozyme;
KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
XX
OS Homo sapiens.
XX
PN US2003134806-A1.
XX
PD 17-JUL-2003.
XX
PF 23-FEB-2001; 2001US-00792818.
XX
PR 10-FEB-2000; 2000US-0181594P.
XX
PA (JARV//) JARVIS T.
PA (CARL//) CARLOWITZ I V.
PA (MCSW//) MCSWIGGEN J.
PA (HAMB//) HAMBLIN P A.
PA (ELLI//) ELLIS J H.
XX
PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
XX

XX Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
PI WPI; 2003-829646/77.
XX
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX
PS Claim 4; SEQ ID NO 361; 74pp; English.
XX
XX The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyne, DNazyme,
CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule,
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequences (encoding at least the novel
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX
SQ Sequence 17 BP; 5 A; 8 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 976 GCAGCAGCAGCAGCAGC 992
DB 1 GCAGCAGCAGCAGCAGC 17

RESULT 251
ADM54299
ID ADM54299 standard; mRNA; 17 BP.
XX
AC ADM54299;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human GRID mRNA substrate sequence #609.
XX
XX Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
KW NCH ribozyme; G-cleaver ribozyme; Zinzyne; DNazyme; amberzyme; Inozyme;
KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
XX
OS Homo sapiens.
XX
PN US2003134806-A1.
XX
PD 17-JUL-2003.
XX
PF 23-FEB-2001; 2001US-00792818.
XX
PR 10-FEB-2000; 2000US-0181594P.
XX
PA (JARV//) JARVIS T.
PA (CARL//) CARLOWITZ I V.
PA (MCSW//) MCSWIGGEN J.
PA (HAMB//) HAMBLIN P A.
PA (ELLI//) ELLIS J H.
XX
PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
XX

DR WPI; 2003-829646/77.
XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.
XX
XX Claim 4; SEQ ID NO 609; 74pp; English.
XX
XX The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNazyme,
CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule, and
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequence (encoding at least the novel
CC nucleic acid molecule in a manner that allows its expression), a
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX
XX Sequence 17 BP; 5 A; 9 C; 3 G; 0 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 986 CAGCAGCAGCAGCC 1002
DB 1 CAGCAGCAGCAGCC 17

RESULT 252
AAQ91051/C
ID AAQ91051 standard; DNA; 18 BP.
XX
XX AAQ91051;
AC
XX 30-JAN-1996 (first entry)
DT
XX HHV-6 associated MS genetic marker 38E external primer 38E8.
DE
XX Human herpes virus-6; HHV-6; multiple sclerosis; genetic marker; 38E;
KW external primer 38E8; diagnosis; ss.
KW
XX Synthetic.
OS
XX WO9512313-A1.
PN
XX 11-MAY-1995.
PD
XX 04-NOV-1994; 94WO-US012655.
PF
XX 05-NOV-1993; 93US-00149176.
PR 24-MAR-1994; 94US-00218029.
PR 05-AUG-1994; 94US-00287942.
PR 04-NOV-1994; 94US-00334482.
XX
XX (PATH-) PATHOGENESIS CORP.
PA
XX Burmer GC, Challoner PB, Smith KT, Brown JP, Parker JD;
PI Nowinski RC;
PI
XX WPI; 1995-215032/28.
DR
XX Treatment of human herpes-virus-6-associated multiple sclerosis - using
PT an antiviral agent, e.g. a nucleoside analogue, administered to the

PT cerebrospinal fluid.
XX
XX Disclosure; Page 35; 116pp; English.
XX
CC AAQ91050 and AAQ91051 are an external primer pair for the human herpes
CC virus-6 (HHV-6) associated multiple sclerosis (MS) genetic marker, 38E
CC (AAQ91054). The primers can be used in the diagnosis of MS
XX
XX Sequence 18 BP; 3 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1972 TGCTCCCAAGATCAGA 1988
DB 17 TGCTCCCAAGATCAGA 1

RESULT 253
AAV94830
ID AAV94830 standard; RNA; 18 BP.
XX
XX AAV94830;
AC
XX 24-FEB-1999 (first entry)
DT
XX Human IL-2 receptor g-chain substrate position 256.
DE
XX
KW Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
KW autoimmune disease; psoriasis; allergy; inflammatory disease;
KW graft rejection; ss.
XX
XX Homo sapiens.
OS
XX WO9824913-A2.
PN
XX 1-JUN-1998.
PD
XX 02-DEC-1997; 97WO-US021748.
PF
XX 03-DEC-1996; 96US-00758306.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Stinchcomb DT, Mcswiggen JA;
PI
XX WPI; 1998-333332/29.
DR
XX Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer,
PT autoimmune disease and allergies.
PT
XX Claim 4; Page 38; 61pp; English.
XX
XX The present sequence invention describes ribozymes targeted to modulate
CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.
CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and
CC AAV94575 to AAV95260 represent specifically claimed substrate sequences
CC from the present invention. The ribozymes can be used for the treatment
CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy
CC and other inflammatory conditions. The ribozymes are also used to induce
CC tolerance in a recipient to alloantigen from a donor
XX
XX Sequence 18 BP; 5 A; 10 C; 2 G; 0 T; 1 U; 0 Other;
SQ

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 993 AGCACCAGCCTACCAAC 1009
DB 1 AGCCCCAGCCUACCAAC 17

RESULT 254
 ID AAA10553 standard; DNA; 18 BP.
 XX
 AC AAA10553;
 XX
 DT 29-JUN-2000 (first entry)
 XX
 DE Smad2 antisense oligonucleotide sequence #6 (ISIS# 27783).
 XX
 KW Smad2; MADH2; MADR2; JVI8-1; transcription factor; inflammation;
 KW chromosome 18q21; antisense compound; treat; prevent; infection; tumour;
 KW diagnostic reagent; research reagent; ss; cancer.
 XX
 OS Synthetic.
 XX
 PN US6037142-A.
 XX
 PD 14-MAR-2000.
 XX
 PF 23-FEB-1999; 99US-00255912.
 XX
 PR 23-FEB-1999; 99US-00255912.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Cowbert LM;
 XX
 DR WPI; 2000-269886/23.
 XX
 KW New antisense compound that inhibits human Smad2, useful e.g. for
 PT treating or preventing infection, inflammation and tumors.
 XX
 PS Claim 11; Col 39; 31pp; English.
 XX
 CC This sequence represents an antisense nucleotide sequence targeting human
 CC Smad2. Smad2 is also known as MADH2, MADR2, hMAD2 and JVI8-1, and is a
 CC member of a subgroup of Smad family transcription factors which are
 CC cytosolic proteins regulated by transforming growth factor-beta (TGF-
 CC beta) and actinins. Smads exist as monomers in unstimulated cells as homo
 CC - or heterodimerise and translocate to the nucleus and activate target
 CC gene transcription upon ligand binding. The Smad2 gene is located on
 CC chromosome 18q21. The invention relates to antisense compounds (see
 CC AAA10548-A10587) targeted to the Smad2 nucleotide sequence. The antisense
 CC oligonucleotide sequences inhibit Smad2 expression by hybridising to DNA
 CC or RNA. The antisense nucleotides are used to treat or prevent diseases
 CC associated with expression of Smad2, e.g. infection, inflammation and
 CC tumours. The oligonucleotides can also be used as diagnostic or research
 CC reagents
 XX
 SQ Sequence 18 BP; 0 A; 11 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 73 GAAGCAGCGGAGGAGA 89
 Db 18 GGAGCAGCGGAGGAGA 2
 RESULT 255
 ID AAS07309 standard; DNA; 18 BP.
 XX
 AC AAS07309;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE CPS1/TES1 genomic DNA sequencing primer FP11.
 XX

KW CPS1; peptide synthetase; peptide toxin; fungal pathogen;
 KW corn crop infection; ss; sequencing primer; FP11.
 XX
 OS Cochliobolus heterostrophus.
 XX
 PN WO200138489-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032227.
 XX
 PR 23-NOV-1999; 99US-00448215.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Yoder OC, Turgeon BC, Lu S;
 XX
 DR WPI; 2001-367672/38.
 XX
 KW New isolated nucleic acid molecule from a plant pathogen useful in
 PT preventing plant pathogenic infections.
 XX
 PS Example 1; Page 54; 132pp; English.
 XX
 CC The sequence represents a sequencing primer used to sequence a genomic
 CC clone from Cochliobolus heterostrophus which contains the CPS1 and TES1
 CC peptide synthetase genes. CPS1 is an enzyme thought to be involved in the
 CC production of peptide toxins, which are involved in the pathogenic
 CC infection of corn crops. The nucleic acids and proteins can be used as
 CC targets for anti-fungal compounds to prevent fungal corn infection and
 CC the nucleic acids can be used in gene therapy to alter the biosynthetic
 CC pathway for the peptide toxins to lower the pathogenicity of the fungi
 XX
 SQ Sequence 18 BP; 0 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 978 AGCAGCACCAGCAGCAG 994
 Db 18 AGAGCAGCACCAGCAGCAG 2
 RESULT 256
 ABL40838
 ID ABL40838 standard; DNA; 18 BP.
 XX
 AC ABL40838;
 XX
 DT 03-JUL-2002 (first entry)
 XX
 DE P. putida exbB and exbD genes amplifying RT-PCR primer.
 XX
 KW exbB; exbD; tonB; antibiotic; toluene; PHBA; aromatic compound; parabene;
 KW para-hydroxybenzoic acid; RT-PCR; primer; ss.
 XX
 OS Pseudomonas putida.
 XX
 PN WO200229034-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 28-SEP-2001; 2001WO-US031180.
 XX
 PR 30-SEP-2000; 2000US-0236879P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Ramos JL, Ben-Bassat A, Godoy P, Ramos-Gonzales MI, Duque E;
 XX
 DR WPI; 2002-340103/37.
 XX

PT Novel isolated nucleic acid of the tonB operon from *Pseudomonas*, useful
 PT for producing transformed bacterial strains which are more sensitive to
 PT antibiotics, and toluene.
 XX
 PS Disclosure; Page 80; 81pp; English.
 XX
 CC The invention relates to a novel gene cluster comprising the exbB, exbD
 CC and tonB genes from *P. putida*. These genes are useful for producing
 CC bacterial cells more sensitive to antibiotics, toluene, pHA (para-
 CC hydroxybenzoic acid), aromatic compounds, parabenes, and aromatic amino
 CC acids. Methods are also provided to identify pHA tolerant genes, and
 CC pHA tolerant strains, useful for producing pHA. The present sequence
 CC represents a primer for RT-PCR amplification of *P. putida* exbB and exbD
 CC mRNA
 XX
 SQ Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 977 CAGCAGCACCAGCAGCA 993
 DB 1 CAGCAGCACCAGCATCA 17
 RESULT 257
 ABS68433/C
 ID ABS68433 standard; DNA; 18 BP.
 AC ABS68433;
 XX
 DT 19-NOV-2002 (first entry)
 XX
 DE Sequencing primer #24 for fungal DNA flanking REMI insertion site.
 XX
 KW Fungal pathogen; peptide synthetase gene cluster; iron reductase;
 KW permease; major facilitator superfamily transporter; MFS transporter;
 KW anti-fungal agent; fungicide; pathogenic fungi; plant pathogen; CPS1;
 KW animal pathogen; fungal infection; wild grass; cereal; corn; mycocide;
 KW leaf spot maize; immunocompromised vertebrate; pneumonia; arthritis;
 KW military disease; bone infection; joint infection; skin disease;
 KW aseptophagitis; vaginitis; onychomycosis; inflammation; urinary tract;
 KW kidney; liver; brain; gastrointestinal tract; lung; fungicidal;
 KW mycoid; antiarthritic; antiinflammatory; dermatological; CoA ligase;
 KW sequencing; primer; ss.
 XX
 OS Cochliobolus heterostrophus.
 OS Synthetic.
 XX
 PN WO200242444-A2.
 XX
 PD 30-MAY-2002.
 XX
 XX 21-NOV-2001; 2001WO-US043381.
 XX
 XX 22-NOV-2000; 2000US-0252649P.
 PR
 PR 22-NOV-2000; 2000US-0252732P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA (CORR) CORNELL RES FOUND INC.
 PA (YODE/) YODER O.
 PA (TURG/) TURGEON B G.
 PA (LUSS/) LU S.
 XX
 XX Yoder O, Turgeon BG, Lu S;
 PI
 XX WPI; 2002-666824/71.
 DR
 XX
 XX Nucleic acid molecules comprising fungal, e.g. Cochliobolus
 PT heterostrophus, genes from a peptide synthetase gene cluster, useful for
 PT identifying anti-fungal agents for treating fungal infections such as
 PT pneumonia and arthritis.

XX Example 1; Page 189; 315pp; English.
 PS
 XX The present invention relates to nucleic acid molecules comprising
 CC fungal, e.g. Cochliobolus heterostrophus, genes from a peptide synthetase
 CC gene cluster, encoding e.g. an iron reductase and/or a permease, or a
 CC major facilitator superfamily (MFS) transporter protein. The
 CC polynucleotides and polypeptides are useful for identifying a novel
 CC fungicidal or mycocidal mode of action which permits rapid discovery of
 CC novel inhibitors of gene products that are useful as fungicides or
 CC mycocides. Anti-fungal agents identified using the polynucleotide and
 CC polypeptide sequences of the invention, and antisense DNA are useful as
 CC fungicides to suppress the growth of pathogenic fungi. The fungal
 CC pathogens include plant pathogens such as *Septoria tritici*, or Cochliobolus
 CC heterostrophus, or animal pathogens such as *Candida albicans*. The anti-
 CC fungal agents are useful for treating fungal infections in plants such as
 CC wild grasses or cereals (e.g. corn). For example they can be used to
 CC treat a disease called leaf spot maize caused by the pathogen C.
 CC heterostrophus. The anti-fungal agents are particularly useful for
 CC treating fungal infections of vertebrates, including immunocompromised
 CC vertebrates, for e.g. pneumonia, arthritis, military disease, bone and
 CC joint infection, skin disease, aseptophagitis, vaginitis, onychomycosis,
 CC and inflammation of the urinary tract, kidney, liver, brain,
 CC gastrointestinal tract and lung. ABS68410-ABS68443 represent sequencing
 CC primers used to sequence C. heterostrophus DNA flanking the REMI vector
 CC insertion site in the examples of the present invention
 XX
 SQ Sequence 18 BP; 0 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 1.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 978 AGCAGCACCAGCAGCAG 994
 DB 18 AGAAGCACCAGCAGCAG 2
 RESULT 258
 ADG88997
 ID AG88997 standard; DNA; 18 BP.
 XX
 AC AG88997;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE *Pseudomonas putida* exbB and exbD gene amplifying RT-PCR primer #2.
 XX
 KW Antibiotic; tonB operon; *Pseudomonas*; bactericidal agent; RT-PCR;
 KW reverse transcription; primer; ss.
 XX
 OS *Pseudomonas putida*.
 OS
 PN US2003158397-A1.
 XX
 PD 21-AUG-2003.
 XX
 XX 01-OCT-2001; 2001US-00968122.
 PF
 PF 01-OCT-2001; 2001US-00968122.
 XX
 XX (RAMO/) RAMOS J L.
 XX (BENE/) BEN-BASSAT A.
 PA (DUQU/) DUQUE E.
 PA (GODO/) GODOY P.
 PA (RAMO/) RAMOS-GONZALEZ M I.
 XX
 XX Ramos JL, Ben-Bassat A, Duque E, Godoy P, Ramos-Gonzalez MI;
 PI WPI; 2003-801890/75.
 DR
 XX New nucleic acid fragment of the tonB operon from *Pseudomonas*, useful for
 PT designing antibiotics, for generating microbes with enhanced biocatalytic

PT potential or for controlling microbial tolerance to pHBA or aromatic compounds.

XX Disclosure; SEQ ID NO 9; 34pp; English.

XX The present invention relates to new isolated nucleic acid fragment of the tonB operon from Pseudomonas. The invention is useful for designing antibiotics or bacteriostatic agents, for generating microbes with enhanced biocatalytic potential and controlling microbial tolerance to pHBA, aromatic compounds or amino acids, antibiotics or bactericidal agents. The present sequence is Pseudomonas putida exbB and exbD gene amplifying RT-PCR primer.

XX Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 977 CAGCAGCACCAGCAGCA 993
Db 1 CAGCAGCACCAGCATCA 17

RESULT 259

AA82737
ID AAA82737 standard; DNA; 19 BP.

XX AA82737;

DT 04-DEC-2000 (first entry)

DE cdk3 ribozyme binding site #22.

KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

OS Mammalia.

PN WO200032765-A2.

PD 08-JUN-2000.

PF 06-DEC-1999; 99WO-US028772.

PR 04-DEC-1998; 98US-0110954P.

PA (IMMU-) IMMUSOL INC.

PI Tritz R, Welch PJ, Barber JR, Robbins JM;

DR WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.

PS Disclosure; Page 51; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment

XX Sequence 19 BP; 3 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2942 TTTGACTTCTCTAGCCA 2958
Db 3 TTTGAGTTCTCTAGCCA 19

RESULT 260

AA82738
ID AAA82738 standard; DNA; 19 BP.

XX AA82738;

DT 04-DEC-2000 (first entry)

DE cdk3 ribozyme binding site #23.

KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

OS Mammalia.

PN WO200032765-A2.

PD 08-JUN-2000.

PF 06-DEC-1999; 99WO-US028772.

PR 04-DEC-1998; 98US-0110954P.

PA (IMMU-) IMMUSOL INC.

PI Tritz R, Welch PJ, Barber JR, Robbins JM;

DR WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.

PS Disclosure; Page 51; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment

XX Sequence 19 BP; 3 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2942 TTTGACTTCTCTAGCCA 2958
Db 2 TTTGAGTTCTCTAGCCA 18

RESULT 261

AAH57900
ID AAH57900 standard; DNA; 19 BP.

XX AAH57900;

DT 10-SEP-2001 (first entry)

DE Cell-cycle dependent kinase cdk3 ribozyme binding site SEQ ID NO:324.

XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; recognition site; target; ribozyme binding site; eye disease; vulnary; proliferative disease; skin disease; psoriasis; diabetic retinopathy; cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;

KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisklicking; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 XX 26-OCT-2000; 2000WO-US029500.
 XX
 PF 26-OCT-1999; 99US-0161532P.
 XX
 PR (IMMU-) IMMUSOL INC.
 XX
 PA Robbins JM, Tritz R;
 XX
 PI WPI; 2001-300427/31.
 DR
 XX
 DR Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX
 XX Example 1; Page 95; 408pp; English.
 XX
 CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisklicking,
 CC ophthalmological, vulnary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 3 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 1; Indels 0; Gaps 0;
 Qy 2942 TTTGACTTCTCAGCCA 2958
 Db 2 TTTGAGTTCTCAGCCA 18
 |||||
 RESULT 262
 AAH57899
 ID AAH57899 standard; DNA; 19 BP.
 XX
 AC AAH57899;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 XX Cell-cycle dependent kinase cdk3 ribozyme binding site SEQ ID NO:323.
 DE Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnary;

KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisklicking; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 XX 26-OCT-2000; 2000WO-US029500.
 XX
 PF 26-OCT-1999; 99US-0161532P.
 XX
 PR (IMMU-) IMMUSOL INC.
 XX
 PA Robbins JM, Tritz R;
 XX
 PI WPI; 2001-300427/31.
 DR
 XX
 DR Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX
 XX Example 1; Page 95; 408pp; English.
 XX
 CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisklicking,
 CC ophthalmological, vulnary, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 3 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 1; Indels 0; Gaps 0;
 Qy 2942 TTTGACTTCTCAGCCA 2958
 Db 3 TTTGAGTTCTCAGCCA 19
 |||||
 RESULT 263
 AAL54233/c
 ID AAL54283 standard; DNA; 19 BP.
 XX
 AC AAL54283;
 XX
 DT 27-MAR-2003 (first entry)
 XX
 DE Mouse Cbfal PCR primer #2.

KW Antiinflammatory; rat periodontium; cell strain; bioactivity;
 KW tooth disease; periodontitis; periodontosis; mouse; murine; PCR; primer;
 KW ss.
 XX
 OS Mue sp.
 XX
 PN JP2002262862-A.
 XX
 PD 17-SEP-2002.
 XX
 XX 12-MAR-2001; 2001JP-00069249.
 PF
 XX 12-MAR-2001; 2001JP-00069249.
 PR
 XX (TOHO-) TOHOKU TECHNOARCH KK.
 PA
 XX WPI; 2003-132121/13.
 DR
 XX A new cell strain derived from rat periodontium useful for treating or
 PT preventing tooth diseases such as periodontitis.
 XX
 PS Example 1; Page 9; 28pp; Japanese.
 XX
 CC The invention relates to a cell strain which is derived from rat
 CC periodontium and can be maintained in passage. The methods of the
 CC invention are useful for acquiring a cell strain, establishing a cell
 CC strain, and measuring the bioactivity against the cell of a rat-derived
 CC periodontium. The cell strain can be used for treating and preventing
 CC tooth diseases such as periodontitis and periodontosis. This
 CC polynucleotide sequence represents a PCR primer used in the
 CC exemplification of the invention
 XX
 SQ Sequence 19 BP; 0 A; 2 C; 5 G; 12 T; 0 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 1; Indels 0; Gaps 0;
 QY 1575 AACAAACACAGCAACAA 1591
 Db 19 AACAAACACACAAACAA 3
 |||||
 RESULT 264
 ID ADN34019/c
 XX
 XX ADN34019 standard; RNA; 19 BP.
 AC
 XX ADN34019;
 DT 01-JUL-2004 (first entry)
 XX
 DE Upper strand of cyclin D1 targeted double stranded siNA #39.
 XX
 XX short interfering nucleic acid; siNA; cyclin; Cytostatic; Vasotropic;
 KW cancer; cell-proliferation disorder; restenosis; drug screening;
 KW genetic engineering; pharmacogenomics; gene mapping;
 KW single nucleotide polymorphisms; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003072705-A2.
 XX
 XX 04-SEP-2003.
 XX
 XX 06-FEB-2003; 2003WO-US0003662.
 PF
 XX 20-FEB-2002; 2002US-0358580P.
 PR
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 17-SEP-2002; 2002US-0411275P.
 PR 17-SEP-2002; 2002US-0411275P.

PR 15-JAN-2003; 2003US-0440129P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Thompson J, Mcswiggen J, Beigelman L;
 PI
 XX WPI; 2003-689983/65.
 DR
 XX New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer and restenosis, down regulates expression of at least
 PT one cyclin gene.
 XX
 XX Example 3; SEQ ID NO 39; 144pp; English.
 PS
 XX The present invention relates to a short interfering nucleic acid (siNA)
 CC that down regulates expression of at least one cyclin gene by RNA
 CC interference. siNA are used to modulate expression of cyclin genes, in
 CC cells, tissue explants or organisms, e.g. for treating a wide range of
 CC cancers and other cell-proliferation disorders such as restenosis, but
 CC also for drug screening, diagnosis, target identification and validation;
 CC genetic engineering, pharmacogenomics, studying gene function and gene
 CC mapping (e.g. of single-nucleotide polymorphisms). The present sequence
 CC represents the upper strand of cyclin D1 targeted double stranded siNA
 CC which is identical to the cyclin D1 transcript target sequence.
 XX
 SQ Sequence 19 BP; 4 A; 6 C; 1 G; 0 T; 8 U; 0 Other;
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
 Matches 16; Conservative 0; Indels 1; Indels 0; Gaps 0;
 QY 549 AGGAAGTGTTCATGAA 565
 Db 17 AGGAAGTGTTCATGAA 1
 |||||
 RESULT 265
 ID ADN34258
 XX
 XX ADN34258 standard; RNA; 19 BP.
 AC
 XX ADN34258;
 DT 01-JUL-2004 (first entry)
 XX
 DE Lower strand of cyclin D1 targeted double stranded siNA #39.
 XX
 XX short interfering nucleic acid; siNA; cyclin; Cytostatic; Vasotropic;
 KW cancer; cell-proliferation disorder; restenosis; drug screening;
 KW genetic engineering; pharmacogenomics; gene mapping;
 KW single nucleotide polymorphisms; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003072705-A2.
 XX
 XX 04-SEP-2003.
 PD
 XX 06-FEB-2003; 2003WO-US0003662.
 PF
 XX 20-FEB-2002; 2002US-0358580P.
 PR
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 17-SEP-2002; 2002US-0411275P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Thompson J, Mcswiggen J, Beigelman L;
 PI
 XX WPI; 2003-689983/65.
 DR

```
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer and restenosis, down regulates expression of at least
PT one cyclin gene.
XX
XX Example 3; SEQ ID NO 278; 144pp; English.
XX
XX The present invention relates to a short interfering nucleic acid (siRNA)
CC that down regulates expression of at least one cyclin gene by RNA
CC interference. siRNA are used to modulate expression of cyclin genes, in
CC cells, tissue explants or organisms, e.g. for treating a wide range of
CC cancers and other cell-proliferation disorders such as restenosis, but
CC also for drug screening, diagnosis, target identification and validation;
CC genetic engineering, pharmacogenomics, studying gene function and gene
CC mapping (e.g. of single-nucleotide polymorphisms). The present sequence
CC represents the lower strand of cyclin D1 targeted double stranded siRNA.
XX
XX Sequence 19 BP; 8 A; 1 C; 6 G; 0 T; 4 U; 0 Other;
SQ
    Query Match      0.4%; Score 15.4; DB 1; Length 19;
    Best Local Similarity 70.6%; Pred. No. 2e+02;
    Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY      549 AGGAACCTCTCAATGAA 565
DB      ||||| :|||:||||
        3 AGGAAGUGUCAUGAA 19
RESULT 266
ADH01571
ID ADH01571 standard; RNA; 19 BP.
AC ADH01571;
XX
DT 11-MAR-2004 (first entry)
DE
DE Protein tyrosine phosphatase siRNA sequence, SEQ ID No 183.
XX
XX small interfering RNA; siRNA; protein tyrosine phosphatase; PTP; PTP1B;
KW insulin receptor protein phosphorylation; Jak2; antidiabetic; anorectic;
KW antiinflammatory; neuroprotective; cytotatic; immunosuppressive;
KW antimicrobial; gene therapy; ss; siRNA.
XX
XX Unidentified.
OS
XX WO2003099227-A2.
PN
XX 04-DEC-2003.
PD
XX
XX 23-MAY-2003; 2003WO-US016651.
PF
XX
XX 23-MAY-2002; 2002US-0383249P.
PR
XX 14-APR-2003; 2003US-0462942P.
PR
XX
XX (CEPT-) CEPTYR INC.
PA
XX
XX Lewis SP, Klinghoffer R, Wilson LK;
PI
XX
XX WPI; 2004-035036/03.
DR
XX
XX New small interfering polynucleotide that modulates protein tyrosine
PT phosphatase (PTP)1B polypeptide signal transduction, useful for treating
PT disorders associated with altered PTP1B signal transduction, e.g.
PT diabetes or cancer.
XX
XX Example 3; SEQ ID NO 183; 234pp; English.
PS
XX
XX The invention relates to a novel isolated small interfering RNA (siRNA)
CC polynucleotide, comprising at least one nucleotide sequence from any of
CC the 20 fully defined sequences given in the specification. The invention
CC further relates to a pharmaceutical composition comprising a new siRNA
CC polynucleotide and a physiological carrier; a recombinant nucleic acid
CC construct, comprising a polynucleotide that is capable of directing
CC
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```
CC transcription of an siRNA; a host cell transformed or transfected with
CC the above recombinant nucleic acid construct; a method for interfering
CC with expression of a protein tyrosine phosphatase (PTP)1B polypeptide, or
CC its variant; a method for identifying a component of a PTP1B signal
CC transduction pathway; a method for modulating an insulin receptor protein
CC phosphorylation state in a cell; a method for altering a Jak2 protein
CC phosphorylation state in a cell; and a method for treating a Jak2-
CC associated disorder. The siRNA has the following activities:
CC antidiabetic, anorectic, antiinflammatory, neuroprotective, cytotatic,
CC immunosuppressive, and antimicrobial. The novel siRNA polynucleotides can
CC be used in gene therapy to treat disorders. The composition and methods
CC are useful in treating disorders associated with PTP1B-mediated signal
CC transduction, such as diabetes, obesity, hyperglycaemia-induced
CC apoptosis, inflammation, neurodegenerative disorders, cancer, autoimmune
CC diseases or infection. This polynucleotide sequence represents an siRNA
CC used for modulating the signal transduction of a protein tyrosine
CC phosphatase of the invention.
XX
XX Sequence 19 BP; 5 A; 8 C; 2 G; 0 T; 4 U; 0 Other;
SQ
    Query Match      0.4%; Score 15.4; DB 1; Length 19;
    Best Local Similarity 70.6%; Pred. No. 2e+02;
    Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY      3674 CCATATTCCTCTCTCAC 3690
DB      ||||| :|||:||||
        2 CCAUAUUCACACCTCCAC 18
RESULT 267
ADR80899/c
ID ADR80899 standard; DNA; 19 BP.
XX
XX ADR80899;
AC
XX
DT 16-DEC-2004 (first entry)
DE
DE Human glucose-6-phosphatase oligonucleotide seqid 5398.
XX
XX antilipemic; cardiatic; vasotropic; antiarteriosclerotic; antidiabetic;
KW cytotatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW RNA interference; iRNA; antisense technology; lipid metabolism;
KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW coronary artery disease; CAD; coronary heart disease; CHD;
KW atherosclerosis; hepatic glucose production;
KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW colon cancer; lung cancer; neurological disease; Huntington disease;
KW spinocerebellar ataxia; viral disease; AIDS; glucose-6-phosphatase; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2004080406-A2.
PN
XX
XX 23-SEP-2004.
PD
XX
XX 08-MAR-2004; 2004WO-US007070.
PF
XX
XX 07-MAR-2003; 2003US-0452682P.
PR
XX 12-MAR-2003; 2003US-0454265P.
PR
XX 13-MAR-2003; 2003US-0454962P.
PR
XX 13-MAR-2003; 2003US-0455050P.
PR
XX 14-APR-2003; 2003US-0462894P.
PR
XX 17-APR-2003; 2003US-0463772P.
PR
XX 25-APR-2003; 2003US-0465665P.
PR
XX 25-APR-2003; 2003US-0465802P.
PR
XX 09-MAY-2003; 2003US-0469612P.
PR
XX 08-AUG-2003; 2003US-0493986P.
PR
XX 11-AUG-2003; 2003US-0494597P.
PR
XX 26-SEP-2003; 2003US-0506341P.
PR
XX 09-OCT-2003; 2003US-0510246P.
PR
XX 10-OCT-2003; 2003US-0510318P.
PR
XX 07-NOV-2003; 2003US-0518453P.
XX
```

PA (ALNY-) ALNYLAM PHARM.
 XX Manoharan M, Bumcrot D;
 XX MPI; 2004-677362/66.
 DR
 XX
 XX Interference RNA agent useful for treating dyslipidemias, coronary artery
 PT disease, diabetes, cancer or neurological disease, comprises sense
 PT sequence and antisense sequence which has specific modifications.
 XX
 XX Example 5; SEQ ID NO 5398; 378pp; English.
 XX
 CC The invention describes a RNA interference (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequences have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC introducing one or more asymmetrical modification in the sequence, where
 CC the modification decreases nuclease sensitivity while not decreasing its
 CC activity; a kit comprising (I) and instruction for its use; and a device
 CC that can be dispense or administer a composition comprising (I). (I) is
 CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
 CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
 CC The subject is suffering from a disorder characterised by elevated or
 CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
 CC inhibit hepatic glucose production or for treating glucose-metabolism-
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
 CC lung cancer), neurological disease (e.g., Huntington disease or
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
 CC represents a human glucose-6-phosphatase antisense oligonucleotide that
 CC can be used to control glucose-6-phosphatase gene expression.
 XX
 XX Sequence 19 BP; 6 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3352 TGTGGTGTCAATGTGTA 3368
 Db 18 TGTGGTGTCAATGTGGA 2
 RESULT 268
 ADR80898/c
 ID ADR80898 standard; DNA; 19 BP.
 XX
 XX ADR80898;
 XX
 XX 16-DEC-2004 (first entry)
 DT
 XX Human glucose-6-phosphatase oligonucleotide seqid 5397.
 DE
 XX
 XX antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
 KW cytosstatic; anticonvulsant; nootropic; muscula; anti-HIV;
 KW RNA interference; iRNA; antisense technology; lipid metabolism;
 KW cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
 KW coronary artery disease; CAD; coronary heart disease; CHD;
 KW atherosclerosis; hepatic glucose production;
 KW glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
 KW colon cancer; lung cancer; neurological disease; Huntington disease; ss.
 KW spinocerebellar ataxia; viral disease; AIDS; glucose-6-phosphatase;
 XX
 OS Homo sapiens.

XX
 PN WO2004080406-A2.
 XX
 XX 23-SBP-2004.
 XX
 XX 08-MAR-2004; 2004WO-US007070.
 XX
 XX 07-MAR-2003; 2003US-0452682P.
 PR 12-MAR-2003; 2003US-0454265P.
 PR 13-MAR-2003; 2003US-0454962P.
 PR 13-MAR-2003; 2003US-0455050P.
 PR 14-APR-2003; 2003US-0462894P.
 PR 17-APR-2003; 2003US-0463772P.
 PR 25-APR-2003; 2003US-0465665P.
 PR 25-APR-2003; 2003US-0465802P.
 PR 08-MAY-2003; 2003US-0469612P.
 PR 08-AUG-2003; 2003US-0493986P.
 PR 11-AUG-2003; 2003US-0494597P.
 PR 26-SEP-2003; 2003US-0506341P.
 PR 09-OCT-2003; 2003US-0510246P.
 PR 10-OCT-2003; 2003US-0510318P.
 PR 07-NOV-2003; 2003US-0518453P.
 XX
 XX (ALNY-) ALNYLAM PHARM.
 PA
 XX Manoharan M, Bumcrot D;
 XX MPI; 2004-677362/66.
 XX
 XX Interference RNA agent useful for treating dyslipidemias, coronary artery
 PT disease, diabetes, cancer or neurological disease, comprises sense
 PT sequence and antisense sequence which has specific modifications.
 XX
 XX Example 5; SEQ ID NO 5397; 378pp; English.
 XX
 CC The invention describes a RNA interference (iRNA) agent (I) comprising a
 CC sense sequence and an antisense sequence, where the sense sequences have
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense
 CC sequences have one or more asymmetrical phosphorothioate modifications
 CC and the antisense sequence targets a human gene sequence. Also described
 CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);
 CC stabilising (I), involves selecting a sequence with activity and
 CC introducing one or more asymmetrical modification in the sequence, where
 CC the modification decreases nuclease sensitivity while not decreasing its
 CC activity; a kit comprising (I) and instruction for its use; and a device
 CC that can be dispense or administer a composition comprising (I). (I) is
 CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
 CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
 CC The subject is suffering from a disorder characterised by elevated or
 CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,
 CC dyslipidaemias, hypercholesterolaemia, statin-resistant
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
 CC inhibit hepatic glucose production or for treating glucose-metabolism-
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
 CC lung cancer), neurological disease (e.g., Huntington disease or
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
 CC represents a human glucose-6-phosphatase antisense oligonucleotide that
 CC can be used to control glucose-6-phosphatase gene expression.
 XX
 XX Sequence 19 BP; 6 A; 9 C; 1 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 15.4; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3352 TGTGGTGTCAATGTGTA 3368
 Db 17 TGTGGTGTCAATGTGGA 1

```
RESULT 269
ACD82527
ID ACD82527 standard; DNA; 17 BP.
XX
XX
AC ACD82527;
XX
XX
DT 19-SEP-2003 (first entry)
XX
XX
DE Nucleic acid cloning associated adaptor molecule #228.
XX
XX
KW Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
internal deletion mutagenesis analysis; cloning vehicle; ss.
XX
XX
OS Synthetic.
XX
XX
PN US2003044791-A1.
XX
XX
PD 06-MAR-2003.
XX
XX
PF 13-JUN-2001; 2001US-00880313.
XX
XX
PR 13-JUN-2001; 2001US-00880313.
XX
XX
PA (FLEM/) FLEMINGTON E K.
XX
XX
PI Flemington EK;
XX
XX
DR WPI; 2003-521745/49.
XX
XX
PT New adaptor molecules, useful for cloning nucleic acid molecules that
does not require the design and synthesis of oligonucleotides or PCR
primers.
XX
XX
PS Claim 12; Fig 5; 100pp; English.
XX
XX
CC The invention describes adaptor molecules, where each end of the adaptor
is compatible with a nucleic acid digested with a restriction enzyme or a
nucleic acid comprising an end that is compatible with a nucleic acid
digested with a restriction enzyme. The adaptor molecules, compositions,
kits and arrays are useful for cloning nucleic acid molecules that does
not require the design and synthesis of oligonucleotides or PCR primers.
The adaptors, kits and arrays are also useful for ligating two ends of a
single nucleic acid molecule, or ligating two or more nucleic acid
molecules. The kits can also be used for performing internal deletion
mutagenesis analysis. The adaptor molecules are ligated to a cloning
vehicle, making the cloning procedure more rapid and efficient, and less
error-prone. This sequence represents a nucleic acid cloning associated
adaptor molecule
XX
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX
Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2586 GTACACCTGCAGCCT 2600
Db 1 GTACACCTGCAGCCT 15
XX
XX
RESULT 270
ADC37816
ID ADC37816 standard; DNA; 17 BP.
XX
XX
AC ADC37816;
XX
XX
DT 18-DEC-2003 (first entry)
XX
XX
DE Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:165.
XX
XX
KW human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
```

```
KW AMLP1a; ss.
XX
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
PN WO2003037931-A2.
XX
XX
PD 08-MAY-2003.
XX
XX
PF 01-NOV-2002; 2002WO-US035129.
XX
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX
PI Shannon M, Phan T;
XX
XX
DR WPI; 2003-430501/40.
XX
XX
PT New isolated nucleic acid molecule encoding a human angiominotin-like
protein, useful for treating or preventing a disorder associated with
decreased or increased expression or activity of AMLP1.
XX
XX
PS Example 2; SEQ ID NO 165; 172pp; English.
XX
XX
CC The present invention describes the human angiominotin-like protein 1
(AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
compositions of the present invention can be used for treating or
preventing a disorder associated with decreased or increased expression
or activity of AMLP1. The present sequence represents a scanning
oligonucleotide for human AMLP1a, which is used in an example from the
present invention.
XX
XX
SQ Sequence 17 BP; 6 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
XX
XX
Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAACA 1443
Db 3 GCAGCAGCAGCAACA 17
XX
XX
RESULT 271
ADI50157/c
ID ADI50157 standard; DNA; 17 BP.
XX
XX
AC ADI50157;
XX
XX
DT 15-APR-2004 (first entry)
XX
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID2660.
XX
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
primer; PCR; gene chip; antisense; viral disease; tumour;
cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX
OS Homo sapiens.
XX
XX
PN WO2003025177-A2.
XX
XX
PD 27-MAR-2003.
XX
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX
PI Telerman A, Anson R, Tuijnder M;
```

XX WPI; 2003-313354/30.

XX New isolated nucleic acid, useful for treating viral diseases associated

PT with tumors and cell degeneration, also related polypeptides, antibodies

PT and transfected cells.

XX Disclosure; SEQ ID NO 2660; 30pp; French.

XX This invention relates to novel isolated nucleic acid sequences involved

CC in the phenomena of tumour suppression, tumour reversion, apoptosis

CC and/or resistance to viruses. The invention may be useful for the

CC development of compounds with a cytostatic, virucide, neuroprotective,

CC neurotropic or neuroleptic activity. The DNA sequences may be useful as

CC probes and primers for detecting, identifying, quantifying and/or

CC amplifying nucleic acid, for example as one component of a gene chip, in

CC vitro as antisense reagents and for production of recombinant

CC polypeptides. The invention may therefore be useful for preparation of

CC pharmaceuticals for prevention and/or treatment of viral diseases that

CC are characterised by development of tumours or cell degeneration,

CC specifically cancer but also Alzheimer's disease and schizophrenia. The

CC present sequence is that of a nucleic acid sequence of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/publishednpt_sequences

XX

XX Sequence 17 BP; 5 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

XX

Query Match 0.4%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 GGTTCCTTGAAGA 163

Db 17 GGTTCCTTGAAGA 3

RESULT 272

AD40522

ID ADC40522 standard; DNA; 18 BP.

XX

XX

AC ADC40522;

XX

XX 18-DEC-2003 (first entry)

XX

XX Human G-protein coupled receptor (GPCR) related reverse primer.

XX

XX gene expression analysis; collective quantitative analysis;

KW G protein coupled receptor; tyrosine oxidase receptor family;

KW ion channel gene family; cancer; EDG-1; EDG-2 receptor; atherosclerosis;

KW myocardial infarction; infarct; ischaemic disease; GPCR; primer; PCR; ss.

XX

XX Unidentified.

XX

XX WO2003052096-A1.

XX

XX

XX 26-JUN-2003.

XX

XX 13-DEC-2002; 2002WO-JP013097.

XX

XX 14-DEC-2001; 2001JP-00382053.

XX

XX 21-FEB-2002; 2002JP-00045104.

XX

XX 15-MAY-2002; 2002JP-00140111.

XX

XX 18-NOV-2002; 2002JP-00333769.

XX

XX (TAKE) TAKEDA CHEM IND LTD.

XX

XX Hinuma S, Kobayashi M, Arai T, Fukusumi S, Fujii R, Komatsu H;

PI Matsumura F, Kawamata Y, Ogi K;

XX

XX WPI; 2003-533023/50.

XX

XX Method for gene expression analysis for treatment of cancers.

XX Example 2; SEQ ID NO 6; 261pp; Japanese.

XX

CC The invention relates to a novel method for gene expression analysis by

CC collective quantitative analysis of the expression of a number of genes

CC to identify those that are promoted or inhibited in a given cell or

CC tissue. The genes are preferably gene families such as the G protein

CC coupled receptor family, tyrosine oxidase receptor family, or ion channel

CC gene family. The methods may be used in treatment of cancers, including

CC prostate, ovarian, stomach, bladder, breast, and cancer of the

CC intestines. EDG-1 and EDG-2 receptor agonists and antagonists may be used

CC in the treatment and prevention of atherosclerosis, myocardial

CC infarction, infarct or ischaemic disease of the brain. This

CC polynucleotide sequence represents a PCR primer used in the

CC exemplification of the invention.

XX

XX Sequence 18 BP; 6 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

XX

Query Match 0.4%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3447 AAACCCCATGTCATG 3461

Db 4 AAACCCCATGTCATG 18

RESULT 273

ADN08161/C

ID ADN08161 standard; DNA; 18 BP.

XX

XX

AC ADN08161;

XX

XX 17-JUN-2004 (first entry)

XX

XX Human S9-RNA RT-PCR primer #2.

XX

XX Human; ss; PCR; endocrine gland vascular endothelial growth factor;

KW EG-VEGF; EG-VEGF receptor; endometrial disease; uterine receptivity;

KW endometriosis; endometrial carcinoma; dysfunctional bleeding;

KW gene therapy; primer; RT-PCR; reverse transcriptase PCR; S9-RNA.

XX

XX Homo sapiens.

XX

XX DE10229379-A1.

XX

XX 29-JAN-2004.

XX

XX 26-JUN-2002; 2002DE-01029379.

XX

XX 26-JUN-2002; 2002DE-01029379.

XX

XX (SCHD) SCHERING AG.

XX

XX Haendler B, Hess-Stumpp H, Schmidt A;

XX

XX WPI; 2004-134408/14.

XX

XX Treatment and prevention of endometrial disease, e.g. endometriosis or

PT carcinoma, by inhibiting endocrine gland vascular endothelial growth

PT factor, also diagnosis.

XX

XX Example 1; Page 5; 13pp; German.

XX

XX The invention relates to a composition that contains, as active agent, an

CC endocrine gland vascular endothelial growth factor (EG-VEGF) nucleic

CC acid, polypeptide or antisense nucleic acid, antibody against EG-VEGF or

CC its receptor (EG-VEGF-R), or EG-VEGF-R antisense nucleic acid, is useful

CC for the treatment or prevention of endometrial diseases. Also included

CC are a method for detecting uterine receptivity (by determining the amount

CC of EG-VEGF polypeptide and/or nucleic acid, using the new composition) or

CC a test system for identifying antagonists of EG-VEGF-R. Also disclosed as

CC new is a splice variant of the human GPR73a receptor. It contains an

CC additional exon which includes a stop codon, so produces a truncated
 CC protein that can not mediate signal transduction, i.e. it functions as a
 CC dominant-negative inhibitor. The composition is used to treat
 CC endometriosis, endometrial carcinoma or dysfunctional bleeding, e.g. by
 CC gene therapy, to diagnose endometriosis or endometrial carcinoma and to
 CC detect uterine receptivity (especially to determine the best time for
 CC implantation of eggs fertilised in vitro). Also the test system that
 CC comprises cells that express the EG-VEGF receptor is used to screen for
 CC receptor antagonists, potentially useful for treating endometriosis. The
 CC present sequence is a human S9-RNA control RT-PCR (reverse transcriptase
 CC PCR) primer used in the isolation of the EG-VEGF cDNA.
 XX
 SQ Sequence 18 BP; 6 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1022 CCTCTCTCTGCTGGA 1036
 Db 16 CCTCTCTCTGCTGGA 2

RESULT 274
 AAQ98457/c
 ID AAQ98457 standard; cDNA; 31 BP.

XX AAQ98457;

XX 23-APR-1996 (first entry)

XX Sense probe CAG-30.

XX Probe; trinucleotide repeat; myotonic dystrophy; DM; Mt-PK gene;
 KW fluorescent label; fluorescein isothiocyanate; fragile X syndrome;
 KW muscular dystrophy; Huntington's disease; ss.

XX Synthetic.

XX WO9525179-A1.

XX 21-SEP-1995.

XX 08-MAR-1995; 95WO-US002861.

XX 17-MAR-1994; 94US-00214823.

XX (UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.

XX Singer RH, Taneja KL;

XX WPI; 1995-336982/43.

XX Detecting trinucleotide repeat expansion by in situ hybridisation - with
 PT detection sensitive enough to distinguish between probe bound to expanded
 PT and normal repeat regions, esp. for myotonic dystrophy diagnosis.

XX Disclosure; Page 38; 51pp; English.

XX The sequences represented by AAQ98457 and AAQ98458 are synthetic probes
 CC for the trinucleotide repeat CTG. These probes can be used in a method of
 CC in situ hybridisation for the detection of a trinucleotide repeat
 CC expansion. These probes were used specifically to identify myotonic
 CC dystrophy (DM). DM is associated with an expanded CTG repeat in the 3'
 CC untranslated region of the Mt-PK gene. These probes are labelled with a
 CC fluorescent label (e.g. fluorescein isothiocyanate) and then used to
 CC treat nucleated cells. The hybridisation of the probe to the expanded
 CC trinucleotide repeat can then be detected by fluorescence microscopy. Due
 CC to the large variation between expanded repeat size, and normal repeat
 CC size in DM (5-27 repeats in non-expanded, 50-2000 repeats in expanded),
 CC the expanded repeat will bind more probes. Only the expanded repeat will
 CC bind enough of the probes to give a detectable fluorescent signal. By
 CC detecting the number of transcripts in a cell of a diagnosed individual,

CC progress of treatment, and severity of the disease can be monitored. This
 CC method can also be used to diagnose other diseases associated with
 CC trinucleotide repeat expansions, such as fragile X syndrome, muscular
 CC dystrophy and Huntington's disease. For some of these diseases a greater
 CC detection specificity would be required due to the smaller difference in
 CC repeat number between normal and infected individuals
 XX
 SQ Sequence 31 BP; 10 A; 10 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 15; DB 1; Length 31;
 Best Local Similarity 67.7%; Pred. No. 5.4e+02;
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1924 ACAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
 Db 31 ACTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 275
 AAZ24996/c
 ID AAZ24996 standard; DNA; 31 BP.

XX AAZ24996;

XX 24-DEC-1999 (first entry)

XX Oligonucleotide CAG30 targeted to myotonic-protein kinase gene.

XX Trinucleotide repeat; myotonic-protein kinase; myotonic dystrophy; probe;
 KW in situ hybridisation; detection; expansion; fragile X syndrome; ss.

XX Synthetic.

XX Homo sapiens.

XX US95962332-A.

XX 05-OCT-1999.

XX 11-DEC-1995; 95US-00570155.

XX 17-MAR-1994; 94US-00214823.

XX 07-MAR-1995; 95US-00399499.

XX (UYMA-) UNIV MASSACHUSETTS.

XX Taneja KL, Singer RH;

XX WPI; 1999-579615/49.

XX Detection of trinucleotide repeats.

XX Disclosure; Col 25; 18pp; English.

XX Oligonucleotides AAZ24983-Z24995 are targeted to the CTG trinucleotide
 CC repeats found in the myotonic-protein kinase (Mt-PK) gene. Excessive
 CC numbers of the trinucleotide repeats in the Mt-PK gene leads to the
 CC disease myotonic dystrophy. The oligonucleotides are used to probe the 5'
 CC -most 7 exons of 14 in the Mt-PK gene. This sequence is used as an
 CC antisense control oligonucleotide for the hybridisation reaction. The
 CC invention relates to a method for the detection of trinucleotide repeat
 CC expansion, e.g. in the Mt-PK gene or FMR1 gene (leading to fragile X
 CC syndrome) by in situ hybridization

Query Match 0.4%; Score 15; DB 1; Length 31;
 Best Local Similarity 67.7%; Pred. No. 5.4e+02;
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1924 ACAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
 Db 31 ACTGCTGCTGCTGCTGCTGCTGCTGCTG 1


```

RESULT 276
AAQ90869
ID AAQ90869 standard; DNA; 18 BP.
XX
XX AC AAQ90869;
XX
XX DT 04-MAR-1996 (first entry)
XX
XX DE hMLH1 gene exon 9 first stage amplification primer N-18765.
XX
XX hMLH1; MutL homologue; cancer diagnosis; mismatch repair; tumour;
KW susceptibility; mutation detection; exon 9; primer N-18765;
KW first stage amplification; ss.
XX
XX OS Synthetic.
XX
XX PN W09516793-A1.
XX
XX PD 22-JUN-1995.
XX
XX PF 16-DEC-1994; 94WO-US014746.
XX
XX PR 17-DEC-1993; 93US-00168877.
XX
XX PR 08-MAR-1994; 94US-00209521.
XX
XX PR 09-DEC-1994; 94US-00352302.
XX
XX PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX PA (DAND ) DANA FARBEN CANCER INST INC.
XX
XX PI Baker SM, Bollag RJ, Kolodner RD, Bronner CE, Liskay RM;
XX
XX WPI; 1995-231583/30.
XX
XX DR Determn. of a mutation in a mutL homologue or gene prod. in a tissue -
XX used to diagnose cancer susceptibility, and to identify and classify a
XX DNA mismatch-repair-defective tumour.
XX
XX PS Claim 13; Fig 4B-2; 168pp; English.
XX
XX CC AAQ90869 and AAQ90870 are a primer pair for the 1st stage amplification
XX of the hMLH1 (a MutL homologue) gene exon 9. A mutation in an analogous
XX segment of a hMLH1 or hPMS1 nucleic acid isolated from a subject, can be
XX detected by comparing it with the above gene fragment. This method can be
XX used to diagnose cancer susceptibility, or to identify and classify a DNA
XX mismatch-repair defective tumour
XX
XX SQ Sequence 18 BP; 7 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1223 CAAAAGCTTCAGATCTC 1240
Db 1 CAAAAGCTTCAGATCTC 18

RESULT 277
AAQ71721
ID AAQ71721 standard; RNA; 18 BP.
XX
XX AC AAQ71721;
XX
XX DT 28-JUL-1999 (first entry)
XX
XX DE Human KDR VEGF receptor hairpin ribozyme substrate #19.
XX
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.

XX
XX OS Homo sapiens.
XX
XX PN W09715662-A2.
XX
XX PD 01-MAY-1997.
XX
XX PF 25-OCT-1996; 96WO-US017480.
XX
XX PR 26-OCT-1995; 95US-0005974P.
XX
XX PR 11-JAN-1996; 96US-00584040.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PA (CHIR ) CHIRON CORP.
XX
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
XX CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX PS Claim 4; Page 119; 218pp; English.
XX
XX CC The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
XX SQ Sequence 18 BP; 5 A; 7 C; 4 G; 0 T; 2 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1094 ACATTCAGCCACAGAGC 1111
Db 1 ACAUGCAGCCACUGAGC 18

RESULT 278
AAZ59187/C
ID AAZ59187 standard; DNA; 18 BP.
XX
XX AC AAZ59187;
XX
XX DT 15-SEP-2003 (revised)
XX
XX DT 20-APR-2000 (first entry)
XX
XX DE Reverse primer for construct MWpSp-MwPmp5 DNA.
XX
XX KW Fusion protein; Bacillus; cell wall protein; promoter; cleavage site;
XX TEV protease; PCR primer; ss.
XX
XX OS Brevibacillus brevis.
XX
XX PN JP11341991-A.
XX
XX PD 14-DEC-1999.
XX
XX PF 30-MAR-1999; 99JP-00089488.
XX
XX PR 31-MAR-1998; 98JP-00087339.
XX
XX PA (ITO-) ITOHAM FOODS INC.
XX
XX PA (UDAK/) UDAKA S.

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```
ID AA286831 standard; DNA; 18 BP.
XX
AC AA286831;
XX
XX 26-APR-2000 (first entry)
DT
XX Human Smad1 antisense inhibitor ISIS #28190.
XX
XX Antisense inhibitor; human; Smad1; disease therapy; ss.
KW
XX
XX Homo sapiens.
OS
XX US6013522-A.
PN
XX 11-JAN-2000.
XX
XX 23-FEB-1999; 99US-00255911.
XX
XX 23-FEB-1999; 99US-00255911.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Cowsett LM;
XX
XX WPI; 2000-136324/12.
DR
XX Antisense oligonucleotides useful for inhibiting expression of human
XX Smad1 in vitro or in vivo.
XX
XX Claim 11; Col 38; 31pp; English.
PS
XX This sequence represents an antisense inhibitor of human Smad1 of the
XX invention. The antisense compounds are useful for inhibiting Smad1
XX expression in human cells or tissues in vitro or in vivo for the
XX treatment of diseases associated with Smad1 expression
XX
XX Sequence 18 BP; 1 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
SQ
    Query Match      0.4%; Score 14.8; DB 1; Length 18;
    Best Local Similarity 88.9%; Pred. No. 2.1e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCAAC 1442
DB 18 AGCAGCAGCAGCAGCTAC 1

RESULT 282
AAZ89196/c
ID AAZ89196 standard; DNA; 18 BP.
XX
XX AAZ89196;
AC
XX 09-JUN-2000 (first entry)
DT
XX Human riboprotein L21 reverse PCR primer.
XX
XX Human; expression profile: Three Prime End Amplification; TPEA;
XX riboprotein L21; RFL21; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200008208-A2.
PN
XX 17-FEB-2000.
XX
XX 05-AUG-1999; 99WO-GB002579.
XX
XX 05-AUG-1998; 98GB-00017055.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
PA
XX Freeman TC, Richardson PJ, Dixon AK;
PI
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XX
DR WPI; 2000-224033/19.
XX
XX Reverse transcription of mRNA species used for expression profiling of
XX single cells by employing a first heeled primer to provide first strand
XX cDNA species and then a second heeled primer population to generate
XX second strand cDNAs.
XX
XX Example 1; Page 29; 50pp; English.
XX
XX This invention describes a novel process (M1) of reverse transcribing
XX mRNA species present in a sample from an organism by: (a) reverse
XX transcribing the mRNA species using a first heeled primer, to provide a
XX first strand cDNA species; and (b) synthesizing second cDNA species using
XX a second heeled primer population, the nucleotide sequences of the non-
XX heel portions of the second heeled primers being such that the reverse
XX transcribed first strand cDNA species are capable of hybridizing to at
XX least one second primer. The processes can be used for expression
XX profiling of single cells. The polynucleotide comprising an oligo d(T)
XX sequence and a heel sequence 5' can be used for the reverse transcription
XX of mRNA species in a sample. The polynucleotide primer population of
XX claim (4) can be used for the synthesis of second strand cDNA from a
XX population of first strand cDNA species. Single cell cDNA libraries can
XX be made for subsequent detailed analysis of gene expression and the
XX discovery of novel genes. Small samples can be used and allow the
XX utilization of the large amount of sequence data available for further
XX understanding of disease processes and the cellular physiology of complex
XX issues. The invention provides a rapid, robust and reproducible procedure
XX called Three Prime End Amplification (TPEA), optionally with PCR (TPEA-
XX PCR). Prior art methods for the analysis of gene expression within single
XX cells or small tissue samples are limiting. Whilst in situ hybridization
XX techniques provide detailed information about the cellular expression
XX pattern of a gene in intact tissue the technique is laborious and unable
XX to analyze multiple transcripts in a single preparation. The methods
XX presented in the disclosure provide a more straightforward, reproducible
XX and reliable cDNA amplification procedure for small mRNA samples where
XX expression profiling can be conducted. The amplification technique can be
XX carried out in a single tube with a need for only limited manual
XX intervention and large numbers of samples can be analyzed. There is a
XX bias towards more uniform length cDNA molecules ensuring that even
XX relatively low abundance mRNA species are transcribed and optionally
XX amplified at the same level of efficiency as more abundant mRNA species.
XX AAZ89191-289253 represent the primers described in the method of the
XX invention
XX
XX Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
SQ
    Query Match      0.4%; Score 14.8; DB 1; Length 18;
    Best Local Similarity 88.9%; Pred. No. 2.1e+02;
    Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 536 GATCCTGAGCTGCAGGAA 553
DB 18 GAGCCTGAGCTGCTGGAA 1

RESULT 283
AAZ88307/c
ID AAF88307 standard; DNA; 18 BP.
XX
XX AAF88307;
AC
XX 22-AUG-2001 (first entry)
DT
XX C. officinalis calendulic acid desaturase primer 1.
XX
XX Calendula; calendulic acid desaturase; unsaturated fatty acid; oil;
XX triglyceride; transgenic plant; primer; ss.
XX
XX Calendula officinalis.
OS
XX DE19941609-A1.
PN
XX
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PD 08-MAR-2001.
XX
XX
XX 01-SEP-1999; 99DE-01041609.
XX
XX 01-SEP-1999; 99DE-01041609.
XX
XX (IPBP-) IPB INST PFLANZENBIOCHEMIE.
XX
XX Feussner I, Hornung E, Fritsche K, Peitzsch N, Renz A;
XX
XX WPI; 2001-283028/30.
XX
XX New nucleic acid sequence encoding Calendula officinalis calendulic acid
XX desaturase, useful for e.g. producing transgenic plants having oil with
XX an increased unsaturated fatty acid content,.
XX
XX Example 3; Page 10; 22pp; German.
XX
XX This invention describes a novel isolated nucleic acid sequence (I)
XX encoding a Calendula officinalis calendulic acid desaturase polypeptide.
XX The invention also describes (1) a process for producing unsaturated
XX fatty acids, comprising introducing at least one copy of (I) or (II) into
XX an oil-producing organism, growing the organism, isolating oil from the
XX organism and releasing fatty acids from the oil; (2) a process for
XX producing triglycerides with an increased unsaturated fatty acid content,
XX comprising introducing at least one copy of (I) or (II) into an oil-
XX producing organism, growing the organism and isolating oil from the
XX organism; (3) a process for producing saturated fatty acids, comprising
XX introducing at least one nonfunctional copy of (I) or (II) into an oil-
XX producing organism, growing the organism, isolating oil from the organism
XX and releasing fatty acids from the oil; (4) a process for producing
XX triglycerides with an increased saturated fatty acid content, comprising
XX introducing at least one nonfunctional copy of (I) or (II) into an oil-
XX producing organism, growing the organism and isolating oil from the
XX organism; (5) an enzyme capable of converting a diunsaturated fatty acid
XX of to a triunsaturated fatty acid. Transgenic organisms (especially
XX plants) containing one or more copies of (I) are useful for producing
XX oils with an increased unsaturated fatty acid content. Transgenic
XX organisms (especially plants) containing one or more nonfunctional copies
XX of (I) are useful for producing oils with an increased saturated fatty
XX acid content. (I) and fragments of (I) are also useful for isolating
XX genomic sequences by homology screening. This sequence represents a
XX primer used in the isolation of the calendulic acid desaturase described
XX in the method of the invention
XX
XX Sequence 18 BP; 1 A; 5 C; 4 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. NO. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 42 AATTCAGCGAGAAGATCG 59
Db 18 AATACAGCGAGAAGACCG 1
RESULT 284
AAS20963
ID AAS20963 standard; DNA; 18 BP.
XX
XX AAS20963;
XX
XX 09-APR-2002 (first entry)
XX
XX PCR primer Igf2r-I2 relating to gene imprinting invention.
XX
XX Human; genomic imprinting; pluripotent mouse embryonic germ cell line;
XX EG; methylated CpG island; DNA methylation; gene imprinting;
XX post-translational modification of histone; cancer; birth defect;
XX diabetes; aberrant imprinting; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX
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PN WO200190313-A2.
XX
XX 29-NOV-2001.
XX
XX 22-MAY-2001; 2001WO-US016253.
XX
XX 22-MAY-2000; 2000US-0206158P.
XX
XX 22-MAY-2000; 2000US-0206161P.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Feinberg A, Strichman-Almashanu L, Jiang S;
XX WPI; 2002-083100/11.
XX
XX Forming embryonic germ cells useful as model system to study imprinting
XX involves mating genetically divergent male and female mammal of same
XX species, dissecting and dissociating embryo obtained from pregnant
XX mammal.
XX
XX Disclosure; Page 54; 125pp; English.
XX
XX The present invention relates to a model system for genomic imprinting
XX using pluripotent mouse embryonic germ (EG) cell lines derived from an
XX interspecific cross. Also disclosed is a library containing methylated
XX CpG islands and a method for assaying methylation in one or more
XX impritable genes. The gene imprinting assay is carried out by single-
XX strand conformation polymorphism (SSCP), quantitative sequencing, single
XX nucleotide primer extension or hot stop PCR. The assays are carried out
XX to determine the post-translational modification of histones. The method
XX further involves identifying a test substance as a candidate drug for
XX treating cancer if the test substance enhances imprinting of a gene whose
XX imprinting is lost in cancer, or if the test substance inhibits
XX imprinting of a gene whose imprinting is gained in cancer. The methylated
XX CpG islands are useful for providing an assessment of the risk of
XX developing cancer, or for providing diagnostic information relative to
XX cancer which involves determining the methylation status of the CpG
XX island in a patient's DNA. The EG cells allow the accession of imprinted
XX genes which are useful for detecting birth defects, diabetes and cancers
XX associated with aberrant imprinting. The EG cell lines represent the
XX first in vitro model system in which genomic imprinting can be followed
XX dynamically and the two alleles can be distinguished. AAS20953-AAS20969
XX represent PCR primers described in the present invention
XX
XX Sequence 18 BP; 1 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. NO. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1024 CTCCTCTGCTGGACCATC 1041
Db 1 CTCCTCTGCTGGGCGCATC 18
RESULT 285
ABT04994
ID ABT04994 standard; DNA; 18 BP.
XX
XX ABT04994;
XX
XX 11-OCT-2002 (first entry)
XX
XX TNFR1 expression modulation related antisense oligo SEQ ID No 24.
XX
XX Antisense compound; tumour necrosis factor receptor 1; liver disease;
XX TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
XX human; ds.
XX
XX Homo sapiens.
XX
XX WO200248168-A1.
XX
XX
```


CC the gene with intronic primers for the human MLH1 gene and analysing the
 CC sequence to identify any mutants; (3) a method of identifying mutants in
 CC splice donor or acceptor sites of a human MSH2 gene, comprising
 CC sequencing splice donor or acceptor sites of the gene with intronic
 CC primers for the human MSH2 gene and analysing the sequence to identify
 CC any mutants; and (4) a transgenic model system for colorectal cancer
 CC comprising cells expressing the variant MLH1 or MSH2 gene. The hMLH1 and
 CC hMSH2 variants are used to diagnose or determine a patient's
 CC susceptibility to hereditary non-polyposis colorectal cancer. ABL01648 to
 CC ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene
 CC fragments from the present invention. ABL01832 to ABL01839 represent
 CC mutagenic primers used in the exemplification of the present invention
 XX
 XX
 SQ Sequence 18 BP; 7 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1223 CAAAAGCCTCAGGATCTC 1240
 ||||| ||||| ||||| |||||
 Db 1 CAAAAGCTTCAGATCTC 18

RESULT 288

ABX80015
 ID ABX80015 standard; cDNA; 18 BP.

XX AC ABX80015;

DT 17-APR-2003 (first entry)

XX DE EST polymorphic DNA repeat polynucleotide #340.

XX KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
 KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
 KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
 KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
 KW Friedreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
 KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX OS Homo sapiens.

XX PN US6472154-B1.

XX PD 29-OCT-2002.

XX PF 31-DEC-1999; 99US-00475947.

XX PR 31-DEC-1999; 99US-00475947.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Garner HR, Wren JD, Minna JD, Fondon JW;

XX DR WPI; 2003-208818/20.

XX PT Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.

XX PS Example; Col 1165; 588pp; English.

XX CC The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic

CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 XX
 SQ Sequence 18 BP; 5 A; 8 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428
 ||||| ||||| ||||| |||||
 Db 1 GCAGCAGCAGCCCCAGCA 18

RESULT 289

AA556267

ID AAD56267 standard; DNA; 18 BP.

XX AC AAD56267;

XX DT 07-AUG-2003 (first entry)

XX DE Hepatitis E virus target oligonucleotide #2.

XX KW Antiviral; viral infection; antisense therapy; virucide; ss.

XX OS Hepatitis E virus.

XX PN WO2003033657-A2.

XX PD 24-APR-2003.

XX PF 16-OCT-2002; 2002WO-US032868.

XX PR 16-OCT-2001; 2001US-0329815P.

XX PA (AVIB-) AVI BIOPHARMA INC.

XX PI Stein DA, Skilling DE, Iversen PL, Smith AW;

XX DR WPI; 2003-403210/38.

XX PT New antiviral compound directed against RNA viruses, e.g. picornavirus,
 PT comprising morpholino oligomer, supporting sequence complementary to
 PT viral target sequence that spans first open reading frame of virus
 PT genome.

XX PS Example 4; Page 41; 63pp; English.

XX CC The invention relates to antisense antiviral compounds and methods of
 CC their use in inhibition of growth of viruses of the picornavirus, of
 CC calicivirus, togavirus or flavivirus families as in treatment of viral
 CC infection. The antiviral compound is useful for inhibiting replication of
 CC an RNA virus. The method is useful for determining the effectiveness of
 CC treating a picornavirus, calicivirus, togavirus or flavivirus infection.
 CC It is also useful for determining the family or genus of an infecting
 CC picornavirus, calicivirus, togavirus or flavivirus. Determining the
 CC family or genus of an infecting virus is useful for identifying a
 CC specific infecting picornavirus, calicivirus, togavirus or flavivirus.
 CC The invention is used in antisense therapy. The present sequence is
 CC Hepatitis E virus target oligonucleotide used to illustrate the method of
 CC the invention

XX SQ Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1271 GCCATGAGCCCGTCAG 1288
Db 1 GCCATGAGCCCGTCAG 18
|||||
RESULT 290
AAD56287/c
ID AAD56287 standard; DNA; 18 BP.
XX AC
XX AD56287;
XX 07-AUG-2003 (first entry)
XX DT
XX DE Hepatitis E virus targeting antisense oligonucleotide #2.
XX DE
XX KW Antiviral; viral infection; antisense therapy; virucide; antisense; ss.
XX OS Hepatitis E virus.
XX PN WO2003033657-A2.
XX PD
XX PD 24-APR-2003.
XX PF
XX PF 16-OCT-2002; 2002WO-US032868.
XX XX
XX PR 16-OCT-2001; 2001US-0329815P.
XX PA (AVIB-) AVI BIOPHARMA INC.
XX PI Stein DA, Skilling DE, Iversen PL, Smith AW;
XX DR WPI; 2003-403210/38.
XX PT New antiviral compound directed against RNA viruses, e.g. picornavirus,
XX PT comprising morpholino oligomer, supporting sequence complementary to
XX PT viral target sequence that spans first open reading frame of virus
XX PT genome.
XX PS Claim 12; Page 23; 63pp; English.
XX CC The invention relates to antisense antiviral compounds and methods of
XX CC their use in inhibition of growth of viruses of the picornavirus,
XX CC calicivirus, togavirus or flavivirus families as in treatment of viral
XX CC infection. The antiviral compound is useful for inhibiting replication of
XX CC an RNA virus. The method is useful for determining the effectiveness of
XX CC treating a picornavirus, calicivirus, togavirus or flavivirus infection.
XX CC It is also useful for determining the family or genus of an infecting
XX CC picornavirus, calicivirus, togavirus or flavivirus. Determining the
XX CC family or genus of an infecting virus is useful for identifying a
XX CC specific infecting picornavirus, calicivirus, togavirus or flavivirus.
XX CC The invention is used in antisense therapy. The present sequence is
XX CC Hepatitis E virus targeting antisense oligonucleotide used to illustrate
XX CC the method of the invention
XX SQ Sequence 18 BP; 2 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1271 GCCATGAGCCCGTCAG 1288
Db 18 GCCATGAGCCCGTCAG 1
|||||
RESULT 291
ADC69962
ID ADC69962 standard; DNA; 18 BP.
XX AC
XX AC ADC69962;
XX XX
XX DT 18-DEC-2003 (first entry)
XX OS
XX ES Escherichia coli.

Primer oligo used for analysing CpG islands in genomic DNA (SeqID 451).
PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;
adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;
cytosine methylation state.
Unidentified.
WO2003052135-A2.
26-JUN-2003.
10-DEC-2002; 2002WO-EP014026.
14-DEC-2001; 2001DE-01061625.
(EPIG-) EPIGENOMICS AG.
Burger M, Field JK, Genc B, Liloglou T, Lipscher E, Maier S;
Nimmrich I;
WPI; 2003-533029/50.
Detecting and differentiating cytosine methylation state of genomic DNA,
useful for diagnosing, treating prognosticating and/or monitoring lung
cell proliferative disorders e.g. adenocarcinoma and squamous cell
carcinoma.
Claim 15; SEQ ID NO 451; 58pp; English.
This invention relates to a novel method for detecting and
differentiating between lung cell proliferative disorders associated with
at least one gene and/or their regulatory regions. Specifically, it
refers to a method comprising contacting a target nucleic acid in a
biological sample with at least one reagent, wherein the reagent is able
to distinguish between methylated and non-methylated CpG dinucleotides
present in the target DNA. As such, it is possible to further
differentiate and diagnose medical conditions including adenocarcinoma
and squamous cell carcinoma, and their respective adjacent lung tissue.
The present invention describes cytostatic oligomers and PNA-oligomers
that are useful as probes for determining the cytosine methylation state
or single nucleotide polymorphisms (SNPs) of the target sequence. This
oligonucleotide sequence is a primer oligomer used for the analysis of
CpG positions within genomic DNA, used in an exemplification of the
invention.
Sequence 18 BP; 3 A; 0 C; 5 G; 10 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3583 TATAGTTTGTGGAGT 3600
Db 1 TTAGGTTTGTGGAGT 18
|||||
RESULT 292
ADD28828/c
ID ADD28828 standard; DNA; 18 BP.
XX AC
XX AC ADD28828;
XX DT
XX DT 15-JAN-2004 (first entry)
XX DE Escherichia coli 0157:H7 VNTR amplicon sequence SEQ ID NO:447.
XX KW molecular sub-typing system; Escherichia coli;
XX KW variable number tandem repeat; VNTR; genetic data;
XX KW epidemiological database; research; gene; ds.
XX OS
XX ES Escherichia coli.

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PN WO2003050269-A2.
 XX 19-JUN-2003.
 XX 11-DEC-2002; 2002WO-US039914.
 XX 11-DEC-2001; 2001US-0339687P.
 XX (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P.
 PA (KEYS/) KEYS C.
 XX Keim P, Keys C;
 XX WPI; 2003-864934/80.
 XX Molecular sub-typing system for Escherichia coli, comprises observing and
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA
 PT sample.
 PS Claim 7; SEQ ID NO 447; 166pp; English.
 XX The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (1) for sub-typing E. coli O157:H7; (2) primers
 CC (II) for amplifying (1); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails
 CC of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
 CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
 CC producing discrete genetic data for an epidemiological database. (I) is
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an E. coli VNTR loci related
 CC amplicon sequence which is used in the exemplification of the present
 CC invention.
 XX Sequence 18 BP; 0 A; 2 C; 4 G; 12 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1579 ACAACAGCAACACAGCA 1596
 Db 18 AAAACAGCAACACAGCA 1
 RESULT 293
 ADD28830/c
 ID ADD28830 standard; DNA; 18 BP.
 XX ADD28830;
 AC ADD28830;
 XX 15-JAN-2004 (first entry)
 DT Escherichia coli O157:H7 VNTR amplicon sequence SEQ ID NO:449.
 DE molecular sub-typing system; Escherichia coli;
 XX

KW variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; gene; ds.
 XX Escherichia coli.
 OS WO2003050269-A2.
 PN 19-JUN-2003.
 XX 11-DEC-2002; 2002WO-US039914.
 XX 11-DEC-2001; 2001US-0339687P.
 XX (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P.
 PA (KEYS/) KEYS C.
 XX Keim P, Keys C;
 XX WPI; 2003-864934/80.
 XX Molecular sub-typing system for Escherichia coli, comprises observing and
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA
 PT sample.
 PS Claim 7; SEQ ID NO 449; 166pp; English.
 XX The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (1) for sub-typing E. coli O157:H7; (2) primers
 CC (II) for amplifying (1); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails
 CC of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
 CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC coli O157:H7 strains by multiplex, comprising (III), and amplifying
 CC reagents for maintaining hybridisation and amplification condition in a
 CC multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub
 CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
 CC producing discrete genetic data for an epidemiological database. (I) is
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an E. coli VNTR loci related
 CC amplicon sequence which is used in the exemplification of the present
 CC invention.
 XX Sequence 18 BP; 0 A; 2 C; 4 G; 12 T; 0 U; 0 Other;
 SQ Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1579 ACAACAGCAACACAGCA 1596
 Db 18 AAAACAGCAACACAGCA 1
 RESULT 294
 ADD28831
 ID ADD28831 standard; DNA; 18 BP.
 XX ADD28831;
 AC ADD28831;
 XX

DT 15-JAN-2004 (first entry)
 XX Escherichia coli 0157:H7 VNTR amplicon sequence SEQ ID NO:450.
 DE molecular sub-typing system; Escherichia coli;
 XX variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; gene; ds.
 KW Escherichia coli.
 XX WO2003050269-A2.
 XX 19-JUN-2003.
 XX 11-DEC-2002; 2002WO-US039914.
 XX 11-DEC-2001; 2001US-0339687P.
 XX (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P.
 PA (KEYS/) KEYS C.
 XX Keim P, Keys C;
 XX WPI; 2003-864934/80.
 XX Molecular sub-typing system for Escherichia coli, comprises observing and
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA
 PT sample.
 XX Claim 7; SEQ ID NO 450; 166pp; English.
 XX The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (I) for sub-typing E. coli O157:H7; (2) primers
 CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails
 CC (III) for multiplex amplification of (I) comprising two or more primers
 CC of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
 CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC coli O157:H7 strains by multiplex, comprising (III), and amplifying
 CC reagents for maintaining hybridisation and amplification condition in a
 CC multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub
 CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
 CC producing discrete genetic data for an epidemiological database. (I) is
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an E. coli VNTR loci related
 CC amplicon sequence which is used in the exemplification of the present
 CC invention.
 XX Sequence 18 BP; 12 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1579 ACAACAGCAACAACAGCA 1596
 Db 1 AAAAAAGCAAAAAACAGCA 18

RESULT 295

ADD28829
 ID ADD28829 standard; DNA; 18 BP.
 XX
 AC ADD28829;
 XX
 DT 15-JAN-2004 (first entry)
 XX Escherichia coli 0157:H7 VNTR amplicon sequence SEQ ID NO:448.
 DE molecular sub-typing system; Escherichia coli;
 KW variable number tandem repeat; VNTR; genetic data;
 KW epidemiological database; research; gene; ds.
 XX Escherichia coli.
 OS
 XX WO2003050269-A2.
 XX 19-JUN-2003.
 XX 11-DEC-2002; 2002WO-US039914.
 XX 11-DEC-2001; 2001US-0339687P.
 XX (UYAR-) UNIV ARIZONA.
 PA (KEIM/) KEIM P.
 PA (KEYS/) KEYS C.
 XX Keim P, Keys C;
 XX WPI; 2003-864934/80.
 XX Molecular sub-typing system for Escherichia coli, comprises observing and
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA
 PT sample.
 XX Claim 7; SEQ ID NO 448; 166pp; English.

The present invention describes a molecular sub-typing system (S) for
 CC Escherichia coli, which comprises observing and recording variable number
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also
 CC described: (1) VNTR loci (I) for sub-typing E. coli O157:H7; (2) primers
 CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus
 CC comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails
 CC (III) for multiplex amplification of (I) comprising two or more primers
 CC of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for
 CC maintaining hybridisation and amplification condition in a PCR instrument
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.
 CC coli O157:H7 strains by multiplex, comprising (III), and amplifying
 CC reagents for maintaining hybridisation and amplification condition in a
 CC multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub
 CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more
 CC primers for amplifying loci comprising VNTR, where the primers have an
 CC observable indicator; (b) obtaining single-stranded sample DNA from the
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA
 CC and amplifying reagents under hybridising and amplifying conditions in a
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)
 CC separating the amplicons by size; (e) evaluating numbers and sizes of
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for
 CC producing discrete genetic data for an epidemiological database. (I) is
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.
 CC coli. The present sequence represents an E. coli VNTR loci related
 CC amplicon sequence which is used in the exemplification of the present
 CC invention.

Sequence 18 BP; 12 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1579 ACAACAGCAACAACAGCA 1596

```
Db      1  AAAACAGCAAAAACAGCA 18
|||||
RESULT 296
ABZ97839
ID      ABZ97839 standard; DNA; 18 BP.
XX
AC      ABZ97839;
XX
DT      17-OCT-2003 (first entry)
XX
DE      Human eotaxin oligonucleotide sequence.
XX
KW      Human; antisense; lung dysfunction; nasal airway dysfunction;
KW      antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
KW      antiasthmatic; hypotensive; immunosuppressive; cycostatic; gene therapy;
KW      antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW      adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW      lung inflammation; respiratory disease; ds.
XX
OS      Homo sapiens.
XX
PN      WO200285308-A2.
XX
PD      31-OCT-2002.
XX
PF      23-APR-2002; 2002WO-US013135.
XX
PR      24-APR-2001; 2001US-0286137P.
XX
PA      (EPIG-) EPIGENESIS PHARM INC.
XX
PI      Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI      Miller S, Tang L, Shahabuddin S;
XX
WPI; 2003-229219/22.
XX
PT      Pharmaceutical composition for treating ailments associated with impaired
PT      respiration, has oligo(s) antisense to specific gene(s) or its
PT      corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT      ubiquinone.
XX
PS      Disclosure; SEQ ID NO 13081; 872pp; English.
XX
CC      The invention relates to a novel pharmaceutical composition, which has a
CC      first active agent comprising an oligonucleotide antisense to the
CC      initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC      5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC      junctions of genes encoding a polypeptide associated with lung and/or
CC      nasal airway dysfunction and a second active agent comprising an
CC      antiinflammatory steroid and ubiquinone. A composition of the invention
CC      has antiinflammatory, antiasthmatic, hypotensive,
CC      immunosuppressive, and cycostatic activity. The composition may have a
CC      use in antisense gene therapy. The composition is useful for treating or
CC      preventing a respiratory, lung or malignant disease or condition, also
CC      for enhancing the prophylactic or therapeutic respiratory effect of an
CC      antiinflammatory steroid in a subject, for reducing or depleting levels
CC      of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC      receptor, producing bronchodilation, increasing levels of ubiquinone or
CC      lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC      lung inflammation, lung allergies, or a respiratory disease or condition.
CC      Note: The sequence data for this patent is not represented in the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1183 CCCCTCAGCCCGGTTGG 1200

Db      1  AAAACAGCAAAAACAGCA 18
|||||
RESULT 297
ADM92720
ID      ADM92720 standard; DNA; 18 BP.
XX
AC      ADM92720;
XX
DT      03-JUN-2004 (first entry)
XX
DE      SNP-containing cardiovascular associated gene primer #50.
XX
KW      SNP; single nucleotide polymorphism; cardiovascular associated gene;
KW      allelic variation; atherosclerosis; ischemia; reperfusion; hypertension;
KW      restenosis; arterial inflammation; myocardial infarction; stroke; primer;
KW      ss.
XX
OS      Homo sapiens.
XX
PN      WO2003057911-A2.
XX
PD      17-JUL-2003.
XX
PF      07-JAN-2003; 2003WO-EP0000060.
XX
PR      08-JAN-2002; 2002EP-00000153.
XX
PA      (FARB ) BAYER AG.
XX
PI      Stropp U, Schwerts S, Kallabis H;
XX
WPI; 2003-577532/54.
XX
PT      New isolated polynucleotides comprising single nucleotide polymorphisms
PT      of the cardiovascular gene, useful for assessing predisposition or
PT      susceptibility to a cardiovascular disease, e.g. atherosclerosis,
PT      restenosis or stroke.
XX
PS      Disclosure; Page 68; 187pp; English.
XX
CC      The invention relates an isolated polynucleotide (I) encoded by a
CC      cardiovascular associated (CA) gene, having allelic variation contained
CC      in a functional surrounding like full length cDNA for CA gene
CC      polypeptide, and with or without the CA gene promoter sequence. (I) is a
CC      polynucleotide comprising single nucleotide polymorphisms predicting
CC      cardiovascular disease. The polynucleotides are useful for assessing
CC      predisposition or susceptibility to a cardiovascular disease, e.g.
CC      atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial
CC      inflammation, myocardial infarction, and stroke. These may also be used
CC      to predict personal medication schemes omitting adverse drug reactions,
CC      or as probes for detecting genetic polymorphisms and as templates for the
CC      recombinant production of normal or variant peptides/polypeptides encoded
CC      by the genes. This sequence corresponds to a PCR primer to amplify one of
CC      the genes of the invention.
XX
SQ      Sequence 18 BP; 1 A; 8 C; 1 G; 8 T; 0 U; 0 Other;
Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1344 CTTCTGTTTGGCCTTCCC 1361
|||||
Db      1  CTTCTGTTTGGCCTTCCC 18
|||||
RESULT 298
ADM92724
ID      ADM92724 standard; DNA; 18 BP.
XX
AC      ADM92724;
XX
```

XX 03-JUN-2004 (first entry)
 XX SNP-containing cardiovascular associated gene primer #54.
 XX
 XX SNP; single nucleotide polymorphism; cardiovascular associated gene;
 KW allelic variation; atherosclerosis; ischemia; reperfusion; hypertension;
 KW restenosis; arterial inflammation; myocardial infarction; stroke; primer;
 KW ss.
 XX Homo sapiens.
 OS WO2003057911-A2.
 XX 17-JUL-2003.
 XX 07-JAN-2003; 2003WO-EP000060.
 XX 08-JAN-2002; 2002EP-00000153.
 XX (FARB) BAYER AG.
 XX Stropp U, Schwes S, Kallabis H;
 XX WPI; 2003-577532/54.
 XX New isolated polynucleotides comprising single nucleotide polymorphisms
 PT of the cardiovascular gene, useful for assessing predisposition or
 PT susceptibility to a cardiovascular disease, e.g. atherosclerosis,
 PT restenosis or stroke.
 XX Disclosure; Page 68; 187pp; English.
 XX The invention relates an isolated polynucleotide (I) encoded by a
 CC cardiovascular associated (CA) gene, having allelic variation contained
 CC in a functional surrounding like full length cDNA for CA gene
 CC polypeptide, and with or without the CA gene promoter sequence. (I) is a
 CC polynucleotide comprising single nucleotide polymorphisms predicting
 CC cardiovascular disease. The polynucleotides are useful for assessing
 CC predisposition or susceptibility to a cardiovascular disease, e.g.
 CC atherosclerosis, ischemia/reperfusion, hypertension, restenosis, arterial
 CC inflammation, myocardial infarction, and stroke. These may also be used
 CC to predict personal medication schemes omitting adverse drug reactions,
 CC or as probes for detecting genetic polymorphisms and as templates for the
 CC recombinant production of normal or variant peptides/polypeptides encoded
 CC by the genes. This sequence corresponds to a PCR primer to amplify one of
 CC the genes of the invention.
 XX SQ Sequence 18 BP; 1 A; 8 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1344 CTTCTGTTTCCTCCCTCC 1361
 DB 1 CTTCTCTATGCTTCCTCC 18
 RESULT 299
 ADM77392
 ID ADM77392 standard; DNA; 18 BP.
 XX
 XX ADM77392;
 AC
 DT 03-JUN-2004 (first entry)
 XX Human fibrocystin (PKHD1) gene DHPLC PCR primer #100.
 DE human; fibrocystin;
 XX treating autosomal recessive polycystic kidney disease; PKHD1; DHPLC PCR;
 KW ss; primer.
 XX

OS Homo sapiens.
 XX WO2003062453-A2.
 XX 31-JUL-2003.
 XX 23-JAN-2003; 2003WO-US002038.
 XX 23-JAN-2002; 2002US-0351110P.
 XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
 XX Harris PC, Ward CJ, Rossetti S, Torres VE;
 PI WPI; 2003-618286/58.
 DR
 XX New isolated nucleic acid comprising a sequence encoding a fibrocystin
 PT polypeptide, useful for diagnosing and treating autosomal recessive
 PT polycystic kidney disease.
 XX Example 4; SEQ ID NO 147; 136pp; English.
 XX The invention comprises the amino acid and coding sequences of
 CC fibrocystin proteins. The DNA and protein sequences of the invention are
 CC useful for diagnosing and treating autosomal recessive polycystic kidney
 CC disease. The present DNA sequence represents a DHPLC PCR primer that was
 CC used to screen for mutations in the human fibrocystin (PKHD1) gene.
 XX SQ Sequence 18 BP; 12 A; 5 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1575 AACACACACACACACAC 1592
 DB 1 AACACACACACACACAC 18
 RESULT 300
 ABD30870
 ID ABD30870 standard; DNA; 18 BP.
 XX
 XX ABD30870;
 AC
 DT 29-JUL-2004 (first entry)
 XX Human eotaxin-derived oligonucleotide SEQ ID 13081.
 DE Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ss; primer.
 XX Homo sapiens.
 OS
 XX WO200285309-A2.
 XX 31-OCT-2002.
 PD
 XX 23-APR-2002; 2002WO-US013143.
 PF
 XX 24-APR-2001; 2001US-0286036P.
 PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX

DR WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
XX oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX Claim 15; SEQ ID NO 13081; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposcretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
XX Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1183 CCCCTCAGCCAGGTGG 1200
Db 1 CCCCTCAGCTCAGTGG 18

RESULT 301
ADJ59713
ID ADJ59713 standard; DNA; 18 BP.
XX
XX AC ADJ59713;
XX
XX 06-MAY-2004 (first entry)
XX
XX Concatemer of Eotaxin U46573 oligonucleotides.
DE
XX
XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; ds.
XX
XX Homo sapiens.
XX
XX WO2004011613-A2.
XX
XX 05-FEB-2004.
XX
XX 25-JUL-2003; 2003WO-US023509.

XX 29-JUL-2002; 2002US-0399076P.
PR (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX
XX WPI; 2004-203534/19.
DR
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
PT initiation codons and introns of respiratory disease-relevant genes e.g.,
PT CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
PT disease e.g., asthma.
XX
XX Claim 2; SEQ ID NO 569; 85pp; English.
PS
XX The present invention relates to an oligonucleotide anti-sense to e.g.,
CC initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
CC end of nucleic acid target comprising gene(s) chosen from e.g.
CC interleukin (IL)-4 receptor, IL-5 receptor or salts of the
CC oligonucleotide and optionally surfactant operatively linked to the
CC oligonucleotide. The method is useful for preventing or treating a
CC respiratory or lung disease, which involves administering to the airways
CC of a subject an effective amount of an inhibitor. The oligonucleotide is
CC useful for production of a medicament for the prevention and/or treatment
CC of a respiratory or lung disease. The respiratory or lung disease is
CC chosen from airway inflammation, allergy(ies), asthma, impeded
CC respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
CC (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
CC (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
CC obstruction. The present sequence represents a concatemer of
CC oligonucleotides of the invention.
XX
XX Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1183 CCCCTCAGCCAGGTGG 1200
Db 1 CCCCTCAGCTCAGTGG 18

RESULT 302
ADJ59712
ID ADJ59712 standard; DNA; 18 BP.
XX
XX AC ADJ59712;
XX
XX 06-MAY-2004 (first entry)
XX
XX Oligonucleotide associated to Eotaxin U46573 #1.
DE
XX
XX interleukin; IL-4 receptor; IL-5 receptor; lung disease;
KW airway inflammation; allergy; asthma; impeded respiration;
KW cystic fibrosis; acute respiratory distress syndrome;
KW pulmonary hypertension; lung inflammation; bronchitis; oligonucleotide;
KW ss.
XX
XX Homo sapiens.
XX
XX WO2004011613-A2.
XX
XX 05-FEB-2004.
XX
XX 25-JUL-2003; 2003WO-US023509.
XX
XX 29-JUL-2002; 2002US-0399076P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX

```

PI Nyce JW, Tang L, Sandrasagra A, Aguilar D, Miller S;
PI Shahabuddin S, Lu H, Cong H;
XX WPI; 2004-203534/19.
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
XX initiation codons and introns of respiratory disease-relevant genes e.g.,
XX CCR1, RANTES, MCP4, useful for prophylaxis or treating respiratory
XX disease e.g., asthma.
XX Claim 2; SEQ ID NO 568; 85pp; English.
XX The present invention relates to an oligonucleotide anti-sense to e.g.,
XX initiation codon, coding region with 2-10 nucleotides of 5'-end and 3'-
XX end of nucleic acid target comprising gene(s) chosen from e.g.
XX interleukin (IL)-4 receptor, IL-5 receptor or salts of the
XX oligonucleotide and optionally surfactant operatively linked to the
XX oligonucleotide. The method is useful for preventing or treating a
XX respiratory or lung disease, which involves administering to the airways
XX of a subject an effective amount of an inhibitor. The oligonucleotide is
XX useful for production of a medicament for the prevention and/or treatment
XX of a respiratory or lung disease. The respiratory or lung disease is
XX chosen from airway inflammation, allergy(ies), asthma, impeded
XX respiration, cystic fibrosis (CF), chronic obstructive pulmonary diseases
XX (COPD), allergic rhinitis (AR), acute respiratory distress syndrome
XX (ARDS), pulmonary hypertension, lung inflammation, bronchitis, airway
XX obstruction. The present sequence represents an oligonucleotide of the
XX invention.
XX Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1183 CCCCTCAGCCAGGTTGG 1200
Db 1 CCCCTCAGCTCAGTGTGG 18
XX
RESULT 303
ADO45203
ID ADO45203 standard; DNA; 18 BP.
XX
XX ADO45203;
XX
XX 15-JUL-2004 (first entry)
XX Human oligonucleotide #569.
XX
XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
XX CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
XX tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
XX lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
XX asthma; lung allergy; inflammation; inflammatory disease;
XX airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
XX chronic obstructive pulmonary disease; COPD; allergic rhinitis;
XX acute respiratory distress syndrome; pulmonary hypertension;
XX lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
XX Homo sapiens.
XX
XX US2004049022-A1.
XX
XX 11-MAR-2004.
XX
XX 25-JUL-2003; 2003US-00627930.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 23-APR-2002; 2002WO-US013143.
XX
XX (NYCE/) NYCE J W.
XX (SAND/) SANDRASAGRA A.

```

```

PA (TANG/) TANG L.
PA (AGUI/) AGUILAR D.
PA (MILL/) MILLER S.
PA (SHAH/) SHAHABUDDIN S.
PA (LUHH/) LU H.
PA (CONG/) CONG H.
XX
XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX WPI; 2004-293804/27.
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
XX initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
XX RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
XX asthma.
XX Claim 2; SEQ ID NO 569; 174pp; English.
XX
XX The invention relates to oligonucleotides anti-sense to an initiation
XX codon, coding region, 5' or 3' intron-exon junction, intron or region
XX with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
XX chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
XX -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
XX tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
XX also relates to a method of screening a candidate compound that binds to
XX one or more nucleic acid target(s) or expressed product(s), for the
XX prevention and/or treatment of a respiratory or lung disease. The
XX oligonucleotides are useful for reducing or inhibiting expression of a
XX gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
XX CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
XX tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
XX useful for preventing or treating a respiratory or lung disease. The
XX respiratory or lung disease is associated with hyper-responsiveness to
XX and/or increased levels of, adenosine and/or levels of adenosine A
XX receptor(s), and/or asthma and/or lung allergies associated with
XX inflammation or an inflammatory disease. The respiratory or lung disease
XX is chosen from airway inflammation, allergy, asthma, impeded respiration,
XX cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
XX allergic rhinitis, acute respiratory distress syndrome, pulmonary
XX hypertension, lung inflammation, bronchitis, airway obstruction or
XX bronchoconstriction. This sequence represents an oligonucleotide of the
XX invention.
XX
XX Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1183 CCCCTCAGCCAGGTTGG 1200
Db 1 CCCCTCAGCTCAGTGTGG 18
XX
RESULT 304
ADO45202
ID ADO45202 standard; DNA; 18 BP.
XX
XX ADO45202;
XX
XX 15-JUL-2004 (first entry)
XX Human oligonucleotide #568.
XX
XX Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
XX CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
XX tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
XX lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
XX asthma; lung allergy; inflammation; inflammatory disease;
XX airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
XX chronic obstructive pulmonary disease; COPD; allergic rhinitis;
XX acute respiratory distress syndrome; pulmonary hypertension;
XX
XX

```

```
KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX Homo sapiens.
XX US2004049022-A1.
XX 11-MAR-2004.
XX 25-JUL-2003; 2003US-00627930.
XX 23-APR-2002; 2002WO-US013135.
XX 23-APR-2002; 2002WO-US013143.
XX (NYCE/) NYCE J W.
XX (SAND/) SANDRASAGRA A.
XX (TANG/) TANG L.
XX (AGUI/) AGUILAR D.
XX (MILL/) MILLER S.
XX (SHAH/) SHAHABUDDIN S.
XX (LUHH/) LU H.
XX (CONG/) CONG H.
XX
XX Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
XX Shahabuddin S, Lu H, Cong H;
XX WPI; 2004-293804/27.
XX
XX Novel single or multiple target oligonucleotide anti-sense to e.g.
XX initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
XX RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
XX asthma.
XX
XX Claim 2; SEQ ID NO 568; 174pp; English.
XX
XX The invention relates to oligonucleotides anti-sense to an initiation
XX codon, coding region, 5' or 3' intron-exon junction, intron or region
XX with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
XX chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
XX -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
XX tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
XX also relates to a method of screening a candidate compound that binds to
XX one or more nucleic acid target(s) or expressed product(s), for the
XX prevention and/or treatment of a respiratory or lung disease. The
XX oligonucleotides are useful for reducing or inhibiting expression of a
XX gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
XX CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
XX tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
XX useful for preventing or treating a respiratory or lung disease. The
XX respiratory or lung disease is associated with hyper-responsiveness to
XX and/or increased levels of, adenosine and/or levels of adenosine A
XX receptor(s), and/or asthma and/or lung allergies associated with
XX inflammation or an inflammatory disease. The respiratory or lung disease
XX is chosen from airway inflammation, allergy, asthma, impeded respiration,
XX cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
XX allergic rhinitis, acute respiratory distress syndrome, pulmonary
XX hypertension, lung inflammation, bronchitis, airway obstruction or
XX bronchoconstriction. This sequence represents an oligonucleotide of the
XX invention.
XX
XX Sequence 18 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
XX Query Match 0.4%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1183 CCCCTCAGCCCGGTGG 1200
DB 1 CCCCTCAGCTCAGTGG 18
RESULT 305
ADR06027
ID ADR06027 standard; DNA; 18 BP.
```

```
XX ADR06027;
XX 21-OCT-2004 (first entry)
XX Human TNFR1 antisense oligonucleotide seqid 25.
XX cytostatic; gene therapy; apoptosis inhibitor;
XX radiation-induced apoptosis; tumour necrosis factor receptor 1; TNFR1;
XX human; antisense oligonucleotide; antisense technology; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..18
XX /mod_base= b
XX /mod_base= OTHER
XX /note= "OTHER= Phosphorothioate backbone"
XX modified_base 1..4
XX /mod_base= a
XX /mod_base= OTHER
XX /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
XX nucleotides"
XX modified_base 15..18
XX /mod_base= c
XX /mod_base= OTHER
XX /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
XX nucleotides"
XX US2004147471-A1.
XX 29-JUL-2004.
XX 06-NOV-2003; 2003US-00702817.
XX 26-JUN-1998; 98US-00106038.
XX 17-JUN-1999; 99WO-US013763.
XX 24-OCT-2000; 2000US-00695451.
XX (ZHAN/) ZHANG H.
XX Zhang H;
XX WPI; 2004-561407/54.
XX Inhibiting radiation-induced apoptosis in a cell or tissue comprises
XX administering to the cell or tissue an antisense oligonucleotide targeted
XX to a nucleic acid molecule encoding tumor necrosis factor receptor 1.
XX Example 10; SEQ ID NO 25; 24pp; English.
XX The invention describes a method of inhibiting radiation-induced
XX apoptosis in a cell or tissue comprising administering to the cell or
XX tissue an antisense oligonucleotide of 8-30 nucleotides in length
XX targeted to a nucleic acid molecule encoding tumour necrosis factor
XX receptor 1 (TNFR1). The method and antisense oligonucleotides are useful
XX for inhibiting radiation-induced apoptosis in a cell or tissue, and for
XX treating diseases associated with the expression of TNFR1. This sequence
XX represents a human tumour necrosis factor receptor 1 (TNFR1) antisense
XX oligonucleotide.
XX
XX Sequence 18 BP; 5 A; 6 C; 7 G; 0 T; 0 U; 0 Other;
XX Query Match 0.4%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 2.1e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 977 CAGCAGCACCAGCAGCAG 994
DB 1 CAGGAGCACCAGCGCAG 18
RESULT 306
```


KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 KW ss.

XX Rattus rattus.

XX OS W09523225-A2.

XX PN 31-AUG-1995.

XX PD 23-FEB-1995; 95WO-IB000156.

XX PF 23-FEB-1994; 94US-00201109.

XX PR 29-MAR-1994; 94US-00218934.

XX PR 07-APR-1994; 94US-00222795.

XX PR 15-APR-1994; 94US-00227958.

XX PR 15-APR-1994; 94US-00228041.

XX PR 18-MAY-1994; 94US-00245736.

XX PR 06-JUL-1994; 94US-00271280.

XX PR 15-AUG-1994; 94US-00291932.

XX PR 16-AUG-1994; 94US-00291433.

XX PR 17-AUG-1994; 94US-00292620.

XX PR 19-AUG-1994; 94US-00293520.

XX PR 02-SEP-1994; 94US-00300000.

XX PR 08-SEP-1994; 94US-00303039.

XX PR 23-SEP-1994; 94US-00311486.

XX PR 23-SEP-1994; 94US-00311749.

XX PR 28-SEP-1994; 94US-00314397.

XX PR 03-OCT-1994; 94US-00316771.

XX PR 07-OCT-1994; 94US-00319492.

XX PR 11-OCT-1994; 94US-00321993.

XX PR 04-NOV-1994; 94US-00334847.

XX PR 10-NOV-1994; 94US-00337608.

XX PR 28-NOV-1994; 94US-00345516.

XX PR 16-DEC-1994; 94US-00357577.

XX PR 23-DEC-1994; 94US-00363233.

XX PR 30-JAN-1995; 95US-00380734.

XX (RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Chowira B, Dorenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FE, Woolf T;
 XX WPI; 1995-351090/45.

XX Ribozymes having modified bases and methods for producing them - for use
 in inhibiting disease related genes.

XX Claim 2; Page 201; 407pp; English.

XX The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
 CC nucleotide base position indicated in the DE line. Regions of the mRNA
 CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 CC inhibit ICAM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 XX correct PI field.)

SQ Sequence 17 BP; 3 A; 7 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;

Best Local Similarity 75.0%; Pred. No. 2e+02; Indels 0; Gaps 0;

Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2349 GGCCACCTACTCTAGG 2364
 |||||:||||:
 DB 1 GGCCCCCUACCUAGG 16

RESULT 309
 AAT33778/c

ID AAT33778 standard; DNA; 17 BP.

XX AC AAT33778;

XX DT 19-DEC-1996 (first entry)

XX DE Primer/probe (CTA) used in manipulation of ob gene control region.

XX KW Ob gene; modulation; control region; cachexia; anorexia; wasting disease;
 KW hyperlipidaemia; hypercholesterolaemia; obesity; infertility;
 KW type II diabetes; ss.

XX OS Synthetic.

XX FN W09629405-A2.

XX PD 26-SEP-1996.

XX PF 19-MAR-1996; 96WO-US003808.

XX PR 20-MAR-1995; 95US-00408584.

XX PR 05-APR-1995; 95US-00418096.

XX PR 02-AUG-1995; 95US-00510584.

XX PR 30-OCT-1995; 95US-00558588.

XX PR 21-NOV-1995; 95US-0007390P.

XX PR 30-NOV-1995; 95US-0007721P.

XX PR 14-DEC-1995; 95US-0008601P.

XX (LIGA-) LIGAND PHARM INC.

XX (INSP) INST PASTEUR LILLE.

XX Briggs MR, Auwerx J, De Vos P, Staels B, Croston GE, Miller SG;
 DR WPI; 1996-443181/44.

XX Control regions isolated from human ob gene - useful in systems to
 identify modulators of ob gene expression, for treatment of anorexia,
 cachexia, diabetes, and obesity.

XX Disclosure; Page 33; 167pp; English.

XX The control regions of the ob gene can be used to identify compounds
 CC which modulate expression of the gene. A host having cachexia, anorexia
 CC or any wasting disease characterised by loss of appetite, insufficient
 CC food intake or body weight loss can be treated by administering a
 CC composition containing a down regulator of ob gene expression. The body
 CC weight or fat content of a host can be changed and a host having
 CC hyperlipidaemia, hypercholesterolaemia, type II diabetes, or obesity
 CC related infertility can be treated by administering a composition
 CC containing an up regulator of ob gene expression. Primers/probes used in
 CC the amplification/identification of the human ob gene control regions are
 CC listed in AAT33760-78

SQ Sequence 17 BP; 1 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.4%;

Best Local Similarity 93.8%; Score 14.4; DB 1; Length 17;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1269 CAGCCATGGAGCCCG 1284

DB 16 CAGGCATGGAGCCCG 1

RESULT 310

AAAX71238
ID AAAX71238 standard; RNA; 17 BP.
XX
AC AAAX71238;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hammerhead ribozyme substrate #250.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
XX WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 104; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 6 A; 2 C; 2 G; 0 T; 7 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 6; Mismatches 1;
OY 3494 AATTGCTCTAATAGA 3509
DB 1 AAUUGUCUUAUUGA 16
RESULT 311
AAA20589/c
ID AAA20589 standard; RNA; 17 BP.
XX
AC AAA20589;
XX
XX 19-JUN-2000 (first entry)
XX
DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:3815.
XX
KW Human; aryl hydrocarbon nuclear transporter; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;
ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
age related macular degeneration; inflammation; neovascular glaucoma;
myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;
Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
Homo sapiens.
WO9950403-A2.
07-OCT-1999.
24-MAR-1999; 99WO-US006507.
27-MAR-1998; 98US-0079678P.
(RIBO-) RIBOZYME PHARM INC.
Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
WPI; 1999-591315/50.
Novel ribozymes for modulating the synthesis, expression and/or stability
of an mRNA encoding an angiogenic factors.
Claim 55; Page 155; 305pp; English.
The present invention describes enzymatic nucleic acid molecules with RNA
cleaving activity, which specifically cleave RNA encoded by an aryl
hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
AAA19154 represent ribozyme sequences for tie-2, and AAA18386 to AAA19086
and AAA19155 to AAA19222 represent their corresponding target sequences;
and AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
AAA21596 to AAA21688 represent their corresponding target sequences;
and AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
sequences for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
AAA23342 represent their corresponding target sequences. The ribozymes of
the invention are used for modulating the synthesis, expression and/or
stability of an mRNA encoding angiogenic factor, especially ARNT,
integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
especially used to treat cancer, diabetic retinopathy, age related
macular degeneration (ARMD), inflammation, and arthritis, as well as
neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
and other syndromes and diseases related to the levels of ARNT, Tie-2,
integrin subunit alpha-6, or integrin subunit beta-3
Sequence 17 BP; 1 A; 3 C; 6 G; 0 T; 7 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1;
OY 1390 CCAACAGCAACAGCAG 1405
DB 17 CCAACAGCAACATCAG 2
RESULT 312
AAA25734/c
ID AAA25734 standard; DNA; 17 BP.
XX
AC AAA25734;
XX
DT 19-JUL-2000 (first entry)

```
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2232.
DE
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX WO9954459-A2.
PN
XX 28-OCT-1999.
PD
XX 19-APR-1999; 99WO-US008547.
PF
XX 20-APR-1998; 98US-0082404P.
PR
XX 23-JUN-1998; 98US-00103636.
PR
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX Claim 77; Page 88; 148pp; English.
PS
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 5 A; 3 C; 1 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 716 GTGATCAAAAGTGAAT 731
DB 17 GTGATCAAAAGTGAAT 2
RESULT 313
AAA25735/C
ID AAA25735 standard; DNA; 17 BP.
XX
XX AAA25735;
AC
XX 19-JUL-2000 (first entry)
DT
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2233.
DE
```

```
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX WO9954459-A2.
PN
XX 28-OCT-1999.
PD
XX 19-APR-1999; 99WO-US008547.
PF
XX 20-APR-1998; 98US-0082404P.
PR
XX 23-JUN-1998; 98US-00103636.
PR
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX Claim 77; Page 88; 148pp; English.
PS
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 5 A; 3 C; 1 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 716 GTGATCAAAAGTGAAT 731
DB 16 GTGATCAAAAGTGAAT 1
RESULT 314
ABK00234
ID ABK00234 standard; RNA; 17 BP.
XX
XX ABK00234;
AC
XX 12-MAR-2002 (first entry)
DT
XX Human NOGO Hammerhead Ribozyme #234.
DE
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW
```


CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a hammerhead ribozyme of the invention

XX SQ Sequence 17 BP; 7 A; 4 C; 1 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 2e+02; Mismatches 5; Indels 0; Gaps 0;
Matches 10; Conservative 5;

QY 1689 TCCTACTTCAGCAAT 1704

Db 1 UCCUACUUCAGAAAU 16

RESULT 316

ABL46891

ID ABL46891 standard; RNA; 17 BP.

XX AC ABL46891;

DT 27-JUN-2003 (first entry)

XX Human GRID G-cleaver ribozyme substrate oligonucleotide #32.

XX Human; Grb2-related with Insert Domain; GRID; T-cell;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytostatic; ss.

XX OS Homo sapiens.

XX PN WO200162911-A2.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-US005957.

XX PR 24-FEB-2000; 2000US-0184594P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (GLAX) GLAXO GROUP LTD.

XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;

XX WPI; 2001-550088/61.

XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.

XX Claim 4; Page 69; 108pp; English.

XX The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful

CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention

XX SQ Sequence 17 BP; 4 A; 7 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1409 CAGCAGCAGCAGCAGC 1424

Db 1 CAGCAGCUGCAGCAGC 16

RESULT 317

ABL46750

ID ABL46750 standard; RNA; 17 BP.

XX AC ABL46750;

XX DT 27-JUN-2003 (first entry)

XX Human GRID NCH ribozyme substrate oligonucleotide #204.

XX Human; Grb2-related with Insert Domain; GRID; T-cell;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytostatic; ss.

XX OS Homo sapiens.

XX PN WO200162911-A2.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-US005957.

XX PR 24-FEB-2000; 2000US-0184594P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (GLAX) GLAXO GROUP LTD.

XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;

XX WPI; 2001-550088/61.

XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.

XX Claim 4; Page 66; 108pp; English.

XX The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention

XX SQ Sequence 17 BP; 4 A; 7 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1409 CAGCAGCAGCAGCAGC 1424

Db 2 CAGCAGCUGCAGCAGC 17

```

RESULT 318
AAS00452/c
ID AAS00452 standard; DNA; 17 BP.
XX
XX AAS00452;
AC
XX
XX 11-SEP-2003 (revised)
DT 15-MAY-2001 (first entry)
XX
XX Lactococcus lactis pyrG gene nested PCR primer pyrg8b.
DE
XX
XX Pyrg; cytidine triphosphate synthetase; CTP; pyrimidine metabolism; UTP;
KW bacteriophage resistant; lactic acid bacterial culture; starter culture;
KW food industry; feed product; dairy product; fermentation process;
KW probiotic; PCR primer; ss.
XX
XX Lactococcus lactis subsp. cremoris; MGL1363.
OS
XX
XX WO200114520-A2.
FN
XX
XX 01-MAR-2001.
PD
XX
XX 10-AUG-2000; 2000WO-DK000446.
PF
XX
XX 19-AUG-1999; 99US-00377152.
PR
XX
XX (CHRH-) CHR HANSEN AS.
PA
XX
XX Wadskov-Hansen SLL, Hammer K, Martinussen J;
PI
XX
XX WPI; 2001-218434/22.
DR
XX
XX Obtaining a derivative of Lactococcus lactis subspecies cremoris having
PT reduced susceptibility to a bacteriophage, useful in food and feed
PT manufacturing, comprises mutating a gene involved in pyrimidine
PT metabolism of a parent bacterium.
XX
XX Example 1; Page 20; 70pp; English.
PS
XX
XX The present sequence for Lactococcus lactis pyrG gene nested PCR primer
CC pyrg8b is 1 of 6 nested PCR primers (AAS00444-AAS00446 and AAS00450-
CC AAS00452) used with partly degenerate primers containing either an EcoRI,
CC HindIII or Sau3AI restriction site (AAS00455-AAS00457) to PCR Lactococcus
CC lactis subspecies cremoris wild type strain MGL1363 pyrG gene. The pyrG
CC gene encodes for cytidine triphosphate (CTP) synthetase which is involved
CC in pyrimidine metabolism by converting UTP to CTP. The wild type CTP
CC synthetase is used to construct bacteriophage resistant lactic acid
CC mutants (AAU00432-AAU00434) that have a reduced susceptibility towards
CC attack by at least one kind of bacteriophage comprising subjecting a
CC population of parent lactic acid bacterial cells, which are initially
CC susceptible towards bacteriophage attack, to mutation in a gene involved
CC in the pyrimidine metabolism. The lactic acid bacterial cultures which
CC have significantly reduced susceptibility towards bacteriophage attacks
CC are useful as starter cultures in the manufacture of food and feed
CC products, e.g. dairy products and in other food fermentation processes.
CC These may also be used as probiotics, which when ingested by humans or
CC animals in the form of viable cells confers good health conditions.
CC Another strain of L. lactis, WB383, is a leaky mutant for the pyrG gene
CC (AAS00458) in that these cells do not require cytidine for growth but
CC have a reduced susceptibility to bacteriophages. (Updated on 11-SEP-2003
CC to standardise OS field)
XX
XX Sequence 17 BP; 1 A; 3 C; 5 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. NO. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1570 GCAGCAACAAACACG 1585
Db 17 GCAGCAACAAACACTG 2

```

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RESULT 319
ABN08476
ID ABN08476 standard; DNA; 17 BP.
XX
XX AC ABN08476;
AC
XX
XX 29-MAY-2002 (first entry)
DT
XX
XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8468.
DE
XX
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200192524-A2.
FN
XX
XX 06-DEC-2001.
PD
XX
XX 25-MAY-2001; 2001WO-US016981.
PF
XX
XX 26-MAY-2000; 2000US-0207456P.
PR
XX
XX 21-SEP-2000; 2000US-0234687P.
PR
XX
XX 27-SEP-2000; 2000US-0236359P.
PR
XX
XX 04-OCT-2000; 2000GB-00024263.
PR
XX
XX 30-JAN-2001; 2001WO-US000661.
PR
XX
XX 30-JAN-2001; 2001WO-US000862.
PR
XX
XX 30-JAN-2001; 2001WO-US000863.
PR
XX
XX 30-JAN-2001; 2001WO-US000864.
PR
XX
XX 30-JAN-2001; 2001WO-US000865.
PR
XX
XX 30-JAN-2001; 2001WO-US000866.
PR
XX
XX 30-JAN-2001; 2001WO-US000867.
PR
XX
XX 30-JAN-2001; 2001WO-US000869.
PR
XX
XX 05-FEB-2001; 2001US-0266860P.
PR
XX
XX (ABOM-) ABOMICA INC.
PA
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI
XX
XX WPI; 2002-179446/23.
DR
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 8468; 214pp; English.
PS
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

```


CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 GACCTTGCTGATGAC 337
|||||
DB 1 GACCTTGCTGATGAC 16

RESULT 322
ABN08475
ID ABN08475 standard; DNA; 17 BP.
XX
AC ABN08475;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:8467.
DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (ABOM-) ABOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI WPI; 2002-179446/23.
XX
DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 8467; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 GACCTGGAGAACATGA 617
|||||
DB 2 GACCTGGAGAACATGA 17

RESULT 323
ABV89862
ID ABV89862 standard; DNA; 17 BP.
XX
AC ABV89862;
XX
XX 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 575.
DE Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
OS Homo sapiens.
XX
XX EPI2339051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.

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PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 575; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
XX Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 1;
QY 2553 CCTGACGCTCTGCAGG 2568
Db 1 CCCAGACGCTCTGCAGG 16
RESULT 324
ABV89861
ID ABV89861 standard; DNA; 17 BP.
XX
XX AC ABV89861;
XX
XX 23-DEC-2002 (first entry)
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 574.
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
XX Homo sapiens.
XX EP1239051-A2.
XX
XX 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.

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PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 574; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
XX Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; Mismatches 0; Gaps 0;
Matches 15; Conservative 0; Indels 1;
QY 2553 CCTGACGCTCTGCAGG 2568
Db 2 CCCAGACGCTCTGCAGG 17
RESULT 325
ACN12567/c
ID ACN12567 standard; RNA; 17 BP.
XX
XX AC ACN12567;
XX
XX 22-APR-2004 (first entry)
XX WNV minus strand Zinzyne substrate SEQ ID NO 12570.
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX viricide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX

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PF 19-OCT-2001; 2001WO-US048350.
XX
XX
PR 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
PI WPI; 2002-706994/76.
XX
XX Claim 23; SEQ ID NO 12570; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 3 A; 1 C; 8 G; 0 T; 5 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1808 AACCCCTGCTCAAAATC 1823
DB |||||:|||||:|
17 AACCCCTGCTCAACTC 2

RESULT 326
ACN04426
ID ACN04426 standard; RNA; 17 BP.
XX
XX ACN04426;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV Zinzyme substrate SEQ ID NO 4429.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNzyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
PI WPI; 2002-706994/76.
XX
XX Claim 23; SEQ ID NO 12570; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX Sequence 17 BP; 3 A; 1 C; 8 G; 0 T; 5 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1808 AACCCCTGCTCAAAATC 1823
DB |||||:|||||:|
17 AACCCCTGCTCAACTC 2

RESULT 327
ABT34779/c
ID ABT34779 standard; DNA; 17 BP.
XX
XX ABT34779;
XX
XX 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID NO 416.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001PR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 82; 720pp; French.

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XX Blatt L, Mcswiggen JA;
PI WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 4429; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, inozyme, G-cleaver, DNzyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 17 BP; 5 A; 8 C; 1 G; 0 T; 3 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1808 AACCCCTGCTCAAAATC 1823
DB |||||:|||||:|
2 AACCCCTGCTCAACUC 17

RESULT 327
ABT34779/c
ID ABT34779 standard; DNA; 17 BP.
XX
XX ABT34779;
XX
XX 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID NO 416.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001PR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 82; 720pp; French.

```

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2778 AGCTAAGCACACAGAT 2793
DB 17 AGCTAAGCACACAGAT 2
|||||||

RESULT 328
ADB05009/C
ID ADB05009 standard; DNA; 17 BP.
XX
AC ADB05009;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MDZ12 scanning oligonucleotide SEQ ID 5995.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5995; 103pp; English.

CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1. MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder,
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1368 AGCCTTCTCTCCTACA 1383
DB 17 AGCCTTCTCTCCTACA 2
|||||||

RESULT 329
ADB05010/C
ID ADB05010 standard; DNA; 17 BP.
XX
AC ADB05010;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MDZ12 scanning oligonucleotide SEQ ID 5996.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5996; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1. MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder,
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic

CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

XX
 SQ Sequence 17 BP; 6 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1368 AGCCTTCTCTCTCTACA 1383
 |||||
 Db 16 AGGCTTCTCTCTCTACA 1

RESULT 330
 ACID62073/c

ID ACID62073 standard; RNA; 17 BP.

AC ACID62073;

DT 23-SEP-2003 (first entry)

DE HCV minus strand DNazyme substrate sequence #384.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; zinzyme;
 KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.

OS WO200281494-A1.

PN 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0286876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEEP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

XX Claim 1; Page 281; 387pp; English.

CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV. The compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention

SQ Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 2e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1660 AAGGTCACCTTTGCCA 1675

|||||
 Db 16 AAGGTCACCTTTGCCA 1

RESULT 331

ACC64185

ID ACC64185 standard; DNA; 17 BP.

XX ACC64185;

AC 01-JUN-2003 (first entry)

DT Murine oligonucleotide associated with tumour suppression, SEQ ID 1432.

DE Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.

XX Mus musculus.

OS WO2003025176-A2.

PN 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004210.

XX 17-SEP-2001; 2001FR-00011979.

XX (MOLE-) MOLECULAR ENGINES LAB.

PA Telerman A, Amson R, Tuijnder M;

PI WPI; 2003-333167/31.

XX New isolated nucleic acid, useful for treating viral diseases associated

PT with tumors and cell degeneration, also related polypeptides, antibodies

PT and transfected cells.

XX Disclosure; Page 198; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,

CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of

CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 4 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3255 ATTCTGTTTAAATC 3270
|||
Db 2 ATCTTGTTTAAATC 17

RESULT 332
ADC37826
ID ADC37826 standard; DNA; 17 BP.

XX
AC ADC37826;

XX 18-DEC-2003 (first entry)

XX Human AMLPia scanning 17-mer oligonucleotide SEQ ID NO:175.

XX human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
KW AMLPia; ss.

XX Synthetic.

OS Homo sapiens.

XX WO2003037931-A2.

XX 08-MAY-2003.

XX 01-NOV-2002; 2002WO-US035129.

XX 01-NOV-2001; 2001US-0334773P.

XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.

XX Shannon M, Phan T;

XX WPI; 2003-430501/40.

XX New isolated nucleic acid molecule encoding a human angiominotin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.

XX Example 2; SEQ ID NO 175; 172pp; English.

XX The present invention describes the human angiominotin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLPia, which is used in an example from the
CC present invention.

XX Sequence 17 BP; 6 A; 4 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1506 AGCAACAGCAGCAGAG 1521
|||
Db 1 AGCAACAGCAGCAGGG 16

RESULT 333

ADB45768/c
ID ADB45768 standard; DNA; 17 BP.

XX
AC ADB45768;

XX 18-DEC-2003 (first entry)

XX Tumour suppression/reversion associated nucleotide #6091.

XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;

KW primer; probe; tumour suppression; tumour reversion; apoptosis;

KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
diagnosis.

XX OS Homo sapiens.

XX WO2003040369-A2.

XX 15-MAY-2003.

XX 17-SEP-2002; 2002WO-IB004219.

XX 17-SEP-2001; 2001FR-00011981.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX NPI; 2003-441574/41.

XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.

XX Disclosure; Page 744; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors) the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules.
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.

XX Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3182 TGGACTACATGAAGAT 3197
|||||
Db 17 TGGACTACATGAAGAT 2

RESULT 334

ADI50387

ID ADI50387 standard; DNA; 17 BP.

XX
AC ADI50387;

PF	17-SEP-2002; 2002WO-IB004523.	
XX		
PR	17-SEP-2001; 2001FR-00011980.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB.	
XX		
PI	Telerman A, Amson R, Tuijnder M;	
XX		
DR	WPI; 2003-313354/30.	
XX		
PT	New isolated nucleic acid, useful for treating viral diseases associated	
PT	with tumors and cell degeneration, also related polypeptides, antibodies	
PT	and transfected cells.	
XX		
PS	Disclosure; SEQ ID NO 4325; 30pp; French.	
XX		
CC	This invention relates to novel isolated nucleic acid sequences involved	
CC	in the phenomena of tumour suppression, tumour reversion, apoptosis	
CC	and/or resistance to viruses. The invention may be useful for the	
CC	development of compounds with a cytostatic, virucide, neuroprotective,	
CC	neotropic or neuroleptic activity. The DNA sequences may be useful as	
CC	probes and primers for detecting, identifying, quantifying and/or	
CC	amplifying nucleic acid, for example as one component of a gene chip, in	
CC	vitro as antisense reagents and for production of recombinant	
CC	polypeptides. The invention may therefore be useful for preparation of	
CC	pharmaceuticals for prevention and/or treatment of viral diseases that	
CC	are characterised by development of tumours or cell degeneration.	
CC	specifically cancer but also Alzheimer's disease and schizophrenia. The	
CC	present sequence is that of a nucleic acid sequence of the invention.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/publishedpat_sequences	
XX		
SQ	Sequence 17 BP; 6 A; 5 C; 1 G; 5 T; 0 U; 0 Other;	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	3330 ATCCAAATTTATCCAAA 3345	
DB		
	2 ATCCCAATTTATCCAAA 17	
RESULT 337		
ACC53755/c		
ID	ACC53755 standard; DNA; 17 BP.	
XX		
AC	ACC53755;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human tumour suppressor sequence #2522.	
XX		
XX	ss; tumour suppressor; antitumour; cytostatic; tumour suppression;	
KW	tumour regression; apoptosis; virus resistance; diagnosis;	
KW	cellular degeneration.	
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
XX		
XX	New nucleic acid sequences associated with tumour suppression, regression,	
PT	apoptosis or virus resistance are useful to diagnose and treat viral	
PT	disease, development of tumor cells and cell degeneration.	
XX		
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	3182 TGGACTACATCGAGAT 3197	
DB		
	17 TGGACTACATCGAGAT 2	
RESULT 338		
ACC52683		
ID	ACC52683 standard; DNA; 17 BP.	
XX		
AC	ACC52683;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human tumour suppressor sequence #1450.	
XX		
XX	ss; tumour suppressor; antitumour; cytostatic; tumour suppression;	
KW	tumour regression; apoptosis; virus resistance; diagnosis;	
KW	cellular degeneration.	
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
XX		
XX	New nucleic acid sequences associated with tumour suppression, regression,	
PT	apoptosis or virus resistance are useful to diagnose and treat viral	
PT	disease, development of tumor cells and cell degeneration.	
XX		
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	3182 TGGACTACATCGAGAT 3197	
DB		
	17 TGGACTACATCGAGAT 2	
RESULT 338		
ACC52683		
ID	ACC52683 standard; DNA; 17 BP.	
XX		
AC	ACC52683;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human tumour suppressor sequence #1450.	
XX		
XX	ss; tumour suppressor; antitumour; cytostatic; tumour suppression;	
KW	tumour regression; apoptosis; virus resistance; diagnosis;	
KW	cellular degeneration.	
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	3182 TGGACTACATCGAGAT 3197	
DB		
	17 TGGACTACATCGAGAT 2	
RESULT 338		
ACC52683		
ID	ACC52683 standard; DNA; 17 BP.	
XX		
AC	ACC52683;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human tumour suppressor sequence #1450.	
XX		
XX	ss; tumour suppressor; antitumour; cytostatic; tumour suppression;	
KW	tumour regression; apoptosis; virus resistance; diagnosis;	
KW	cellular degeneration.	
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	3182 TGGACTACATCGAGAT 3197	
DB		
	17 TGGACTACATCGAGAT 2	
RESULT 338		
ACC52683		
ID	ACC52683 standard; DNA; 17 BP.	
XX		
AC	ACC52683;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human tumour suppressor sequence #1450.	
XX		
XX	ss; tumour suppressor; antitumour; cytostatic; tumour suppression;	
KW	tumour regression; apoptosis; virus resistance; diagnosis;	
KW	cellular degeneration.	
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	3182 TGGACTACATCGAGAT 3197	
DB		
	17 TGGACTACATCGAGAT 2	
RESULT 338		
ACC52683		
ID	ACC52683 standard; DNA; 17 BP.	
XX		
AC	ACC52683;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human tumour suppressor sequence #1450.	
XX		
XX	ss; tumour suppressor; antitumour; cytostatic; tumour suppression;	
KW	tumour regression; apoptosis; virus resistance; diagnosis;	
KW	cellular degeneration.	
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	3182 TGGACTACATCGAGAT 3197	
DB		
	17 TGGACTACATCGAGAT 2	
RESULT 338		
ACC52683		
ID	ACC52683 standard; DNA; 17 BP.	
XX		
AC	ACC52683;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human tumour suppressor sequence #1450.	
XX		
XX	ss; tumour suppressor; antitumour; cytostatic; tumour suppression;	
KW	tumour regression; apoptosis; virus resistance; diagnosis;	
KW	cellular degeneration.	
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	3182 TGGACTACATCGAGAT 3197	
DB		
	17 TGGACTACATCGAGAT 2	
RESULT 338		
ACC52683		
ID	ACC52683 standard; DNA; 17 BP.	
XX		
AC	ACC52683;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human tumour suppressor sequence #1450.	
XX		
XX	ss; tumour suppressor; antitumour; cytostatic; tumour suppression;	
KW	tumour regression; apoptosis; virus resistance; diagnosis;	
KW	cellular degeneration.	
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	3182 TGGACTACATCGAGAT 3197	
DB		
	17 TGGACTACATCGAGAT 2	
RESULT 338		
ACC52683		
ID	ACC52683 standard; DNA; 17 BP.	
XX		
AC	ACC52683;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human tumour suppressor sequence #1450.	
XX		
XX	ss; tumour suppressor; antitumour; cytostatic; tumour suppression;	
KW	tumour regression; apoptosis; virus resistance; diagnosis;	
KW	cellular degeneration.	
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	3182 TGGACTACATCGAGAT 3197	
DB		
	17 TGGACTACATCGAGAT 2	
RESULT 338		
ACC52683		
ID	ACC52683 standard; DNA; 17 BP.	
XX		
AC	ACC52683;	
XX		
DT	27-JUN-2003 (first entry)	
XX		
DE	Human tumour suppressor sequence #1450.	
XX		
XX	ss; tumour suppressor; antitumour; cytostatic; tumour suppression;	
KW	tumour regression; apoptosis; virus resistance; diagnosis;	
KW	cellular degeneration.	
OS	Homo sapiens.	
XX		
FN	FR2826373-A1.	
XX		
PD	27-DEC-2002.	
XX		
PF	20-JUN-2001; 2001FR-00008139.	
XX		
PR	20-JUN-2001; 2001FR-00008139.	
XX		
PA	(MOLE-) MOLECULAR ENGINES LAB SA.	
XX		
PI	Tuijnder M, Telerman A, Amson R;	
XX		
DR	WPI; 2003-250498/25.	
Query Match 0.4%; Score 14.4; DB 1; Length 17;		
Best Local Similarity 93.8%; Pred. No. 2e+02;		

Best Local Similarity 93.8%; Pred. NO. 2e+02;		Best Local Similarity 93.8%; Pred. NO. 2e+02;	
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	3330 ATCCAAATTATCCAAA 3345	QY	2650 CCAGAGGGCAGTGGCT 2665
DB	2 ATCCAAATTATCCAAA 17	DB	17 CCAGACGGCAGTGGCT 2
RESULT 339		RESULT 340	
ID	ADL47232/C	ID	ADL46972/C
XX	ADL47232 standard; RNA; 17 BP.	XX	ADL46972 standard; RNA; 17 BP.
AC	ADL47232;	AC	ADL46972;
XX		XX	
DT	20-MAY-2004 (first entry)	DT	20-MAY-2004 (first entry)
XX		XX	
DE	Human NOGO receptor zinzyme substrate sequence #219.	DE	Human NOGO receptor inozyme substrate sequence #405.
XX		XX	
KW	antisense oligonucleotide; neurite growth inhibitor; NOGO;	KW	antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW	prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;	KW	prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
KW	protein kinase PKR; cerebrovascular accident;	KW	protein kinase PKR; cerebrovascular accident;
KW	central nervous system injury; CNS injury; spinal cord injury; cancer;	KW	central nervous system injury; CNS injury; spinal cord injury; cancer;
KW	melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;	KW	melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW	restenosis; asthma; Crohn's disease; diabetes; obesity;	KW	restenosis; asthma; Crohn's disease; diabetes; obesity;
KW	autoimmune disease; lupus; multiple sclerosis; transplant rejection;	KW	autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW	graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;	KW	graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
KW	allergy; asthma; allergic rhinitis; atopic dermatitis;	KW	allergy; asthma; allergic rhinitis; atopic dermatitis;
KW	NOGO receptor zinzyme; substrate; ds.	KW	NOGO receptor inozyme; substrate; ds.
XX		XX	
OS	Unidentified.	OS	Unidentified.
XX		XX	
FN	WO200281628-A2.	FN	WO200281628-A2.
XX		XX	
PD	17-OCT-2002.	PD	17-OCT-2002.
XX		XX	
PF	03-APR-2002; 2002WO-US010512.	PF	03-APR-2002; 2002WO-US010512.
XX		XX	
PR	05-APR-2001; 2001US-00827395.	PR	05-APR-2001; 2001US-00827395.
PR	29-MAY-2001; 2001US-0294412P.	PR	29-MAY-2001; 2001US-0294412P.
PR	28-AUG-2001; 2001US-0315315P.	PR	28-AUG-2001; 2001US-0315315P.
XX		XX	
PA	(RIBO-) RIBOZYME PHARM INC.	PA	(RIBO-) RIBOZYME PHARM INC.
XX		XX	
PI	Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;	PI	Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;
XX		XX	
XX	WPI; 2003-058513/05.	XX	WPI; 2003-058513/05.
DR		DR	
XX		XX	
PT	Novel enzymatic nucleic acid that down-regulates expression of neurite	PT	Novel enzymatic nucleic acid that down-regulates expression of neurite
PT	growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or	PT	growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
PT	protein kinase PKR genes, for treating cancer and inflammatory disease.	PT	protein kinase PKR genes, for treating cancer and inflammatory disease.
XX		XX	
PS	Claim 9; SEQ ID NO 765; 317pp; English.	PS	Claim 9; SEQ ID NO 505; 317pp; English.
XX		XX	
CC	The invention comprises nucleic acids (e.g. antisense oligonucleotides)	CC	The invention comprises nucleic acids (e.g. antisense oligonucleotides)
CC	that down regulate the expression or inhibit the function of a receptor	CC	that down regulate the expression or inhibit the function of a receptor
CC	for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),	CC	for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
CC	IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the	CC	IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the
CC	invention are useful for treating: cerebrovascular accident, central	CC	invention are useful for treating: cerebrovascular accident, central
CC	nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,	CC	nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
CC	lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,	CC	lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
CC	restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune	CC	restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
CC	disease, lupus, multiple sclerosis, transplant/graft rejection,	CC	disease, lupus, multiple sclerosis, transplant/graft rejection,
CC	ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic	CC	ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
CC	conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The	CC	conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
CC	nucleic acids of the invention are also useful for down-regulating the	CC	nucleic acids of the invention are also useful for down-regulating the
CC	expression of a target gene and as a diagnostic tool to examine genetic	CC	expression of a target gene and as a diagnostic tool to examine genetic
CC	drifts and mutations within diseased cells or to detect the presence of a	CC	drifts and mutations within diseased cells or to detect the presence of a
CC	target RNA in a cell. The present RNA sequence represents a human NOGO	CC	target RNA in a cell. The present RNA sequence represents a human NOGO
CC	receptor zinzyme substrate sequence.	CC	receptor inozyme substrate sequence.
XX		XX	
SQ	Sequence 17 BP; 2 A; 7 C; 5 G; 0 T; 3 U; 0 Other;	SQ	Sequence 17 BP; 1 A; 7 C; 6 G; 0 T; 3 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 17;		Query Match 0.4%; Score 14.4; DB 1; Length 17;	

Best Local Similarity 93.8%; Pred. No. 2e+02; Mismatches 0; Indels 1; Gaps 0;

QY 2649 CCCAGAGCGCAGTGGC 2664
|||||
Db 16 CCCAGAGCGCAGTGGC 1

RESULT 341
ADM54108
ID ADM54108 standard; mRNA; 17 BP.
XX
AC ADM54108;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human GRID mRNA substrate sequence #383.

XX Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
KW NCH ribozyme; G-cleaver ribozyme; Zinzyme; DNazyme; amberzyme; Inozyme;
KW hairpin ribozyme; tissue rejection; graft rejection; leukaemia.

XX Homo sapiens.

XX US2003134806-A1.

XX 17-JUL-2003.

XX 23-FEB-2001; 2001US-00792818.

XX 10-FEB-2000; 2000US-0181594P.

XX (JARV/) JARVIS T.

XX (CARL/) CARLOWITZ I V.

XX (MCSW/) MCSWIGGEN J.

XX (HAMB/) HAMBLIN P A.

XX (ELLI/) ELLIS J H.

XX Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;

XX WPI; 2003-829646/77.

XX New nucleic acid molecule that down-regulates expression of Grb2-related
PT with insert domain (GRID) gene, useful for treating a condition
PT associated with the level of GRID, e.g. tissue/graft rejection and
PT leukemia.

XX Claim 4; SEQ ID NO 383; 74pp; English.

XX The invention relates to a nucleic acid molecule that down-regulates
CC expression of Grb2-related with insert domain (GRID) gene, e.g. a
CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNazyme,
CC amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
CC including the novel nucleic acid molecule, reducing GRID activity in a
CC cell by contacting the cell with the novel nucleic acid molecule,
CC treating a patient having a condition associated with the level of GRID
CC (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
CC contacting the cell with the novel nucleic acid molecule, an expression
CC vector comprising a nucleic acid sequences (encoding at least the novel
CC nucleic acid molecule in a manner that allows its expression), a
CC mammalian cell including the expression vector and an enzymatic nucleic
CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.

XX Sequence 17 BP; 4 A; 7 C; 5 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGC 1424
|||||
Db 2 CAGCAGCUGCAGCAGC 17

RESULT 342
ADI85415/C

ID ADI85415 standard; RNA; 17 BP.

XX AC ADI85415;

XX 03-JUN-2004 (first entry)

XX HCV DNazyme substrate sequence #2661.

XX ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;
KW HCV infection; type I interferon; DNazyme.

XX Hepatitis C virus.

XX US2003125270-A1.

XX 03-JUL-2003.

XX 18-DEC-2000; 2000US-00740332.

XX 18-DEC-2000; 2000US-00740332.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J.

XX (ROBE/) ROBERTS E.

XX (PAVC/) PAVCO P A.

XX (MACE/) MACEJACK D.

XX Blatt L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;

XX WPI; 2004-031273/03.

XX Enzymatic nucleic acid molecules which specifically cleave RNA derived
PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,
PT especially in combination with type I interferon therapy.

XX Claim 1; SEQ ID NO 2661; 198pp; English.

XX The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which
CC the binding arms of the enzymatic nucleic acid molecule comprises
CC sequences complementary to any of the defined substrate sequences given
CC in the specification. The nucleic acid molecule may be administered for
CC the treatment of HCV infections, especially in combination with type I
CC interferons. The present sequence represents a HCV DNazyme substrate
CC sequence.

XX Sequence 17 BP; 4 A; 4 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1660 AAGGTCACCTTTGCCA 1675

Db 16 AAGGTCACCTTTGCCA 1

RESULT 343

ADR27873

ID ADR27873 standard; DNA; 17 BP.

XX ADR27873;

XX 04-NOV-2004 (first entry)

XX Murine VE-statin b PCR primer, SEQ ID 13.

XX Cytostatic; Ophthalmological; Vasotropic; Antiarteriosclerotic;
 KW VE-statin; endothelium; perivascular smooth muscle cell; angiogenesis;
 KW cancer; retinopathy; atherosclerosis; restenosis; gene therapy; PCR;
 KW primer; ss; mouse.
 XX Mus musculus.
 OS FR2851249-Al.
 PN 20-AUG-2004.
 PD 17-FEB-2003; 2003FR-00001875.
 PF 17-FEB-2003; 2003FR-00001875.
 PR (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 PA Soncin F, Mattot V;
 XX WPI; 2004-618122/60.
 DR Using VE-statins to inhibit recruitment of perivascular smooth muscle
 PT cells, for treating e.g. cancer and retinopathy, also new VE-statins,
 PT related nucleic acids and antibodies.
 XX Claim 10; SEQ ID NO 13; 63pp; French.
 PS The present invention relates to a method for preparing a composition for
 CC inhibiting recruitment of perivascular cells of smooth muscle type using
 CC a VE-statin protein (I; ADR27861-ADR27863 and ADR27902). VE-statins,
 CC soluble factors secreted by endothelial cells of the blood vessels, block
 CC recruitment of perivascular smooth muscle cells (but do not affect their
 CC proliferation), so inhibit angiogenesis. VE-statins, also their peptide
 CC fragments, nucleic acids encoding them and vectors containing this
 CC nucleic acid, are used for treating cancer, retinopathy, atherosclerosis
 CC and restenosis, including in gene therapy. The VE-statin nucleic acids
 CC can also be used to produce transgenic animals (for studying the VE-
 CC statin proteins and genes); the VE-statins are used to screen for
 CC specific (ant)agonists, and antibodies specific for VE-statins can be
 CC used to determine expression profiles, particularly for diagnosis of
 CC diseases associated with VE-statins. The present sequence is a primer
 CC used to illustrate the invention.
 XX Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. NO. 2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1084 TGGTCAGCAGACATTC 1099
 Db 1 TGGCAGCAGACATTC 16
 |||||
 RESULT 344
 ACN70300
 ID ACN70300 standard; DNA; 17 BP.
 XX ACN70300;
 AC 02-DEC-2004 (first entry)
 XX Human GDMLP-1 probe SEQ ID NO:7202.
 DE Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX Homo sapiens.
 OS US2004137589-Al.
 XX
 PN

PD 15-JUL-2004.
 XX 26-NOV-2003; 2003US-00723361.
 PF 26-MAY-2000; 2000US-0207456P.
 XX 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0286860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX (GUY/) GU Y.
 PA (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 PI WPI; 2004-533378/51.
 DR Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX Disclosure; SEQ ID NO 7202; Opp; English.
 PS The invention relates to a novel polypeptide (I) comprising a sequence
 CC (SI) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (SI), 95% deviation from (SI) which are conservative substitutions, and
 CC 65% identity to (SI). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. NO. 2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 322 GACCTTCCTATGAGC 337
 Db 1 GACCTTCCTATGAGC 16
 |||||
 RESULT 345
 ACN71565
 ID ACN71565 standard; DNA; 17 BP.
 XX ACN71565;
 AC 02-DEC-2004 (first entry)
 XX Human GDMLP-1 probe SEQ ID NO:8467.
 DE
 XX

KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
XX 15-JUL-2004.
XX
PD 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0268660P.
PR 25-MAY-2001; 2001US-00866108.
XX
XX (GUY/) GU Y.
PA (JIVY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon MB;
PI WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
XX Disclosure; SEQ ID NO 8467; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
XX Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 602 GAACCTGGAGAACATGA 617
DB 2 GAGCTGGAGAACATGA 17
RESULT 346
ACN70299

ID ACN70299 standard; DNA; 17 BP.
XX
AC ACN70299;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMPLP-1 probe SEQ ID NO:7201.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
XX Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0268660P.
PR 25-MAY-2001; 2001US-00866108.
XX
XX (GUY/) GU Y.
PA (JIVY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon MB;
PI WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
XX Disclosure; SEQ ID NO 7201; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as a agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
XX Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 GACCTTGCTGATGAC 337
 ACN71566
 |||||
 Db 2 GACCTTGCGATGAC 17
 ACN71566;
 02-DEC-2004 (first entry)
 Human GDMPLP-1 probe SEQ ID NO:8468.
 Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 skeletal muscle function.
 XX Homo sapiens.
 OS
 XX US2004137589-A1.
 PN
 XX 15-JUL-2004.
 PD
 XX 26-NOV-2003; 2003US-00723361.
 PF
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX (GUY/) GU Y.
 PA (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 PI WPI; 2004-533378/51.
 DR Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX Disclosure; SEQ ID NO 8468; Opp; English.
 PS
 XX The invention relates to a novel polypeptide (1) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.

CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 SQ Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 602 GAACCTGGAGAACATGA 617
 |||||
 Db 1 GAGCTGGAGAACATGA 16
 RESULT 348
 AAV51900/c
 ID AAV51900 standard; DNA; 18 BP.
 XX
 AC AAV51900;
 XX
 DT 02-FEB-1999 (first entry)
 XX
 DE Zea mays genome reverse PCR primer #196.
 XX
 KW Polymorphic marker; allele-specific; probe; amplification; PCR primer;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back-cross; hybrid; ancestry; corn; ss.
 XX Synthetic.
 OS Zea mays.
 OS
 XX WO9824796-A1.
 PN
 XX 11-JUN-1998.
 PD
 XX 01-DEC-1997; 97WO-US021782.
 PF
 XX 02-DEC-1996; 96US-0032069P.
 PR 07-MAR-1997; 97US-00813507.
 XX (AFFY-) AFFYMETRIX INC.
 XX Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;
 PI WPI; 1998-333252/29.
 DR Brassica species allele-specific oligonucleotide probes and primers -
 PT useful for plant breeding.
 XX Example 1; Page 53; 65pp; English.
 PS
 XX AAV51705-V52008 are reverse PCR primers used to amplify fragments of the
 CC Zea mays genome in order to detect polymorphic markers. Such markers can
 CC be used in the construction of allele-specific primers and probes for
 CC amplification or hybridisation, e.g. to determine common or disparate
 CC ancestry between 2 or more plants, to monitor the genetic contribution of
 CC an ancestral plant, to trace the progeny of proprietary plants, in
 CC certification of a hybrid plant or to identify the progeny of a back-
 CC crossed plant with an ancestral plant
 XX
 SQ Sequence 18 BP; 0 A; 4 C; 9 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1532 GCCCAACGACGACGACG 1547
 |||||
 Db 18 GCCCACCACGACGACGACG 3
 RESULT 349
 AAX10193/c

```

ID AAX10193 standard; DNA; 18 BP.
XX
XX
AC AAX10193;
XX
XX 24-MAR-1999 (first entry)
DT
XX Human biallelic polymorphic marker downstream primer #499.
DE
XX Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW treatment; marker; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO9820165-A2.
XX
XX 14-MAY-1998.
PD
XX 05-NOV-1997; 97WO-US020313.
XX
XX 06-NOV-1996; 96US-0030455P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Lander ES, Wang D, Hudson T;
XX
XX WPI; 1998-286974/25.
XX
XX New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
XX
XX Claim 16; Page 213; 310pp; English.
XX
XX AAX09121-X10268 are allele-specific oligonucleotide primers used in the
XX isolation of various biallelic polymorphic markers found in the human
XX genome (represented in AAX10269-X12937). These primers can be used in a
XX method for determining polymorphic forms in an individual for use in e.g.
XX forensics, paternity testing or for phenotypic typing for diseases such
XX as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
XX hypercholesterolemia, polycystic kidney disease, hereditary
XX spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
XX haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
XX syndrome, osteogenesis imperfecta, acute intermittent porphyria.
XX autoimmune diseases, inflammation, cancer, diseases of the nervous
XX system, infection by pathogenic microorganisms, and characteristics such
XX as longevity, appearance (e.g. baldness, obesity), strength, speed,
XX endurance, fertility, and susceptibility or receptivity to particular
XX drugs or therapeutic treatments. The isolated polymorphic nucleic acid
XX segments can also be used to produce medicaments for the treatment or
XX prophylaxis of such diseases
XX
XX Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2647 TTCCAGAGGCGAGTG 2662
DB 16 TTCCAGAGGCGAGTG 1
RESULT 350
AAX241191/c
ID AAX241191 standard; DNA; 18 BP.
XX
XX AAX241191;
AC
XX 26-JAN-2000 (first entry)
DT

```

```

XX Human AKT-1 phosphorothioate antisense oligonucleotide SEQ ID NO:343.
DE
XX
XX Identification; genetic target; gene modulation; human; probe;
KW antisense oligonucleotide; phosphorothioate; PCR primer;
KW nucleotide sequence-based technology; antisense drug discovery;
KW target validation; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9953101-A1.
XX
XX 21-OCT-1999.
PD
XX 13-APR-1999; 99WO-US008268.
XX
XX 13-APR-1998; 98US-0081483P.
XX
XX 28-APR-1998; 98US-00067638.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowser LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;
XX Chasi C, Wyatt JR, Borchers AH, Vickers TA;
XX
XX WPI; 1999-620446/53.
XX
XX Identifying compounds which modulate expression of nucleic acids, used to
PT provide compounds having defined physical, chemical or bioactive
PT properties, e.g. antisense activity.
XX
XX Example 30; Page 113; 264pp; English.
XX
XX A method has been developed of defining a set of compounds that modulate
XX the expression of a target nucleic acid (tNA) sequence via binding of the
XX compounds with the tNA sequence. The method comprises generating a
XX library of virtual compounds in silico according to defined criteria, and
XX evaluating in silico the binding of the virtual compounds with the tNA
XX according to defined criteria. Also described are: (1) a method of
XX defining a set of oligonucleotides (ONs) that modulate the expression of
XX a tNA sequence via binding of the ONs with the tNA sequence comprising
XX generating a library of virtual compounds in silico according to defined
XX criteria, and evaluating in silico the binding of the virtual ONs with
XX the tNA according to defined criteria; and (2) a method of defining a set
XX of compounds that modulate the expression of a tNA sequence via binding
XX of the compounds with the tNA. The methods can be used for the generation
XX and identification of synthetic compounds having defined physical,
XX chemical or bioactive properties. Information gathered from assays of
XX such compounds is used to identify nucleic acid sequences that are
XX tractable to a variety of nucleotide sequence-based technologies, e.g.
XX antisense drug discovery and target validation. AAX40852 to AAX41220, and
XX AAY52701 to AAY52706, represent sequences used in the exemplification of
XX the present invention
XX
XX Sequence 18 BP; 0 A; 10 C; 1 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 73 GAAGCAGCGGAGGAG 88
DB 18 GAAGCAGCGGAGGAG 3
RESULT 351
AAX22207/c
ID AAX22207 standard; DNA; 18 BP.
XX
XX AAX22207;
AC
XX 26-NOV-1999 (first entry)
DT

```

DE Human Akt-1 mRNA inhibiting antisense oligo ISIS #28890.
XX
KW Human; Akt-1; antisense; diagnostic; therapeutic; prophylaxis; infection;
KW inflammation; tumor formation; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX US5958773-A.
XX
XX 28-SEP-1999.
XX
XX 17-DEC-1998; 98US-00212771.
XX
XX 17-DEC-1998; 98US-00212771.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Cowsett LM;
XX
XX WPI; 1999-561048/47.
XX
XX Antisense compounds complementary to Akt-1 useful for, e.g. diagnostics,
XX therapeutics and as research reagents.
XX
XX Claim 3; Col 39; 32pp; English.
XX
XX The invention provides antisense compounds of 8-30 nucleotides that
XX inhibit the expression of human Akt-1. The antisense compounds may be
XX used for diagnostics, therapeutics (for modulating the expression of Akt-
XX 1), prophylaxis (e.g. to prevent or delay infection, inflammation, or
XX tumor formation), as research reagents (e.g. to distinguish between
XX members of a biological pathway) and in kits. Sequences AA22197-236
XX represent phosphorothioate oligonucleotides used for antisense inhibition
XX of Akt-1 mRNA
XX
XX Sequence 18 BP; 0 A; 10 C; 1 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 73 GAAGCAGCGGAGGAG 88
Db 18 GAAGCAGCGGAGGAG 3
RESULT 352
AAA48769
ID AAA48769 standard; DNA; 18 BP.
XX
XX AAA48769;
AC
XX
XX 08-SEP-2000. (first entry)
XX
XX Human G-alpha-16 antisense oligonucleotide ISIS# 20826.
XX
XX Human; G-alpha-16; G protein; cytostatic; hyperproliferative disorder;
XX cancer, inflammation; infection; antisense inhibition; ss.
XX
XX Homo sapiens.
OS
XX WO200032817-A1.
XX
XX 08-JUN-2000.
XX
XX 25-AUG-1999; 98WO-US019613.
XX
XX 03-DEC-1998; 98US-00205143.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowsett LM;
PI
DE Human Akt-1 mRNA inhibiting antisense oligo ISIS #28890.
XX
KW Human; Akt-1; antisense; diagnostic; therapeutic; prophylaxis; infection;
KW inflammation; tumor formation; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX US5958773-A.
XX
XX 28-SEP-1999.
XX
XX 17-DEC-1998; 98US-00212771.
XX
XX 17-DEC-1998; 98US-00212771.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Cowsett LM;
XX
XX WPI; 1999-561048/47.
XX
XX Antisense compounds complementary to Akt-1 useful for, e.g. diagnostics,
XX therapeutics and as research reagents.
XX
XX Claim 3; Col 39; 32pp; English.
XX
XX The invention provides antisense compounds of 8-30 nucleotides that
XX inhibit the expression of human Akt-1. The antisense compounds may be
XX used for diagnostics, therapeutics (for modulating the expression of Akt-
XX 1), prophylaxis (e.g. to prevent or delay infection, inflammation, or
XX tumor formation), as research reagents (e.g. to distinguish between
XX members of a biological pathway) and in kits. Sequences AA22197-236
XX represent phosphorothioate oligonucleotides used for antisense inhibition
XX of Akt-1 mRNA
XX
XX Sequence 18 BP; 0 A; 10 C; 1 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 73 GAAGCAGCGGAGGAG 88
Db 18 GAAGCAGCGGAGGAG 3
RESULT 352
AAA48769
ID AAA48769 standard; DNA; 18 BP.
XX
XX AAA48769;
AC
XX
XX 08-SEP-2000. (first entry)
XX
XX Human G-alpha-16 antisense oligonucleotide ISIS# 20826.
XX
XX Human; G-alpha-16; G protein; cytostatic; hyperproliferative disorder;
XX cancer, inflammation; infection; antisense inhibition; ss.
XX
XX Homo sapiens.
OS
XX WO200032817-A1.
XX
XX 08-JUN-2000.
XX
XX 25-AUG-1999; 98WO-US019613.
XX
XX 03-DEC-1998; 98US-00205143.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowsett LM;
PI
WPI; 2000-412354/35.
A new antisense compound for inhibiting the expression of human G-alpha-16 and treating, preventing or delaying infections, inflammation or hyperproliferative disorders such as cancer.
Claim 3; Page 73; 100pp; English.
The present sequence is an antisense oligonucleotide used to modulate expression of G-alpha-16. G-alpha-16 is a human G protein which interacts differentially with several receptor types including members of the opioid and chemokine receptor families. A series of antisense oligonucleotides have been designed to target different regions of the human G-alpha-16 RNA. They may be used to inhibit the expression of G-alpha-16 in human cells and tissues and thus to treat diseases associated with G-alpha-16, such as hyperproliferative disorders, especially cancer. Infections, inflammation or tumour formation can be prevented or delayed. The compounds can be used in research and diagnostics in sandwich and other assays. Note: The sequence has a phosphorothioate backbone and may be either an oligodeoxynucleotide or a chimeric oligonucleotide containing 2'-methoxyethyl (2'-MOE) wings and a deoxy gap. The ISIS number given above corresponds to the oligodeoxynucleotide sequence
Sequence 18 BP; 6 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1532 GCCCAACAGCAGCAGC 1547
Db 3 GCCCAAAAGCAGCAGC 18
RESULT 353
AAH02259
ID AAH02259 standard; DNA; 18 BP.
XX
XX AAH02259;
AC
XX
XX 24-JUL-2001 (first entry)
XX
XX aph(3')-Via resistance gene detection nucleotide sequence SEQ ID NO:2252.
XX
XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitica;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;
XX primer; ss.
XX
XX Unidentified.
OS
XX WO200123604-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-CA001150.
XX
XX 28-SEP-1999; 99CA-02283458.
XX
XX 19-MAY-2000; 2000CA-02307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
XX Picard FJ, Roy PH;
XX
XX WPI; 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and primers
XX which can be used to identify and detect the presence of algal, archaeal,
XX bacterial, fungal and parasitica species in a test sample.
PT

```

XX PS Claim 21; Page 1560; 1590pp; English.
XX CC
XX CC The present invention describes a method for generating a repertory of
XX CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
XX CC and/or primers are derived. The method comprises amplifying the nucleic
XX CC acids of determined algal, archaeal, bacterial, fungal and parasitic
XX CC species with a combination of defined primer pairs. The method can be
XX CC used for producing probes and/or primers for detecting one or more
XX CC related microorganisms e.g. algae, archaea, bacteria, fungi and
XX CC parasites, for universal detection and for specific and ubiquitous
XX CC detection and identification of an algal, archaeal, bacterial, fungal and
XX CC parasitic species' genus, family and group. A nucleic acid (I) obtained
XX CC using the method of the invention can be used for the universal detection
XX CC of any bacterium, fungus or parasite in a sample and for the detection of
XX CC at least one antimicrobial agent resistance gene or at least one toxin
XX CC gene. hexA nucleic acids are used for the specific and ubiquitous
XX CC detection and for identification of Streptococcus pneumoniae. (I) can be
XX CC used to design a therapeutic agent which is effective against
XX CC microorganisms. Microbial species or genus or family or phylum or group
XX CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
XX CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
XX CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria
XX CC gonorrhoeae and Staphylococcus sp. . Using DNA based tests provides faster
XX CC results than substrate specificity tests as results can be determined in
XX CC an hour and improved accuracy is also achieved. AAH0010 to AAH002304
XX CC represent nucleotide sequences and primers/probes which are given in the
XX CC exemplification of the present invention
XX CC
XX CC Sequence 18 BP; 4 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
XX CC
XX CC Query Match 0.4%; Score 14.4; DB 1; Length 18;
XX CC Best Local Similarity 93.8%; Pred. No. 2.4e+02;
XX CC Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX CC
XX CC QY 2257 CACATACAGTGTCTCT 2272
XX CC |||||
XX CC Db 2 CACATACAGTGTCTCT 17
XX CC
XX CC RESULT 354
XX CC ABV72657/C
XX CC ID ABV72657 standard; DNA; 18 BP.
XX CC
XX CC AC ABV72657;
XX CC
XX CC DT 29-NOV-2002 (first entry)
XX CC
XX CC DE Human RISC forward PCR primer #1.
XX CC
XX CC KW Serine carboxypeptidase; mammalian; RISC; antihypertensive;
XX CC retinoid-inducible serine carboxypeptidase; antiarteriosclerotic;
XX CC nephrotropic; antiasthmatic; vasotropic; gene therapy; vascular disease;
XX CC vascular hyperplasia; atherosclerosis; restenosis; glomerulonephritis;
XX CC hypertension; obstructive bladder disease; tubuloclerosis; asthma;
XX CC interstitial tubular disease; human; PCR; primer; ss.
XX CC
XX CC OS Homo sapiens.
XX CC
XX CC PN WO200268599-A2.
XX CC
XX CC PD 06-SEP-2002.
XX CC
XX CC PF 22-FEB-2002; 2002WO-US005560.
XX CC
XX CC PR 22-FEB-2001; 2001US-0271183P.
XX CC PR 23-MAY-2001; 2001US-0293097P.
XX CC
XX CC PA (UVRP ) UNIV ROCHESTER.
XX CC
XX CC PI Miano JM, Streb JW, Chen J;
XX CC DR WPI; 2002-713371/77.
XX CC
XX CC
XX CC Claim 30; Page 33; 129pp; English.
XX CC
XX CC The invention relates to a novel mammalian retinoid-inducible serine
XX CC carboxypeptidase (RISC) protein or polypeptide. The proteins of the
XX CC invention have antiarteriosclerotic, antihypertensive, nephrotropic,
XX CC antiasthmatic, and vasotropic activity. The polynucleotides of the
XX CC invention may have a use in gene therapy. The retinoid-inducible serine
XX CC carboxypeptidase protein and the nucleic acid molecule are useful in
XX CC detecting, preventing or treating vascular diseases or disorders, e.g.
XX CC vascular hyperplasia, atherosclerosis, restenosis, glomerulonephritis,
XX CC hypertension, obstructive bladder disease, tubuloclerosis, asthma or
XX CC interstitial tubular disease, in inhibiting smooth muscle cell growth and
XX CC inhibiting the activity of extracellular regulated kinase. The transgenic
XX CC animal is useful in screening and identifying agents that induce or
XX CC suppress the function of the retinoid-inducible genes. The sequence
XX CC represents a PCR primer used in the invention as a primer or probe to the
XX CC human RISC polynucleotide
XX CC
XX CC Sequence 18 BP; 1 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
XX CC
XX CC Query Match 0.4%; Score 14.4; DB 1; Length 18;
XX CC Best Local Similarity 93.8%; Pred. No. 2.4e+02;
XX CC Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX CC
XX CC QY 1429 GCAGCAGCGACACAG 1444
XX CC |||||
XX CC Db 17 GCAGCAGCGACACAG 2
XX CC
XX CC RESULT 355
XX CC ABL57876/C
XX CC ID ABL57876 standard; DNA; 18 BP.
XX CC
XX CC AC ABL57876;
XX CC
XX CC DT 05-AUG-2002 (first entry)
XX CC
XX CC DE Human ABCA7 gene PCR primer ABCA7_AX.
XX CC
XX CC KW Human; ABCA7; promoter; immunomodulatory; antiinflammatory; metabolic;
XX CC ATP-Binding Cassette; lipid metabolism disorder; immune response;
XX CC inflammation; gene therapy; PCR; primer; ss.
XX CC
XX CC OS Homo sapiens.
XX CC
XX CC PN WO200234903-A2.
XX CC
XX CC PD 02-MAY-2002.
XX CC
XX CC PF 17-OCT-2001; 2001WO-FR003219.
XX CC
XX CC PR 24-OCT-2000; 2000FR-00013649.
XX CC PR 28-NOV-2000; 2000US-0253141P.
XX CC
XX CC PA (AVET ) AVENTIS PHARMA SA.
XX CC (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX CC
XX CC PI Deneffe P, Rosier M, Prades C, Arnould-Reguigne I;
XX CC PI Osorio Y ForteaJ, Duverger N, Chimini G;
XX CC
XX CC DR WPI; 2002-362799/39.
XX CC
XX CC New promoter of the ABCA7 gene, useful for identifying modulators of
XX CC transcription and in gene therapy of e.g. disorders of lipid metabolism.
XX CC
XX CC Example 3; Page 98; 126pp; French.
XX CC
XX CC The present invention relates to ABCA7 gene promoter sequences (ABC

```

CC stands for ATP-Binding Cassette), which are used to identify agents (A)
 CC that modulate transcription of nucleic acids placed under control of the
 CC promoter. (A) is potentially useful for treating or preventing defects in
 CC lipid metabolism and defects in mechanisms involved in the immune
 CC response and inflammation. The promoters can also be used in gene therapy
 CC to control expression of therapeutic genes. Analysis of the promoter
 CC sequences can be used diagnostically, particularly to identify subjects
 CC at risk of lipid metabolism disorders. The present sequence is a PCR
 CC primer for human ABCA7, used to illustrate the invention
 XX
 SQ Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1507 GCACAGCAGCAGCAGC 1522
 Db 18 GCACAGCAGCAGCAGC 3

RESULT 356
 ADK95201
 ID ADK95201 standard; DNA; 18 BP.

XX AC ADK95201;

XX DT 06-MAY-2004 (first entry)

XX DE Primer of the invention #921.

XX KW human; single nucleotide polymorphism; SNP; ss; primer.

XX OS Synthetic.

XX FN JP2003259875-A.

XX PD 16-SEP-2003.

XX PF 08-MAR-2002; 2002JP-00064373.

XX PR 08-MAR-2002; 2002JP-00064373.

XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX DR WPI; 2004-093977/10.

XX PT Novel polynucleotide useful for PCR amplification along with two DNA
 fragment from another set of sequences, or for detecting single
 PT nucleotide polymorphism in human gene.

XX PS Claim 2; SEQ ID NO 4230; 2627pp; Japanese.

XX CC The present invention relates to a polynucleotide isolated from a human
 CC gene and is useful for detecting a single nucleotide polymorphism in a
 CC human gene or for diagnosing of disease. The invention enables the
 CC detection of a single nucleotide polymorphism in a human gene. The
 CC present sequence represents a primer of the invention.

XX SQ Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 986 CAGCAGCAGCAGCAGC 1001
 Db 3 CAGCAGCAGCAGCAGC 18

RESULT 357
 ADM69867/c
 ID ADM69867 standard; DNA; 18 BP.

XX AC

ADM69867;

XX DT 03-JUN-2004 (first entry)

XX DE Plant gene polymorphism marker related primer, SEQ ID 746.

XX KW Primer; variation mapping; mutation mapping; plant;
 gene polymorphism marker; ss.

XX OS Synthetic.

XX FN JP2003289885-A.

XX PD 14-OCT-2003.

XX PF 31-JAN-2003; 2003JP-00024620.

XX PR 01-FEB-2002; 2002JP-00025338.

XX PA (RIKA) RIKAGAKU KENKYUSHO.

XX PA (SAIM-) SAI MEDIA KK.

XX PA (MATS/) MATSUI M.

XX PA (NAKA/) NAKAZAWA M.

XX DR WPI; 2004-126231/13.

XX PT A primer set and method useful for mapping at least the
 variation/mutation part of a plant gene using a gene polymorphism marker.

XX PS Claim 7; SEQ ID NO 746; 120pp; Japanese.

XX CC The present invention relates to a primer set and method for mapping at
 least the variation/mutation part of a plant gene using a gene
 CC polymorphism marker. A mutation site of the plant gene is mapped by
 CC utilizing a genetic polymorphism marker as follows: (a) genomic DNA is
 CC prepared from a plant homozygously having a mutation to be an object of
 CC the mapping; (b) A forward primer 1 containing a base corresponding to
 CC the gene polymorphic maker of one ecotype plant, a forward primer 2
 CC containing a base corresponding to the genetic polymorphism of the other
 CC ecotype plant and a reverse primer 3 based on the base sequence common
 CC with both the ecotype plants are prepared; (c) two kinds of
 CC oligonucleotides emitting fluorescence of different colors when the
 CC genetic polymorphism marker is detected are prepared; (d) an
 CC amplification reaction of the genomic DNA is carried out in the presence
 CC of the primers 1, 2 and 3 and the two kinds of the oligonucleotides; (e)
 CC the fluorescence intensity emitted from the resultant reactional product
 CC is detected and (f) the position on the genome of the mutation site is
 CC determined from the results of detection. The present sequence is a
 CC primer, used to illustrate the invention.

XX SQ Sequence 18 BP; 3 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2463 CACCACAGAGAACATC 2478

Db 16 CACCACAGAGACCATC 1

RESULT 358
 ADN06360
 ID ADN06360 standard; DNA; 18 BP.

XX AC ADN06360;

XX DT 15-JUL-2004 (first entry)

XX DE Human FLAP related microsatellite marker SEQ ID NO:8.

XX KW leukotriene synthesis inhibitor; myocardial infarction;


```

ADS94379
ID ADS94379 standard; DNA; 18 BP.
XX
AC ADS94379;
XX
XX
DT 02-DEC-2004 (first entry)
XX
DE Human 5-lipoxygenase activating protein (FLAP) gene PCR primer #5.
XX
KW human; 5-lipoxygenase activating protein; FLAP; chromosome 13q12;
KW single nucleotide polymorphism; SNP; myocardial infarction; PCR; primer;
KW microsatellite marker; ss.
XX
OS Homo sapiens.
XX
XX WO2004035746-A2.
XX
XX 29-APR-2004.
XX
XX 16-OCT-2003; 2003WO-US032805.
XX
XX 17-OCT-2002; 2002US-0419432P.
XX
XX (DECO-) DECODE GENETICS EHF.
XX
XX Helgadottir A, Gulcher JR, Manolescu A;
XX
XX WPI; 2004-348442/32.
XX
XX Novel FLAP (5-lipoxygenase activating protein) nucleic acid useful for
XX diagnosing myocardial infarction and for identifying agent that is useful
XX for treating myocardial infarction.
XX
XX Example; SEQ ID NO 8; 230pp; English.
XX
XX The invention comprises nucleic acid sequences of the human 5-
XX lipoxygenase activating protein (FLAP) gene - present on chromosome
XX 13q12. In particular the invention relates to polymorphisms identified
XX within this gene. The DNA sequences of the invention are useful for
XX diagnosing susceptibility to myocardial infarction and identifying agents
XX that alter expression of FLAP. The present DNA sequence represents a PCR
XX primer that is used to amplify a microsatellite marker from the human
XX FLAP gene.
XX
XX Sequence 18 BP; 4 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1648 CCAGCCTTTGCTAAGG 1663
Db 2 CCAGCCTTTGCTTAGG 17
|||||
|||||

RESULT 361
ABS71093
ID ABS71093 standard; DNA; 26 BP.
XX
AC ABS71093;
XX
XX 27-NOV-2002 (first entry)
XX
XX Human GPCR ligand Bv8 cDNA PCR primer hbv8-F1.
XX
XX G-protein coupled receptor; GPCR; ZAQ; human; ZAQ; ZAQ; rat; ZAQ1;
XX rZAQ1; rZAQ2; mouse; ISE receptor; mISE; GPR73; Bv8 protein;
XX digestive disorder; central nervous system disorder; CNS; diarrhoea;
XX bowel inflammation; constipation; food absorption disorder; nootropic;
XX Alzheimer's disease; Parkinson's disease; schizophrenia; laxative;
XX antiinflammatory; antidiarrhoeic; neuroleptic; neuroprotective; PCR;
XX primer; ss.
XX

OS Homo sapiens.
XX
XX WO200262944-A2.
XX
XX 15-AUG-2002.
XX
XX 01-FEB-2002; 2002WO-JP000852.
XX
XX 02-FEB-2001; 2001JP-00026820.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;
XX Hinuma S;
XX
XX WPI; 2002-627537/67.
XX
XX Screening of compounds modifying the binding of G-protein coupled
XX receptor protein ZAQ and related proteins to their ligands for use in
XX treatment and diagnosis of digestive disorders.
XX
XX Example 3; Page 117; 197pp; Japanese.
XX
XX The present invention relates to a screening method for compounds for
XX their ability to modify the binding of G-protein coupled receptor (GPCR)
XX protein ZAQ and related proteins (human ZAQ, human ZAQ, rat ZAQ1
XX (rZAQ1), rZAQ2, human and mouse ISE (mISE) receptor, and mouse GPR73) to
XX their ligands (the mature form of human, mouse or rat Bv8 protein). The
XX receptor protein and ligand are contacted in the presence or absence of
XX the test compound. The compounds are useful in a drug composition for the
XX treatment, and prevention of digestive and central nervous system (CNS)
XX disorders, including bowel inflammation, diarrhoea, constipation, food
XX absorption disorders, Alzheimer's disease, Parkinson's disease and
XX schizophrenia. The present sequence represents a PCR primer used in the
XX examples of the present invention
XX
XX Sequence 26 BP; 1 A; 9 C; 6 G; 10 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 14.4; DB 1; Length 26;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1931 CTTCTTCTCCAGCAGCAGATGCTG 1954
Db 1 CTACTTCTGCTGCTGCTGCTGCTG 24
|||||
|||||

RESULT 362
ADD69029
ID ADD69029 standard; DNA; 26 BP.
XX
XX ADD69029;
XX
XX 15-JAN-2004 (first entry)
XX
XX Angiogenesis inhibitor-related PCR primer hbv8-F1.
XX
XX angiogenesis inhibitor; cytostatic; antiinflammatory; cancer;
XX ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; ISE; ss;
XX PCR; primer; hbv8-F1.
XX
XX Unidentified.
XX
XX WO2003066860-A1.
XX
XX 14-AUG-2003.
XX
XX 03-FEB-2003; 2003WO-JP001057.
XX
XX 04-FEB-2002; 2002JP-00027299.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX

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Query Match          0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 365
ACA99716/c
ID ACA99716 standard; DNA; 17 BP.
XX
AC ACA99716;
XX
DT 28-JUL-2003 (first entry)
XX
DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #209.
XX
KW Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
XX G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS Homo sapiens.
XX
FN WO2003031621-A2.
XX
PD 17-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032599.
XX
PR 12-OCT-2001; 2001US-0329000P.
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Zhang J;
XX
DR WPI; 2003-381720/36.
XX
New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
investigating and/or treating disorders associated with aberrant
expression or activity of GPCR-A-1, such as tumors and cancers.
Example 2; SEQ ID NO 233; 156pp; English.
The invention describes an isolated nucleic acid encoding a G protein
coupled receptor (GPCR), mutations of which cause cancer, comprising a
2225 or 1921 base pair sequence, or their degenerate variants, encoding a
409 residue amino acid sequence, all given in the specification, with or
without conservative amino acid substitutions, or complements of the
sequence of them. The encoding nucleic acid is not more than 100 kbase in
length. The methods and compositions of the present invention are useful
for diagnosing, investigating and/or treating disorders associated with
aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
This sequence represents an oligonucleotide used to analyse the gene
encoding human G-protein coupled receptor GPCR-A-1
Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2660 GTGGCTCCTCTCTAA 2673
Db 16 GTGGCTCCTCTCTAA 3
RESULT 366
ACA99715/c
ID ACA99715 standard; DNA; 17 BP.
XX
AC ACA99715;
XX
DT 28-JUL-2003 (first entry)
XX
DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #208.
XX
KW Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
XX G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS Homo sapiens.
XX
FN WO2003031621-A2.
XX
PD 17-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032599.
XX
PR 12-OCT-2001; 2001US-0329000P.
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Zhang J;
XX
DR WPI; 2003-381720/36.
XX
New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
investigating and/or treating disorders associated with aberrant
expression or activity of GPCR-A-1, such as tumors and cancers.
Example 2; SEQ ID NO 233; 156pp; English.
The invention describes an isolated nucleic acid encoding a G protein
coupled receptor (GPCR), mutations of which cause cancer, comprising a
2225 or 1921 base pair sequence, or their degenerate variants, encoding a
409 residue amino acid sequence, all given in the specification, with or
without conservative amino acid substitutions, or complements of the
sequence of them. The encoding nucleic acid is not more than 100 kbase in
length. The methods and compositions of the present invention are useful
for diagnosing, investigating and/or treating disorders associated with
aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
This sequence represents an oligonucleotide used to analyse the gene
encoding human G-protein coupled receptor GPCR-A-1
Sequence 17 BP; 5 A; 4 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2660 GTGGCTCCTCTCTAA 2673
Db 16 GTGGCTCCTCTCTAA 3
RESULT 367
ADC37815
ID ADC37815 standard; DNA; 17 BP.
XX
AC ADC37815;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human AMLP1a scanning 17-mer oligonucleotide SEQ ID NO:164.
XX
KW human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
XX AMLP1a; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
FN WO2003037931-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035129.
XX
PR 01-NOV-2001; 2001US-0334773P.
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Shannon M, Phan T;
XX
DR WPI; 2003-430501/40.
XX
```

PT New isolated nucleic acid molecule encoding a human angiotensin-like
PT protein, useful for treating or preventing a disorder associated with
XX decreased or increased expression or activity of AMLP1.
XX
XX Example 2; SEQ ID NO 164; 172pp; English.
XX
XX The present invention describes the human angiotensin-like protein 1
CC (AMLP1). human AMLP1 has cytosolic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1a, which is used in an example from the
CC present invention.
XX
XX
SQ Sequence 17 BP; 5 A; 5 C; 7 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAAC 1442
DB 4 GCAGCAGCAGCAAC 17
RESULT 368
ADF78423/C
ID ADF78423 standard; DNA; 17 BP.
XX
XX AC ADF78423;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE Chromosomal abnormality detection-related APC small deletion DNA 169.
XX
XX KW chromosomal abnormality; maternal locus; genetic disorder; foetus;
KW mutation; translocation; transversion; monosomy; trisomy 21;
KW Chromosome 21; Down's Syndrome; aneuploidies; chromosome deletion;
KW chromosome addition; chromosome amplification; chromosome translocation;
KW chromosome rearrangement; single nucleotide polymorphism detection;
KW SNP detection; pregnant female; APC; adenomatous polyposis coli; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200307423-A2.
XX
XX PD 12-SEP-2003.
XX
XX PF 28-FEB-2003; 2003WO-US006198.
XX
XX PR 01-MAR-2002; 2002US-0360232P.
XX
XX PR 11-MAR-2002; 2002US-00093618.
XX
XX PR 08-MAY-2002; 2002US-0378354P.
XX
XX (DHALL/) DHALLAN R.
XX
XX PI Dhallan R;
XX
XX PT WPI; 2003-845073/78.
XX
XX DR Detection of chromosomal abnormalities e.g. Down's Syndrome, non-
PT invasively in a fetus, comprises forming a ratio of amounts of alleles at
PT a locus of interest and a different heterozygous locus.
XX
XX Example 7; Page 164; 164pp; English.
XX
XX This invention relates to a novel method of detecting chromosomal
XX abnormalities by determining the sequence of alleles of a locus of
CC interest from template DNA, determining which alleles are present and
CC comparing to amounts of alleles at a different, selected heterozygous
CC locus (for example on another chromosome or a maternal locus); relative
CC amounts are expressed as a ratio indicating presence or absence of the

CC abnormality. The method is useful for the detection of genetic disorders,
CC especially in a foetus, including chromosomal abnormalities and
CC mutations, for example translocations, transversions, monosomies,
CC trisomies (for example trisomy 21 in which an additional copy of
CC chromosome 21 results in Down's Syndrome) and other aneuploidies,
CC deletions, additions, amplifications, translocations and rearrangements.
CC It can be used to detect any alterations in a gene sequence, especially
CC single nucleotide polymorphisms (SNPs), and may be used to detect
CC numerous abnormalities simultaneously, for example if several SNPs are
CC associated with a particular disease. The method provides a rapid, non-
CC invasive method for determining the sequence of DNA from a foetus using a
CC sample from a pregnant female, for example to detect genetic disorders as
CC above or to determine if a foetus is a carrier of a disease or
CC predisposed to a disease.

XX SQ Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3174 TGTTTCAGGTGGACT 3187
DB 14 TGTTTCAGGTGGACT 1

RESULT 369
ADH53228/C
ID ADH53228 standard; DNA; 17 BP.

XX AC ADH53228;

XX DT 25-MAR-2004 (first entry)

XX DE Human APC (adenomatous polyposis coli) DNA fragment 165.

XX KW sequence determination; recognition site; restriction endonuclease;
KW human; APC; adenomatous polyposis coli; chromosome 5q21-22;
KW colorectal cancer; ds.

XX OS Homo sapiens.

XX PN WO2003074740-A1.

XX PD 12-SEP-2003.

XX PF 28-FEB-2003; 2003WO-US006376.

XX PR 01-MAR-2002; 2002US-0360232P.

XX PR 11-MAR-2002; 2002US-00093618.

XX PR 08-MAY-2002; 2002US-0378354P.

XX (DHALL/) DHALLAN R.

XX PI Dhallan R;

XX DR WPI; 2003-756772/71.

XX PT Determining a sequence of a locus of interest comprises replicating a

XX region of DNA comprising a locus of interest from a template

XX polynucleotide by using a first and a second primer.

XX Example 5; Page 141; 190pp; English.

XX The invention relates to a novel method for determining the sequence of a
CC locus of interest which comprises replicating a region of DNA comprising
CC a locus of interest from a template polynucleotide by using a first and a
CC second primer where the second primer contains a sequence that generates
CC a recognition site for a restriction enzyme such that digestion with the
CC restriction enzyme generates a 5' overhang containing the locus of
CC interest. The method may be useful for determining the sequences of
CC multiple loci of interest concurrently and for determining the sequence
CC of a mutant allele in the presence of a normal allele. The current

```
CC sequence is that of the human APC (adenomatous polyposis coli) DNA
CC fragment of the invention which is located on chromosome 5q21-22 and in
CC which mutations are associated with colorectal cancer.
XX
SQ Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match      0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3174 TGTTCAGGTGGACT 3187
Db 14 TGTTCAGGTGGACT 1

RESULT 370
ADI50862
ID ADI50862 standard; DNA; 17 BP.
XX
AC ADI50862;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID3365.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytosatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 3365; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match      0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1042 ACCAGGTCCATTG 1055
Db 17 ACCAGGTCCATTG 4

RESULT 372
ADI47898/C
ID ADI47898 standard; DNA; 17 BP.
XX
AC ADI47898;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID401.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytosatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 401; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 5 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

Query Match      0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1042 ACCAGGTCCATTG 1055
Db 17 ACCAGGTCCATTG 4

RESULT 372
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ADR97999/c
ID ADR97999 standard; DNA; 17 BP.
XX
AC ADR97999;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human APC DNA fragment containing deletion at codon 1371.
XX
DE ds; chromosomal abnormality; detection; foetus; translocation;
KW transversion; monosomy; trisomy; aneuploidy; deletion; addition;
KW amplification; prenatal diagnosis; SNP; single nucleotide polymorphism;
KW human; chromosome 5q21-22; adenomatous polyposis coli; mutation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004079011-A1.
XX
PD 16-SEP-2004.
XX
PF 29-AUG-2003; 2003WO-US027308.
XX
PR 28-FEB-2003; 2003WO-US006198.
XX
PA (RAVG-) RAVGEN INC.
XX
PI Dhallan R;
XX
DR WPI; 2004-677127/66.
XX
PT Detecting a chromosomal abnormality, e.g. translocations, transversions,
PT monosomies, trisomies, aneuploidies, deletions, or arrangements, comprises
PT determining the sequence of alleles of a locus of interest in the sample
PT from template DNA.
XX
PS Example 7; Page 156; 429pp; English.
XX
CC This invention describes a novel method for detecting a chromosomal
CC abnormality in a sample which comprises determining the sequence of
CC alleles of a locus of interest in a sample from template DNA where
CC determining the sequence of the alleles comprises amplifying the locus of
CC interest, hybridising the amplified loci to GeneChip array, washing
CC GeneChip array, staining the GeneChip array with detectable reagents, and
CC scanning GeneChip array. The amplification method is self-sustained
CC sequence reaction, ligase chain reaction, rapid amplification of cDNA
CC ends, PCR and ligase chain reaction, Q-beta phage amplification, strand
CC displacement amplification, or splice overlap extension PCR, preferably
CC PCR. The determination of the sequence of the alleles comprises
CC amplifying the locus of interest, fragmenting the amplicon, hybridising
CC fragmented amplicons to CodeLink Arrays, extension reaction to
CC incorporate a nucleotide and detecting incorporated nucleotides. The
CC amplicon fragmentation is by exonuclease digestion. Detecting a
CC chromosomal abnormality in a sample comprises determining the sequence of
CC alleles of a locus of interest from template DNA, where determining the
CC sequence of the alleles comprises using BeadArray Technology. The
CC determination of the sequence of the alleles may also be done by
CC amplifying the locus of interest, dephosphorylation of the unused
CC reagents, in vitro transcription reaction of the products, RNase A
CC cleavage of the products, mixing the products with CleanResin,
CC transferring products to SpectroCHIP, and analysing the SpectroCHIP. The
CC dephosphorylation reaction is with shrimp alkaline phosphatase.
CC Alternatively, the determination of the sequence of the alleles comprises
CC amplifying the locus of interest, dephosphorylation of the unused
CC reagents, hybridising a primer to the locus of interest, incorporating a
CC nucleotide, mixing the products with CleanResin, transferring products to
CC SpectroCHIP, and analysing the SpectroCHIP. The hybridisation of primer
CC is adjacent to the locus of interest. The determination of the sequence
CC of the alleles may also comprise amplifying the locus of interest,
CC treating the products with exonuclease, single stranded DNA is annealed
CC to an oligonucleotide, incorporating a nucleotide using the annealed
CC template and primer, and detecting the incorporated nucleotide. The
CC method is useful for detecting a chromosomal abnormality in a sample.

Specifically, the method is useful for detecting chromosomal
abnormalities in a fetus including translocations, transversions,
monosomies, trisomies, and other aneuploidies, deletions, additions,
amplifications, and arrangements. The method of the invention can also be
used for prenatal diagnosis. This sequence represents a fragment of the
human adenomatous polyposis coli (APC) gene which contains a nucleotide
deletion.
Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3174 TGTTGAGTGGACT 3187
Db 14 TGTTGAGTGGACT 1
RESULT 373
ADS08683/C
ID ADS08683 standard; DNA; 17 BP.
XX
AC ADS08683;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human DNA oligonucleotide #172.
XX
KW Human; nucleic acid detection; cell lysis; chromosomal abnormality;
KW cancer; carcinoma; bladder; breast; bronchus; colon; kidney; liver; lung;
KW oesophagus; gall bladder; ovary; pancreas; stomach; cervix; thyroid;
KW prostate; skin; small cell lung cancer; squamous cell carcinoma;
KW leukaemia; lymphoma; myelodysplastic syndrome; fibrosarcoma;
KW rhabdomyosarcoma; astrocytoma; neuroblastoma; glioma; schwannoma;
KW melanoma; seminoma; teratocarcinoma; osteosarcoma; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004078994-A2.
XX
PD 16-SEP-2004.
XX
PF 01-MAR-2004; 2004WO-US006337.
XX
PR 28-FEB-2003; 2003WO-US006198.
XX
PA (RAVG-) RAVGEN INC.
XX
PI Dhallan R;
XX
DR WPI; 2004-662434/64.
XX
PT Detecting presence or absence of nucleic acid, containing mutation,
PT involves isolating nucleic acid from sample containing cell lysis
PT inhibitor, and detecting presence or absence of nucleic acid.
XX
PS Example 7; Page 165; 440pp; English.
XX
CC The invention relates to a method for detecting a nucleic acid, involving
CC isolating a nucleic acid from a sample, where an agent that impedes cell
CC lysis was added to the sample, and detecting the presence or absence of
CC the nucleic acid. The invention also relates to a method for detecting of
CC chromosomal abnormalities in a DNA sample and determining the sequence of
CC foetal DNA from a sample of a pregnant female. The nucleic acid contains
CC at least one mutation chosen from a single point mutation, multiple point
CC mutations, an insertion, a frameshift, a truncation, a deletion, a
CC duplication and a transversion. The method is useful for detecting
CC nucleic acid in a sample obtained from a source chosen from bacteria,
CC viruses, fungi, mycobacteria, protozoa, molds, yeasts, plants, humans,
CC non-humans, multi-cellular parasites, animals and archaeobacteria. The
CC method is useful for detecting, diagnosing or monitoring a disease such

as cancer chosen from carcinoma of the bladder, breast, bronchus, colon, kidney, liver, lung, oesophagus, gall bladder, ovary, pancreas, stomach, cervix, thyroid, prostate and skin, small cell lung cancer, squamous cell carcinoma, haematopoietic tumours of lymphoid lineage, leukaemia, acute lymphocytic leukaemia, acute lymphoblastic leukaemia, B-cell lymphoma, T-cell lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma, hairy cell lymphoma, Burkett's lymphoma, haematopoietic tumours of myeloid lineage, acute and chronic myelogenous leukaemias, myelodysplastic syndrome and promyelocytic leukaemia, tumours of mesenchymal origin, fibrosarcoma and rhabdomyosarcoma, tumours of the central and peripheral nervous system, astrocytoma, neuroblastoma, glioma and schwannomas, melanoma, seminoma, teratocarcinoma and osteosarcoma. The method is also useful for monitoring response to treatment chosen from surgery, radiation, lifestyle change, dietary protocol and supplementation and administration of a drug. The drug is chosen from chemotherapeutic agents, antibacterial agents, anti-viral agents, anti-fungal agents, targeted-cancer drugs, cytotoxic agents, cytostatic agents and anti-proliferative agents. This sequence represents a DNA oligonucleotide used in the scope of the invention.

Sequence 17 BP; 6 A; 6 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 3174 TGTTCAGTGGACT 3187

Db 14 TGTTCAGTGGACT 1

RESULT 374

AAZ44310/C

ID AA244310 standard; DNA; 30 BP.

XX AA244310;

DT 04-APR-2000 (first entry)

DE Human SCA7 primer 1.

XX SCA7; human; spinocerebellar ataxia type 7; SCA1; SCA2; SCA3; SCA6;

XX repeat expansion detection; RED analysis; detection; primer; ss.

XX Homo sapiens.

XX CA2245310-A.

XX 19-FEB-1999.

XX 19-AUG-1998; 98CA-02245310.

XX 19-AUG-1997; 97US-0056170P.

XX (MINU) UNIV MINNESOTA.

XX Koob MD, Ranum LP;

XX WPI; 2000-098181/09.

XX Identifying individuals at risk of developing spinocerebellar ataxia type 7 by analyzing trinucleotide repeat regions of spinocerebellar ataxia type 7 gene.

XX Disclosure; Page 43; 66pp; English.

XX This invention describes a novel method for identifying individuals at risk for developing spinocerebellar ataxia type 7 (SCA7). The method comprises analyzing the CAG repeat region of a SCA7 gene to detect CAG repeats, where individuals at risk have at least 30 CAG repeats and those not at risk have less than 19 CAG repeats. The method is useful for identifying individuals at risk of developing SCA7 and also those at risk of developing SCA1, 2, 3 or 6. The use of genomic DNA in the repeat

CC expansion detection (RED) analysis allows isolation of any potential trinucleotide repeat expansion regardless of the expression pattern. CC Utilization of different oligonucleotides in the RED assay allows any of the possible trinucleotide repeats to be detected, and the cycled nature of the reaction makes it extremely sensitive. This sequence represents a CC primer used to amplify the human SCA7 gene which is described in the CC method of the invention

XX Sequence 30 BP; 10 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 30;

Best Local Similarity 66.7%; Pred. No. 6e+02; Mismatches 10; Indels 0; Gaps 0;

XX Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1925 CAGCAATTTCTTCTCCAGCAGCAGATGCTG 1954

Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 375

AAS13781/C

ID AAS13781 standard; DNA; 30 BP.

XX AAS13781;

DT 08-MAY-2002 (first entry)

XX Simple sequence repeat, SSR, #52.

XX Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;

XX cereal profiling; grass profiling; seed batch purity testing.

XX Synthetic.

XX NZ509193-A.

XX 25-MAY-2001.

XX 03-JAN-2001; 2001NZ-00509193.

XX 24-DEC-1999; 99AU-00004906.

XX 04-MAY-2000; 2000AU-00007310.

XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.

XX (UYSC-) UNIV SOUTHERN CROSS.

XX (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.

XX (UYAD-) UNIV ADELAIDE.

XX (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.

XX Forster JW, Jones ES;

XX WPI; 2001-512563/56.

XX New simple sequence repeats having 2 or more tandemly repeated nucleotide core elements isolated from ryegrass and fescue, useful for selecting of genes in grass or cereal breeding or profiling grass or cereal species varieties.

XX Claim 13; Page 53; 72pp; English.

XX The invention relates to a substantially purified or isolated nucleic acid (I) from ryegrass or fescue species including a simple sequence repeat (SSR), having 2 or more tandemly repeated nucleotide core elements 2-6 nucleotides in length. Also included are a nucleic acid primer suitable for amplifying an SSR, identifying (M1) an SSR by preparing a library of ryegrass or fescue genomic DNA enriched for SSRs and identifying clones in the library containing SSRs, a library of ryegrass or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for a gene in grass or cereal breeding by identifying an SSR that is closely associated with the gene such that the SSR and the gene are preferentially co-inherited, and selecting for the SSR in the breeding, a method for DNA profiling grass or cereal species varieties by assessing variation between SSR varieties and testing the purity of grass or cereal

CC seed batches by assessing variation within seed batch of an SSR. The SSRs
CC may be used in the selection of genes in grass or cereal breeding, for
CC profiling grass or cereal species varieties, for testing the purity of
CC grass or cereal seed batches, and for DNA profiling to establish the
CC distinct identity, uniformity and/or stability of a cultivar. The present
CC sequence is a rye grass or fescue SSR
XX
SQ Sequence 30 BP; 10 A; 10 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTCTCCAGCAGCAGATGCTG 1954

DB 30 CRGCTGCTGCTGCTGCTGCTGCTGCTG 1

RESULT 376

AAV81598/c

ID AAV81598 standard; DNA; 17 BP.

AC AAV81598;

XX 11-MAY-1999 (first entry)

XX Oligonucleotide used in PNA-DNA-PNA chimeric macromolecule.

XX PNA; peptide nucleic acid; nuclease resistance; diagnostic; ss.

XX Synthetic.

XX WO9514706-A1.

XX 01-JUN-1995.

XX 23-NOV-1994; 94WO-US013523.

XX 24-NOV-1993; 93US-00158352.

XX (ISIS-) ISIS PHARM INC.

PA Cook PD;

XX WPI; 1995-206893/27.

XX New chimeric macromolecules contg. DNA and peptide nucleic acid segments
PT - with good nuclease stability and binding affinity, also activating
PT RNaseH, useful for treating disease, in diagnosis and for identifying
PT chemotherapeutic agents.

XX Disclosure; Page 50; 68pp; English..

XX The patent discloses new macromolecules of formula PNA-DNA-PNA, in which
CC DNA comprises at least one 2'-deoxynucleotide and each PNA comprises at
CC least one peptide nucleic acid subunit. These compounds have increased
CC resistance to nuclease and increased specific binding affinity, and they
CC can activate RNaseH for target strand cleavage. They can hybridise
CC specifically to a nucleic acid strand (especially RNA) and are useful (1)
CC for treating diseases associated with undesirable production of protein,
CC (2) for in-vitro modification of sequence-specific nucleic acid (by
CC contacting a test solution with the macromolecule and RNaseH), or (3) for
CC in-vivo enhancement of polynucleotide hybridisation and RNase activity.
CC They can also be used diagnostically and for screening chemotherapeutic
CC agents

XX SQ Sequence 17 BP; 2 A; 5 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 CGGAATTCAGCGAGAA 54

Db 17 CTGAATGCAGCGAGAA 1

RESULT 377

AAV63806/c

ID AAV63806 standard; RNA; 17 BP.

XX AAV63806;

XX 20-JUL-1999 (first entry)

XX Rabbit stromelysin hammerhead target SEQ ID NO:438.

XX Arthritic condition; graft tolerance; immune response; target; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
XX stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;
XX diagnosis; ss.

XX Oryctolagus cuniculus.

XX WO9618736-A2.

XX 20-JUN-1996.

XX 22-NOV-1995; 95WO-US015516.

XX 13-DEC-1994; 94US-00354920.

XX 23-DEC-1994; 94US-00363253.

XX 23-DEC-1994; 94US-00363254.

XX 17-FEB-1995; 95US-00390850.

XX 20-APR-1995; 95US-00426124.

XX 02-MAY-1995; 95US-00432874.

XX 04-MAY-1995; 95US-00434509.

XX 07-JUL-1995; 95US-0000951P.

XX 07-JUL-1995; 95US-0000974P.

XX 07-AUG-1995; 95US-00512861.

XX 05-OCT-1995; 95US-00541365.

XX (RIBO-) RIBOZYME PHARM INC.

XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;

PI Mcswiggen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;

PI Karpelsky A, Thompson JD, Modak A, Burgin A;

XX WPI; 1996-300653/30.

XX Enzymatic nucleic acid molecules having a hammer-head motif - used for
PT the treatment of arthritis, induction of graft tolerance or treatment of
PT auto-immune diseases.

XX Example 1; Page 153; 307pp; English.

XX The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
CC; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
CC can inhibit collagenase and stromelysin production in the synovial
CC membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention

XX

SQ Sequence 17 BP; 3 A; 3 C; 4 G; 0 T; 7 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 560 AATGAACCTGACCAACAT 576
 DB 17 ACTGAAGTGACCAACAT 1

RESULT 378
 AAX63820/C
 ID AAX63820 standard; RNA; 17 BP.
 XX AC AAX63820;
 XX DT 20-JUL-1999 (first entry)
 XX DE Rabbit stromelysin hammerhead target SEQ ID NO:452.
 XX KW Arthritic condition; graft tolerance; immune response; target; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
 KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
 KW diagnosis; ss.
 XX OS Oryctolagus cuniculus.
 XX PN W09618736-A2.
 XX PD 20-JUN-1996.
 XX PF 22-NOV-1995; 95WO-US015516.
 XX PR 13-DEC-1994; 94US-00354920.
 XX PR 23-DEC-1994; 94US-00363253.
 XX PR 23-DEC-1994; 94US-00363254.
 XX PR 17-FEB-1995; 95US-00390850.
 XX PR 20-APR-1995; 95US-00426124.
 XX PR 02-MAY-1995; 95US-00432874.
 XX PR 04-MAY-1995; 95US-00434509.
 XX PR 07-JUL-1995; 95US-0000951P.
 XX PR 07-JUL-1995; 95US-0000974P.
 XX PR 07-AUG-1995; 95US-00512861.
 XX PR 05-OCT-1995; 95US-00541365.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
 PI Mcswiggen J, Gustofson J, Ueman N, Wincott F, Matulic-Adamic J;
 PI Karpelesky A, Thompson JD, Modak A, Burgin A;
 XX WPT; 1996-300653/30.
 XX Enzymatic nucleic acid molecules having a hammer-head motif - used for
 PT the treatment of arthritis, induction of graft tolerance or treatment of
 PT auto-immune diseases.
 XX Example 1; Page 153; 307pp; English.
 XX The present invention describes a novel enzymatic nucleic acid (ENA)
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
 CC; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
 CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
 CC can inhibit collagenase and stromelysin production in the synovial
 CC membrane of joints for the treatment or prevention of arthritis,
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
 CC be used to treat antigen presenting cells of a donor to induce tolerance
 CC in a recipient to an alloantigen of a donor. They can also be used for
 CC enhancing graft tolerance or for treating autoimmune disease, and for
 CC treating allergies and other inflammatory conditions. The ENA's can also
 CC be used in diagnosis. Ribozyme impacts on the expression of

CC stromelysin without introducing the non-specific effects upon gene
 CC expression which accompany treatment with retinoids and dexamethasone.
 CC The concentration of ribozyme required to affect a therapeutic treatment
 CC is lower than that required of antisense molecules, and is highly
 CC specific. The present sequence is used in the exemplification of the
 CC present invention
 XX SQ Sequence 17 BP; 2 A; 3 C; 6 G; 0 T; 6 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1432 GCAGCAGCAACAGCAGC 1448
 DB 17 GCAGCATCAACAGCATC 1

RESULT 379
 AAX68730
 ID AAX68730 standard; RNA; 17 BP.
 XX AC AAX68730;
 XX DT 28-JUL-1999 (first entry)
 XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #25.
 XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX OS Homo sapiens.
 XX PN W09715662-A2.
 XX PD 01-MAY-1997.
 XX PF 25-OCT-1996; 96WO-US017480.
 XX PR 26-OCT-1995; 95US-0005974P.
 XX PR 11-JAN-1996; 96US-00584040.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (CHIR) CHIRON CORP.
 XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX WPT; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX Claim 4; Page 47; 218pp; English.
 XX The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX SQ Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 52.9%; Pred. No. 2.5e+02;


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XX OS Homo sapiens.
XX PA WO9715662-A2.
XX PN
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 47; 218pp; English.
XX SQ The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX75725 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.5e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Oy 2167 GTCTACTTCTCAGCGGA 2183
Db 1 GUCUGUCUCACAGGA 17
RESULT 383
AAX71615/c
ID AAX71615 standard; RNA; 17 BP.
XX AC AAX71615;
XX DT 28-JUL-1999 (first entry)
XX DE Human KDR VEGF receptor hammerhead ribozyme substrate #627.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 47; 218pp; English.
XX SQ The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX75725 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.5e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
Oy 2167 GTCTACTTCTCAGCGGA 2183
Db 1 GUCUGUCUCACAGGA 17

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XX (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.
XX PS Claim 4; Page 116; 218pp; English.
XX SQ The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX SQ Sequence 17 BP; 1 A; 6 C; 3 G; 0 T; 7 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1509 AACAGCAGCAGAGCTCA 1525
Db 17 AACAGGAGGAGAGCTCA 1
RESULT 384
AAX69119/c
ID AAX69119 standard; RNA; 17 BP.
XX AC AAX69119;
XX DT 28-JUL-1999 (first entry)
XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #414.
XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
XX KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
XX KW foetal liver kinase 1; ss.
XX OS Homo sapiens.
XX PN WO9715662-A2.
XX PD 01-MAY-1997.
XX PF 25-OCT-1996; 96WO-US017480.
XX PR 26-OCT-1995; 95US-0005974P.
XX PR 11-JAN-1996; 96US-00584040.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (CHIR ) CHIRON CORP.
XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX PT rheumatoid arthritis, etc., in a human patient.

```

XX PS Claim 4; Page 59; 218pp; English.

XX CC The present invention describes nucleic acid molecules which modulate the

XX CC synthesis, expression and/or stability of a mRNA encoding 1 or more

XX CC receptors of vascular endothelial growth factor (VEGF). A patient

XX CC (preferably human) having a condition associated with the level of the

XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing

XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

XX CC treated by administering the nucleic acid molecule or the expression

XX CC vector to the patient. AAX75725 to AAX75752 represent specific examples

XX CC of nucleic acid molecules from the present invention

XX SQ Sequence 17 BP; 1 A; 7 C; 3 G; 0 T; 6 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 GGAGCCAGAGAGACTC 446

DB 17 GGAGCCAGAGAGAGACTC 1

RESULT 385

AAX74484

ID AAX74484 standard; RNA; 17 BP.

XX AC AAX74484;

XX OS Mus sp.

XX PN WO9715662-A2.

XX PD 01-MAY-1997.

XX PF 25-OCT-1996; 96WO-US017480.

XX PR 26-OCT-1995; 95US-0005974P.

XX PR 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

PA (CHIR) CHIRON CORP.

XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,

XX rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 155; 218pp; English.

XX CC The present invention describes nucleic acid molecules which modulate the

XX CC synthesis, expression and/or stability of a mRNA encoding 1 or more

XX CC receptors of vascular endothelial growth factor (VEGF). A patient

XX CC (preferably human) having a condition associated with the level of the

XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing

XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

XX CC treated by administering the nucleic acid molecule or the expression

CC vector to the patient. AAX67275 to AAX75752 represent specific examples

CC of nucleic acid molecules from the present invention

XX SQ Sequence 17 BP; 3 A; 5 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 58.8%; Pred. No. 2.5e+02;

Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2167 GTCTACTTCTCAGCGGA 2183

DB 1 GUCUGCUUCACACAGGA 17

RESULT 386

AAX69821

ID AAX69821 standard; RNA; 17 BP.

XX AC AAX69821;

XX DT 28-JUL-1999 (first entry)

XX DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1116.

XX KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;

XX KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

XX KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;

XX KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;

XX KW foetal liver kinase 1; ss.

XX OS Homo sapiens.

XX PN WO9715662-A2.

XX PD 01-MAY-1997.

XX PF 25-OCT-1996; 96WO-US017480.

XX PR 26-OCT-1995; 95US-0005974P.

XX PR 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

PA (CHIR) CHIRON CORP.

XX PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,

XX rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 80; 218pp; English.

XX CC The present invention describes nucleic acid molecules which modulate the

XX CC synthesis, expression and/or stability of a mRNA encoding 1 or more

XX CC receptors of vascular endothelial growth factor (VEGF). A patient

XX CC (preferably human) having a condition associated with the level of the

XX CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing

XX CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

XX CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

XX CC treated by administering the nucleic acid molecule or the expression

XX CC vector to the patient. AAX67275 to AAX75752 represent specific examples

XX CC of nucleic acid molecules from the present invention

XX SQ Sequence 17 BP; 4 A; 3 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 47.1%; Pred. No. 2.5e+02;

Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 224 TCATTTCTTGATCAAA 240

DB 1 TCATTTCTTGATCAAA 240

```

Db      1  UCAUGUCUUGAUUCAA 17

RESULT 387
AAX74483
ID      AAX74483 standard; RNA; 17 BP.
XX
AC      AAX74483;
XX
DT      28-JUL-1999 (first entry)
XX
DE      Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #11.
XX
KW      Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW      KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW      tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW      fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW      foetal liver kinase 1; ss.
XX
OS      Mus sp.
XX
PN      WO9715662-A2.
XX
PD      01-MAY-1997.
XX
PF      25-OCT-1996; 96WO-US017480.
XX
PR      26-OCT-1995; 95US-0005974P.
PR      11-JAN-1996; 96US-00584040.
XX
PA      (RIBO-) RIBOZYME PHARM INC.
PA      (CHIR) CHIRON CORP.
XX
PI      Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
PI      WPI; 1997-259017/23.
XX
DR      Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT      stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT      rheumatoid arthritis, etc., in a human patient.
XX
PS      Claim 4; Page 155; 218pp; English.
XX
CC      The present invention describes nucleic acid molecules which modulate the
CC      synthesis, expression and/or stability of a mRNA encoding 1 or more
CC      receptors of vascular endothelial growth factor (VEGF). A patient
CC      (preferably human) having a condition associated with the level of the
CC      fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC      receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC      angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC      treated by administering the nucleic acid molecule or the expression
CC      vector to the patient. AAX67275 to AAX75752 represent specific examples
CC      of nucleic acid molecules from the present invention
XX
SQ      Sequence 17 BP; 2 A; 5 C; 4 G; 0 T; 6 U; 0 Other;
      Query Match      0.4%; Score 13.8; DB 1; Length 17;
      Best Local Similarity 52.9%; Pred. No. 2.5e+02;
      Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy      2166 TGCTACTTCACACGGG 2182
      :||:|::|::|::|::|
Db      1  UGUCUGUCUUCACACGG 17

RESULT 388
AAV39600
ID      AAV39600 standard; cDNA; 17 BP.
XX
AC      AAV39600;
XX
DT      28-SEP-1998 (first entry)
XX
DE      Pentaplex tc-PROBE apolipoprotein A IV oligonucleotide SEQ ID NO:90.
XX
KW      Mass spectrometry; diagnosis; detection; biological sample; infection;
KW      genetic disease; chromosomal abnormality; identification; heredity;
KW      pathogenic organism; telomerase activity; oncogene mutation;
KW      cancer-specific sequence; primer; ss.
XX
OS      Synthetic.
XX
PN      WO9820166-A2.
XX
PD      14-MAY-1998.
XX
PF      06-NOV-1997; 97WO-US020444.
XX
PR      06-NOV-1996; 96US-00744481.
PR      06-NOV-1996; 96US-00744590.
PR      06-NOV-1996; 96US-00746036.
PR      06-NOV-1996; 96US-00746055.
PR      23-JAN-1997; 97US-00786988.
PR      23-JAN-1997; 97US-00787639.
PR      19-SEP-1997; 97US-00933792.
PR      08-OCT-1997; 97US-00947801.
XX
PA      (SEQU-) SEQUENOM INC.
XX
PI      Koster H, Tang K, Fu D, Siebert CW, Little DP, Higgins GS;
PI      Braun A, Damhoffer-Demar B, Jurinke C, Van Den Boom D, Xiang G;
PI      Lough DM;
XX
WPI; 1998-286975/25.
XX
DR      Sequencing nucleic acid by mass spectrometric analysis - for detecting
PT      nucleic acids, telomerase activity, oncogene mutations, or cancer-
PT      specific sequences, for diagnosis of disease.
XX
PS      Example 24; Page 199; 478pp; English.
XX
CC      A process has been developed for determining the sequence of a target
CC      nucleic acid. The process comprises: (i) generating at least two
CC      fragments (F) from the target nucleic acid; and (ii) analysing F by mass
CC      spectrometry (MS). The sequences in AAV39483 to AAV39592 are specifically
CC      claimed primers for use in the mass spectrometric analysis of the above
CC      process. The process is used to detect genetic diseases (e.g.
CC      haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's
CC      disease, cystic fibrosis and many others) or chromosomal abnormalities
CC      (or predisposition); infections and cancers; also for establishing
CC      identity and heredity. Particular applications are diagnosis of
CC      neuroblastoma, detecting telomerase, determining family relationships and
CC      HLA compatibility, and in genetic fingerprinting. Compared with known
CC      methods using MS, this process requires fewer specific reagents and is
CC      better suited to automation. Extended primers are shorter; primer
CC      annealing is more efficient and the process allows detection of many
CC      sequences simultaneously. The present sequence represent an
CC      oligonucleotide used in an example from the present invention
XX
SQ      Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
      Query Match      0.4%; Score 13.8; DB 1; Length 17;
      Best Local Similarity 88.2%; Pred. No. 2.5e+02;
      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1399 ACAGCAGCAACAGCAGC 1415
      |||||
Db      1  ACAGCAGCAACAGCATC 17

RESULT 389
AAV95022/c
ID      AAV95022 standard; RNA; 17 BP.
XX
AC      AAV95022;
XX
DT      28-SEP-1998 (first entry)
XX

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DT 24-FEB-1999 (first entry)
XX Mouse IL-2 receptor g-chain substrate position 1012.
DE Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;
KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;
KW autoimmune disease; psoriasis; allergy; inflammatory disease;
KW graft rejection; ss.
XX Mus sp.
OS WO9824913-A2.
PN 11-JUN-1998.
XX 02-DEC-1997; 97WO-US021748.
XX 03-DEC-1996; 96US-00758306.
XX (RIBO-) RIBOZYME PHARM INC.
XX Stinchcomb DT, Mcswiggen JA;
PI WPI; 1998-333332/29.
XX Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer,
XX autoimmune disease and allergies.
XX Claim 4; Page 43; 61pp; English.
XX The present sequence invention describes ribozymes targetted to modulate
XX the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.
XX AAV93889 to AAV94574 represent specifically claimed ribozymes, and
XX AAV94575 to AAV95260 represent specifically claimed substrate sequences
XX from the present invention. The ribozymes can be used for the treatment
XX of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy
XX and other inflammatory conditions. The ribozymes are also used to induce
XX tolerance in a recipient to alloantigen from a donor
XX Sequence 17 BP; 5 A; 7 C; 3 G; 0 T; 2 U; 0 Other;
SQ Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 252 TTGGGGAGATCTCTCT 268
DB 17 TTGGGGGAATCTCGCT 1

RESULT 390
AAV08617
ID AAV08617 standard; DNA; 17 BP.
XX AAV08617;
XX 15-FEB-1999 (first entry)
DE Primer ACP/9RB for human ACE gene.
XX PCR primer; human; ACE; angiotensin converting enzyme; angiotensinogen;
KW cardiovascular status; AGT; AT1; type 1 angiotensin II receptor; stroke;
KW polymorphic pattern; blood pressure; electrocardiographic profile;
KW cardiac condition diagnosis; myocardial infarction; atherosclerosis;
KW hypertension; cardiovascular disease; ss.
XX Synthetic.
OS Homo sapiens.
XX WO9845477-A2.
XX 15-OCT-1998.
XX 01-APR-1998; 98WO-IB000475.
XX 04-APR-1997; 97US-0042930P.
XX

PF 01-APR-1998; 98WO-IB000475.
XX 04-APR-1997; 97US-0042930P.
XX (EURO-) EURONA MEDICAL AB.
XX Norberg LT, Andersson MK, Lindstroem PHR;
XX WPI; 1998-568361/48.
XX Assessing cardiovascular status in humans by polymorphic analysis - of
XX genes for angiotensin converting enzyme, angiotensinogen and angiotensin
XX II receptor, used to diagnose predisposition to disease and to predict
XX effect of therapy.
XX Example 1; Page 29; 71pp; English.
XX This sequence represents a PCR primer for the human ACE (angiotensin
XX converting enzyme) gene, and can be used in the method of the invention.
XX The method is for assessing cardiovascular status in humans by
XX determining the sequence of at least one polymorphic site in the ACE
XX (angiotensin converting enzyme), AGT (angiotensinogen) and/or AT1 (type 1
XX angiotensin II receptor) genes, and comparing the polymorphic pattern
XX with that in patients with predetermined markers of status. The method is
XX used to assess blood pressure or electrocardiographic profile, to
XX diagnose a cardiac condition such as (silent) myocardial infarction (MI),
XX hypertension, atherosclerosis or stroke. They can also be used to predict
XX response to treatments with ACE inhibitors, angiotensin II receptor
XX antagonists, diuretics, alpha- or beta-adrenergic receptor antagonists,
XX etc. It is also used to identify susceptibility to cardiovascular
XX disease. Libraries of nucleic acids containing polymorphic positions in
XX the 3 genes, and libraries of targets corresponding to the peptides from
XX the genes are used to screen for cardiovascular agents. The nucleic acids
XX contained in the library can be used as source of probes
XX Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 CAGCAGCAGCAGCAACA 1443
DB 1 CGCGCGCAGCAGCAACA 17

RESULT 391
AAV08623
ID AAV08623 standard; DNA; 17 BP.
XX AAV08623;
XX 15-FEB-1999 (first entry)
DE Primer ACP/16RT for human ACE gene.
XX PCR primer; human; ACE; angiotensin converting enzyme; angiotensinogen;
KW cardiovascular status; AGT; AT1; type 1 angiotensin II receptor; stroke;
KW polymorphic pattern; blood pressure; electrocardiographic profile;
KW cardiac condition diagnosis; myocardial infarction; atherosclerosis;
KW hypertension; cardiovascular disease; ss.
XX Synthetic.
OS Homo sapiens.
XX WO9845477-A2.
XX 15-OCT-1998.
XX 01-APR-1998; 98WO-IB000475.
XX 04-APR-1997; 97US-0042930P.
XX

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PA (EURO-) EURONA MEDICAL AB.
XX
PI Norberg LT, Andersson MK, Lindstroem PHR;
XX
DR WPI; 1998-568361/48.
XX
XX Assessing cardiovascular status in humans by polymorphic analysis - of
PT genes for angiotensin converting enzyme, angiotensinogen and angiotensin
PT II receptor, used to diagnose predisposition to disease and to predict
PT effect of therapy.
XX
XX Example 1; Page 29; 71pp; English.
XX
CC This sequence represents a PCR primer for the human ACE (angiotensin
CC converting enzyme) gene, and can be used in the method of the invention.
CC The method is for assessing cardiovascular status in humans by
CC determining the sequence of at least one polymorphic site in the ACE
CC (angiotensin converting enzyme), AGT (angiotensinogen) and/or AT1 (type 1
CC angiotensin II receptor) genes, and comparing the polymorphic pattern
CC with that in patients with predetermined markers of status. The method is
CC used to assess blood pressure or electrocardiographic profile, to
CC diagnose a cardiac condition such as (silent) myocardial infarction (MI),
CC hypertension, atherosclerosis or stroke. They can also be used to predict
CC response to treatments with ACE inhibitors, angiotensin II receptor
CC antagonists, diuretics, alpha- or beta-adrenergic receptor antagonists,
CC etc. It is also used to identify susceptibility to cardiovascular
CC disease. Libraries of nucleic acids containing polymorphic positions in
CC the 3 genes, and libraries of targets corresponding to the peptides from
CC the genes are used to screen for cardiovascular agents. The nucleic acids
CC contained in the library can be used as source of probes
XX
SQ Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1427 CAGCAGCAGCAGCAACA 1443
Db 1 CGGCGCAGCAGCAACA 17
RESULT 392
AAA20848
ID AAA20848 standard; RNA; 17 BP.
XX
AC AAA20848;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:4074.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 55; Page 171; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21589 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberculous sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 10 A; 1 C; 3 G; 0 T; 3 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 938 AACACAGATAGCTGCTAA 954
Db 1 AACACAGAUAGAUGAUA 17
RESULT 393
AAA22595/c
ID AAA22595 standard; RNA; 17 BP.
XX
AC AAA22595;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin subunit beta 3 substrate sequence SEQ ID NO:5821.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberculous sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX

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PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX
XX WPI; 1999-591315/50.
XX
DR Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 230; 305pp; English.
XX
XX The present invention describes enzymatic cleave RNA molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA223263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 0 A; 4 C; 0 G; 0 T; 13 U; 0 Other;
    Query Match 0.4%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 2.5e+02;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3090 AAAGAAGAAAGGAAGA 3106
Db 17 AAAGAAAGGAAGAAGA 1
RESULT 394
AAA38251
ID AAA38251 standard; DNA; 17 BP.
XX
XX AAA38251;
AC
XX
XX 21-AUG-2000 (first entry)
DT
XX
XX Human ACE regulatory region PCR primer, SEQ ID NO:51.
DE
XX
XX Angiotensin-converting enzyme gene; ACE; regulatory region; polymorphism;
KW
KW polymorphic marker; cardiovascular disease; myocardial infarction;
KW
KW unstable angina; hypertension; atherosclerosis; stroke; prognosis;
KW
KW drug screening; treatment outcome; human; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200022166-A2.
PN
XX
XX 20-APR-2000.
PD
XX

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```

PF 13-OCT-1999; 99WO-IB001678.
XX
XX 14-OCT-1998; 98US-0104286P.
PR 14-OCT-1998; 98US-0104302P.
XX
XX (EURO-) EURONA MEDICAL AB.
PA
XX
XX Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
PI
XX
XX WPI; 2000-318010/27.
XX
XX Assessing cardiovascular status in humans involves comparing test
XX polymorphic pattern comprising polymorphic positions within genes
XX encoding specific proteins, with reference polymorphic pattern.
XX
XX Example 1; Page 51; 126pp; English.
XX
XX The invention relates to a novel method of assessing the cardiovascular
XX status in an individual and to newly identified polymorphisms in the
XX genes encoding angiotensin-converting enzyme (ACE), angiotensin II
XX receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
XX aldosterone synthase, endothelin receptor type A and beta-adrenergic
XX receptors 1 and 2. The method comprises determining the sequence at one
XX or more polymorphic positions within these genes, and comparing the
XX pattern of polymorphisms from the individual with a reference polymorphic
XX pattern obtained from a population of individuals exhibiting a
XX predetermined cardiovascular disease status. The polymorphic markers are
XX useful for determining the predisposition of an individual to
XX cardiovascular disorders such as myocardial infarction, unstable angina,
XX hypertension, atherosclerosis and stroke. They are also useful for
XX predicting the likely cardiovascular status of a patient given a
XX treatment regimen comprising administration of cardiovascular drugs
XX (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
XX blockers) or calcium channel blockers). One or more polymorphic markers
XX provides a basis for predicting the outcome of a treatment regimen.
XX Fragments of the genes comprising a polymorphic site may be used as
XX primers and probes for detecting genetic polymorphisms or in molecular
XX library arrays for high throughput screening. The genes, and the proteins
XX they encode are useful in the screening of potential cardiovascular
XX drugs. Determination of an individual's polymorphic pattern reduces or
XX eliminates trial and error in selecting a treatment for a particular
XX individual cardiovascular patient. It also provides the ability to
XX eliminate patients from clinical trials who are predicted to be non-
XX responsive, or at a risk for an adverse response, to a particular
XX treatment regimen. Adverse results in an early trial can be evaluated to
XX identify polymorphic patterns so that the adverse results can be
XX correlated with a sub-population of the test population, permitting
XX exclusion of such sub-populations from the treatment group. Beneficial
XX drugs can be approved for use in the appropriate population, thereby
XX decreasing the number of patients required for a clinical trial which in
XX turn decreases the duration and cost of such trials. Sequences AAA38240-
XX A38251 represent PCR primers used in an exemplification of the invention
XX to amplify short fragments of the human ACE gene regulatory region
XX (AAA38329) for sequence determination
XX
SQ Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
    Query Match 0.4%; Score 13.8; DB 1; Length 17;
    Best Local Similarity 88.2%; Pred. No. 2.5e+02;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1427 CAGCAGCAGCAGCAACA 1443
Db 1 CGCGCGCAGCAGCAACA 17
RESULT 395
AAA38245
ID AAA38245 standard; DNA; 17 BP.
XX
XX AAA38245;
AC
XX
XX 21-AUG-2000 (first entry)
DT

```


XX Human ACE regulatory region PCR primer, SEQ ID NO:45.
DE Angiotensin-converting enzyme gene; ACE; regulatory region; polymorphism;
XX polymorphic marker; cardiovascular disease; myocardial infarction;
KW unstable angina; hypertension; atherosclerosis; stroke; prognosis;
KW drug screening; treatment outcome; human; PCR primer; ss.
XX Homo sapiens.
OS
XX WO200022166-A2.
PN
XX 20-APR-2000.
PD
XX
XX 13-OCT-1999; 99WO-IB001678.
PF
XX
XX 14-OCT-1998; 98US-0104286P.
PR
XX 14-OCT-1998; 98US-0104302P.
PR
XX (EURO-) EURONA MEDICAL AB.
XX
XX Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
PI WPI; 2000-318010/27.
XX
XX
XX Assessing cardiovascular status in humans involves comparing test
PT polymorphic pattern comprising polymorphic positions within genes
PT encoding specific proteins, with reference polymorphic pattern.
XX
XX Example 1; Page 50; 126pp; English.
PS
XX
XX The invention relates to a novel method of assessing the cardiovascular
CC status in an individual and to newly identified polymorphisms in the
CC genes encoding angiotensin-converting enzyme (ACE), angiotensin II
CC receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin,
CC aldosterone synthase, endothelin receptor type A and beta-adrenergic
CC receptors 1 and 2. The method comprises determining the sequence at one
CC or more polymorphic positions within these genes, and comparing the
CC pattern of polymorphisms from the individual with a reference polymorphic
CC pattern obtained from a population of individuals exhibiting a
CC predetermined cardiovascular disease status. The polymorphic markers are
CC useful for determining the predisposition of an individual to
CC cardiovascular disorders such as myocardial infarction, unstable angina,
CC hypertension, atherosclerosis and stroke. They are also useful for
CC predicting the likely cardiovascular status of a patient given a
CC treatment regimen comprising administration of cardiovascular drugs
CC (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-
CC blockers) or calcium channel blockers). One or more polymorphic markers
CC provides a basis for predicting the outcome of a treatment regimen.
CC Fragments of the genes comprising a polymorphic site may be used as
CC primers and probes for detecting genetic polymorphisms or in molecular
CC library arrays for high throughput screening. The genes, and the proteins
CC they encode are useful in the screening of potential cardiovascular
CC drugs. Determination of an individual's polymorphic pattern reduces or
CC eliminates trial and error in selecting a treatment for a particular
CC individual cardiovascular patient. It also provides the ability to
CC eliminate patients from clinical trials who are predicted to be non-
CC responsive, or at a risk for an adverse response, to a particular
CC treatment regimen. Adverse results in an early trial can be evaluated to
CC identify polymorphic patterns so that the adverse results can be
CC correlated with a sub-population of the test population, permitting
CC exclusion of such sub-populations from the treatment group. Beneficial
CC drugs can be approved for use in the appropriate population, thereby
CC decreasing the number of patients required for a clinical trial, which in
CC turn decreases the duration and cost of such trials. Sequences AAA38240-
CC A38251 represent PCR primers used in an exemplification of the invention
CC to amplify short fragments of the human ACE gene regulatory region
CC (AAA38329) for sequence determination
XX
XX Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1427 CAGCAGCAGCAGCAACA 1443
DB 1 CGGCGGCAGCAGCAACA 17
RESULT 396
AAA25616/C
ID AAA25616 standard; DNA; 17 BP.
XX
XX AAA25616;
AC
XX
XX 19-JUL-2000 (first entry)
DT
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2114.
DE
XX
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9954459-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US008547.
PF
XX
XX 20-APR-1998; 98US-0082404P.
PR
XX 23-JUN-1998; 98US-00103636.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
XX Claim 77; Page 85; 148pp; English.
PS
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA33503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 2 A; 0 C; 8 G; 7 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1384 CTACACCCACAGCAAC 1400
Db 17 CTACACCCATACCAAC 1

RESULT 397
AAA25020/c
ID AAA25020 standard; DNA; 17 BP.
XX
XX
AC AAA25020;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1518.
XX
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN WO954459-A2.
XX
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX
WPI; 2000-013248/01.
XX
New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
Claim 77; Page 65; 148pp; English.
XX
The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24748 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 BP; 2 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 458 AAGCAATGATGGCCA 474
||||| ||| ||||| |||||
```

```
Db 17 AAGCAATGATGGCCA 1

RESULT 398
AAC61251
ID AAC61251 standard; DNA; 17 BP.
XX
XX
AC AAC61251;
XX
DT 30-JAN-2001 (first entry)
XX
DE Human ACE, AGT and AT1 genes polymorphisms PCR primer SEQ ID NO: 51.
XX
KW Human; genetic polymorphism; disease diagnosis; treatment; cancer;
KW cardiovascular system; nervous system; glaucoma; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200056922-A2.
XX
XX
PD 28-SEP-2000.
XX
XX
PF 23-MAR-2000; 2000WO-GB001102.
XX
XX
PR 23-MAR-1999; 99US-0136046P.
PR 23-MAR-1999; 99WO-IB000497.
PR 24-MAR-1999; 99US-0126243P.
PR 23-DEC-1999; 99US-00471890.
XX
XX
PA (GEMI-) GEMINI GENOMICS AB.
XX
XX
PI Lindstrom PHR, Norberg LT, Jonasson L, Olaisson E, Sanders R;
XX
XX
WPI; 2000-638268/61.
XX
Assessing disease status in individual by determining sequence(s) at one
PT or more polymorphic positions within the human genes encoding the
PT protein(s) involved in physiological pathway associated with treatment
PT regime.
XX
XX
PS Example 1; Page 58; 141pp; English.
XX
The present invention is related to methods for determining the
CC polymorphic pattern of an individual and using the results to determine
CC their risk of a number of diseases, including cancer, cardiovascular
CC diseases, glaucoma and nervous system disorders such as depression and
CC neurodegenerative diseases. In addition, the methods can be used to
CC determine the effects of different types of treatment for individuals,
CC and thus enables appropriate therapies to be prescribed. The PCR primers
CC shown in sequences AAC61201-C61371 were all used to demonstrate the
CC methods of the invention
XX
SQ Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 CAGCAGCAGCAGCAACA 1443
||||| ||| ||||| ||||| |||||
Db 1 CGCGCGCAGCAGCAACA 17

RESULT 399
AAC61245
ID AAC61245 standard; DNA; 17 BP.
XX
XX
AC AAC61245;
XX
DT 30-JAN-2001 (first entry)
XX
DE Human ACE, AGT and AT1 genes polymorphisms PCR primer SEQ ID NO: 45.
XX
```

KW Human; genetic polymorphism; disease diagnosis; treatment; cancer;
 KW cardiovascular system; nervous system; glaucoma; PCR primer; ss.
 XX Homo sapiens.
 XX WO200056922-A2.
 XX PD 28-SEP-2000.
 XX PF 23-MAR-2000; 2000WO-GB001102.
 XX PR 23-MAR-1999; 99US-0126046P.
 XX PR 23-MAR-1999; 99WO-IB000497.
 XX PR 24-MAR-1999; 99US-0126243P.
 XX PR 23-DEC-1999; 99US-00471890.
 XX PA (GEMI-) GEMINI GENOMICS AB.
 XX PI Lindstrom PHR, Norberg LT, Jonsson L, Olaisson E, Sanders R.
 XX WPI; 2000-638268/61.
 XX Assessing disease status in individual by determining sequence(s) at one
 PT or more polymorphic positions within the human genes encoding the
 PT protein(s) involved in physiological pathway associated with treatment
 PT regime.
 XX Example 1; Page 57; 141pp; English.
 XX The present invention is related to methods for determining the
 CC polymorphic pattern of an individual and using the results to determine
 CC their risk of a number of diseases, including cancer, cardiovascular
 CC diseases, glaucoma and nervous system disorders such as depression and
 CC neurodegenerative diseases. In addition, the methods can be used to
 CC determine the effects of different types of treatment for individuals,
 CC and thus enables appropriate therapies to be prescribed. The PCR primers
 CC shown in sequences AAC61201-C61371 were all used to demonstrate the
 CC methods of the invention
 XX Sequence 17 BP; 5 A; 6 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1427 CAGCAGCAGCAGCAACA 1443
 DB 1 CGCGCGCAGCAGCAACA 17
 RESULT 400
 AAF07477/c
 ID AAF07477 standard; DNA; 17 BP.
 XX AAF07477;
 AC AAF07477;
 XX 16-FEB-2001 (first entry)
 DT Hammerhead ribozyme substrate #3734.
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 XX WO2000061729-A2.
 XX 19-OCT-2000.
 XX 11-APR-2000; 2000WO-US009721.
 XX 12-APR-1999; 99US-0129390P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 WPI; 2000-647423/62.
 Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor protein,
 interferon alpha and erythropoietin.
 Claim 18; Page 117; 164pp; English.
 The present invention relates to enzymatic and antisense nucleic acid
 molecules that act as inhibitors of the expression of repressor genes
 encoding the TR2 Orphan receptor. EAR3/COUP-TF-1, the GATA transcription
 factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 Inhibition of the repressors removes prevents inhibition (and
 consequently increases expression of) genes involved in the production of
 erythropoietin, granulocyte colony stimulating factor protein and
 interferon alpha

PA (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 WPI; 2000-647423/62.
 Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor protein,
 interferon alpha and erythropoietin.
 Claim 54; Page 141; 164pp; English.
 The present invention relates to enzymatic and antisense nucleic acid
 molecules that act as inhibitors of the expression of repressor genes
 encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 Inhibition of the repressors removes prevents inhibition (and
 consequently increases expression of) genes involved in the production of
 erythropoietin, granulocyte colony stimulating factor protein and
 interferon alpha

Sequence 17 BP; 6 A; 6 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 3351 CTGTGGTGTCAATGTGT 3367
 DB 17 CTGTGGAGTAAATGTGT 1
 RESULT 401
 AAF05460
 ID AAF05460 standard; DNA; 17 BP.
 XX AAF05460;
 AC AAF05460;
 XX 16-FEB-2001 (first entry)
 DT Hammerhead ribozyme substrate #2679.
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX Homo sapiens.
 XX WO2000061729-A2.
 XX 19-OCT-2000.
 XX 11-APR-2000; 2000WO-US009721.
 XX 12-APR-1999; 99US-0129390P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 WPI; 2000-647423/62.
 Enzymatic and antisense nucleic acid inhibition of repressor genes,
 useful for producing e.g. granulocyte colony stimulating factor protein,
 interferon alpha and erythropoietin.
 Claim 18; Page 117; 164pp; English.
 The present invention relates to enzymatic and antisense nucleic acid
 molecules that act as inhibitors of the expression of repressor genes
 encoding the TR2 Orphan receptor. EAR3/COUP-TF-1, the GATA transcription
 factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 Inhibition of the repressors removes prevents inhibition (and
 consequently increases expression of) genes involved in the production of

```
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 7 A; 1 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match      0.4%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 2.5e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3369 ATTAATTGTTGTAATA 3385
Db 1 ATTCATTGTTGTAATA 17

RESULT 402
AAAF04887/c
ID AAFA04887 standard; DNA; 17 BP.
XX
AC AAFA04887;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #2403.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 4; Page 110; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 3 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match      0.4%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 2.5e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3100 GCGAGACAAATTACAA 3116
Db 17 GTGAGACAAATTGACAA 1

RESULT 403
AAAF04439/c
ID AAFA04439 standard; DNA; 17 BP.
XX
```

```
AC AAFA04439;
XX
DT 16-FEB-2001 (first entry)
XX
DE Hammerhead ribozyme substrate #1955.
XX
KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW interferon alpha; ss.
XX
OS Homo sapiens.
XX
PN WO200061729-A2.
XX
PD 19-OCT-2000.
XX
PF 11-APR-2000; 2000WO-US009721.
XX
PR 12-APR-1999; 99US-0129390P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX
DR WPI; 2000-647423/62.
XX
PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT useful for producing e.g. granulocyte colony stimulating factor protein,
PT interferon alpha and erythropoietin.
XX
PS Claim 4; Page 100; 164pp; English.
XX
CC The present invention relates to enzymatic and antisense nucleic acid
CC molecules that act as inhibitors of the expression of repressor genes
CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
CC Inhibition of the repressors removes prevents inhibition (and
CC consequently increases expression of) genes involved in the production of
CC erythropoietin, granulocyte colony stimulating factor protein and
CC interferon alpha
XX
SQ Sequence 17 BP; 3 A; 4 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match      0.4%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 2.5e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3100 GCGAGACAAATTACAA 3116
Db 17 GTGAGACAAATTGACAA 1

RESULT 404
AAAF04439/c
ID AAFA04439 standard; DNA; 17 BP.
XX
AC AAFA04439;
XX
DT 02-FEB-2001 (first entry)
XX
DE Forward primer #39 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
PN WO200058516-A2.
XX
PD 05-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US008069.
XX
PR 26-MAR-1999; 99US-0126473P.
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PR 23-JUN-1999; 99US-0140359P.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (APFY-) APFYMATRIX INC.
XX
XX Pan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX WPI; 2000-656171/63.
XX
XX Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
XX Example 7; Page 51; 70pp; English.
XX
XX The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one of the primers used in
CC the method of the present invention to amplify a polymorphic sample. The
CC amplified nucleic acid product is then used as a template in a SBE
CC reaction with an extension primer. The SBE reaction products are used to
CC form the oligonucleotide array
XX
XX Sequence 17 BP; 1 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 815 TCTGCCCTCTGCACCTC 831
Db 1 TCTGCCCTCTGCACCTC 17
RESULT 405
AA09710
ID AA09710 standard; DNA; 17 BP.
XX
XX AC
XX AD09710;
XX
XX 10-SEP-2001 (first entry)
XX
XX Cryptosporidium parvum S60 gene sequencing PCR primer, S15.R9.
XX
XX S60 antigen; protozoacide; vaccine; intestinal infection; diarrhoea;
XX AIDS; Acquired Immune Deficiency Syndrome; cancer; PCR primer; ss.
XX
XX Cryptosporidium parvum.
XX
XX WO200140248-A1.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-AU001492.
XX
XX 01-DEC-1999; 99AU-00004400.
XX (MACQ-) MACQUARIE RES LTD.
XX
XX Winter G, Slade MB, Williams KL, Gooley AA;
XX WPI; 2001-408274/43.
XX
XX Novel nucleic acids encoding antigenic polypeptides of Cryptosporidium
XX useful in antigenic preparations for immunizing animals against
XX Cryptosporidium.
XX
XX Example; Fig 6; 72pp; English.
XX
CC The invention relates to Cryptosporidium parvum S60 potential vaccine
CC antigen and its corresponding DNA molecule. S60 antigens are used in
CC vaccine preparations for immunising animals, preferably human, against
CC Cryptosporidium. The S60 protein is processed into two glycoproteins S15
CC and S45. This S45 and S15 glycoproteins behave as a single membrane
CC glycoprotein S60. S60 vaccine antigen is used for treating intestinal
CC infections such as diarrhoea in immunosuppressed patients e.g., AIDS
CC (Acquired Immune Deficiency Syndrome), cancer patients and recipients of
CC transplants. The present DNA sequence is PCR primer which is used for
CC sequencing Cryptosporidium parvum S60 gene
XX
XX Sequence 17 BP; 1 A; 2 C; 7 G; 7 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2394 TTGGAGCTGGATCTGTT 2410
Db 1 TTGGTGGGGGATCTGTT 17
RESULT 406
AAH94700/C
ID AAH94700 standard; RNA; 17 BP.
XX
XX AC AAH94700;
XX
XX 09-OCT-2001 (first entry)
XX
XX Human Chk1 ribozyme substrate SEQ ID NO: 125.
DE
XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;
XX RNA cleavage; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200157206-A2.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US0033504.
XX
XX 03-FEB-2000; 2000US-0179983P.
XX (RIBO-) RIBOZYME PHARM INC.
XX (FATT) FATTAEY A R.
XX
XX Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;
XX WPI; 2001-496922/54.
XX
XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
XX molecules, which downregulates expression of a checkpoint kinase-1 gene,
XX useful for treating colorectal, lung, breast or prostate cancers.
XX
XX Claim 4; Page 54; 115pp; English.
XX
XX The present invention provides nucleic acid molecules capable of
XX downregulating the expression of the human checkpoint kinase-1 (chk1)
XX gene. These may be antisense or ribozyme sequences, and are useful in the
XX treatment of diseases associated with conditions affected by Chk1 levels,
XX including cancer. The present sequence is an oligonucleotide described in
XX the exemplification of the invention
XX
XX Sequence 17 BP; 1 A; 7 C; 3 G; 0 T; 6 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 666 AGCAAGCCAGGAGC 682
Db 1 AGCAAGCCAGGAGC 682

```

XX	09-AUG-2001.	
PD	02-FEB-2001; 2001WO-US003504.	
XX	03-FEB-2000; 2000US-0179983P.	
XX	(RIBO-) RIBOZYME PHARM INC.	
PA	(FATT/) FATTAEY A R.	
XX	Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;	
PI	WPI; 2001-496922/54.	
XX	Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid	
XX	molecules, which downregulates expression of a checkpoint kinase-1 gene,	
PT	useful for treating colorectal, lung, breast or prostate cancers.	
PT	Claim 4; Page 71; 115pp; English.	
XX	The present invention provides nucleic acid molecules capable of	
CC	downregulating the expression of the human checkpoint kinase-1 (Chk1)	
CC	gene. These may be antisense or ribozyme sequences, and are useful in the	
CC	treatment of diseases associated with conditions affected by Chk1 levels,	
CC	including cancer. The present sequence is an oligonucleotide described in	
CC	the exemplification of the invention	
XX	Sequence 17 BP; 1 A; 7 C; 3 G; 0 T; 6 U; 0 Other;	
XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;	
XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;	
XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0	
QY	665 CAGCAAGCCAGGAGGAG 681	
DB	17 CAGCAGAGCTAGAGGAG 1	
RESULT 409		
ABK01103		
ID	ABK01103 standard; RNA; 17 BP.	
XX	ABK011103;	
AC	12-MAR-2002 (first entry)	
XX	Human NOGO Inozyme #373.	
DE	Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;	
XX	cerebroprotective; nootropic; neuroprotective; antiparkinsonian;	
XX	muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;	
KW	DNAzyme; inozyme; G-cleavage; amberyze; zinczyme; lymphoma; leukaemia;	
KW	B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;	
KW	human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;	
KW	MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;	
KW	inflammatory arthropathy; central nervous system injury;	
KW	cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;	
KW	chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;	
KW	Parkinson's disease; ataxia; Huntington's disease;	
KW	Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.	
OS	Homo sapiens.	
OS	Synthetic.	
XX	WO200159103-A2.	
PN	16-AUG-2001.	
XX	09-FEB-2001; 2001WO-US004273.	
PF	11-FEB-2000; 2000US-0181797P.	
XX	28-FEB-2000; 2000US-0185516P.	
PR	06-MAR-2000; 2000US-0187128P.	

XX	09-AUG-2001.	
PD	02-FEB-2001; 2001WO-US003504.	
XX	03-FEB-2000; 2000US-0179983P.	
XX	(RIBO-) RIBOZYME PHARM INC.	
PA	(FATT/) FATTAEY A R.	
XX	Fattaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;	
PI	WPI; 2001-496922/54.	
XX	Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid	
XX	molecules, which downregulates expression of a checkpoint kinase-1 gene,	
PT	useful for treating colorectal, lung, breast or prostate cancers.	
PT	Claim 4; Page 71; 115pp; English.	
XX	The present invention provides nucleic acid molecules capable of	
CC	downregulating the expression of the human checkpoint kinase-1 (Chk1)	
CC	gene. These may be antisense or ribozyme sequences, and are useful in the	
CC	treatment of diseases associated with conditions affected by Chk1 levels,	
CC	including cancer. The present sequence is an oligonucleotide described in	
CC	the exemplification of the invention	
XX	Sequence 17 BP; 1 A; 7 C; 3 G; 0 T; 6 U; 0 Other;	
XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;	
XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;	
XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0	
QY	665 CAGCAAGCCAGAGGAG 681	
DB	17 CAGCAGAGCTAGAGGAG 1	
RESULT 409		
ABK01103		
ID	ABK01103 standard; RNA; 17 BP.	
XX	ABK011103;	
AC	12-MAR-2002 (first entry)	
XX	Human NOGO Inozyme #373.	
DE	Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;	
XX	cerebroprotective; nootropic; neuroprotective; antiparkinsonian;	
XX	muscular; C2D0; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;	
XX	DNAzyme; inozyme; G-cleavage; amberszyme; zinczyme; lymphoma; leukaemia;	
XX	B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;	
XX	human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;	
XX	MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;	
XX	inflammatory arthropathy; central nervous system injury;	
XX	cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;	
XX	chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;	
XX	Parkinson's disease; ataxia; Huntington's disease;	
XX	Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.	
OS	Homo sapiens.	
OS	Synthetic.	
XX	WO200159103-A2.	
PN	16-AUG-2001.	
XX	09-FEB-2001; 2001WO-US004273.	
PF	11-FEB-2000; 2000US-0181797P.	
XX	28-FEB-2000; 2000US-0185516P.	
PR	06-MAR-2000; 2000US-0187128P.	


```

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGC 1427
DB 1 GCGGCAGCAGCAGCAGC 17

RESULT 411
ID ABK02892/c
XX ABK02892 standard; RNA; 17 BP.
AC ABK02892;
XX
DT 12-MAR-2002 (first entry)
DE Human CD20 Hammerhead ribozyme #191.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX
WPI; 2001-607195/69.
XX
Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
Claim 30; Page 143; 200pp; English.
XX
The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg2+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more

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CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg2+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is a hammerhead ribozyme of the invention
XX
SQ Sequence 17 BP; 1 A; 3 C; 1 G; 0 T; 12 U; 0 Other;

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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 3416 TAAAAAGGTAATAGAA 3432
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DB 17 TAAAAAGGTAATAGAA 1
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RESULT 412
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ABK02895/c
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```
ID ABK02895 standard; RNA; 17 BP.
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XX AC ABK02895;
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XX DT 12-MAR-2002 (first entry)
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```
XX DE Human CD20 Hammerhead ribozyme #194.
```

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XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX

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OS Homo sapiens.
```

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OS Synthetic.
```

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XX PN WO200159103-A2.
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XX PD 16-AUG-2001.
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XX PF 09-FEB-2001; 2001WO-US004273.
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XX PR 11-FEB-2000; 2000US-0181797P.
```

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XX PR 28-FEB-2000; 2000US-0185516P.
```

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XX PR 06-MAR-2000; 2000US-0187128P.
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XX (RIBO-) RIBOZYME PHARM INC.
```

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XX (BLAT/) BLATT L.
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```
XX (MCSW/) MCSWIGGEN J.
```

```
XX (CHOW/) CHOWRIRA B M.
```

```
XX Blatt L, Mcswiggen J, Chowrira BM;
```


XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

XX central nervous system injury.

PS Claim 30; Page 143; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr

CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targeting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targeting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present

CC sequence is a hammerhead ribozyme of the invention

XX

SQ Sequence 17 BP; 4 A; 3 C; 0 G; 0 T; 10 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3201 ATGCTTAAAAATGGAAA 3217

Db 17 ATGTTTAAAAAAGGAAA 1

RESULT 413

ABK00767

ID ABK00767 standard; RNA; 17 BP.

AC ABK00767;

XX

DT 12-MAR-2002 (first entry)

XX

DE Human NOGO Inozyme #37.

XX

Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; neurotropic; neuroprotective; antiParkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNzyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWIRA B M.

XX

PI Blatt L, Mcswiggen J, Chowira BM;

XX

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

PT central nervous system injury.

XX

XX Claim 88; Page 78; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr

CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targeting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targeting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present

CC sequence is a hammerhead ribozyme of the invention

XX

SQ Sequence 17 BP; 4 A; 6 C; 5 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1411 GCACGACGACGACGACG 1427

Db 1 GCACGACGACGACGACG 17

RESULT 414
 ABK01792
 ID ABK01792 standard; RNA; 17 BP.
 AC
 AC ABK01792;
 DT 12-MAR-2002 (first entry)
 XX
 XX Human NOGO Zinzyne #114.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200159103-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX Claim 88; Page 97; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with an RNA motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a zinzyme molecule of the invention

SQ Sequence 17 BP; 4 A; 6 C; 6 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1425
 Db 1 CGGCAGCAGCUGCAGCA 17
 |||||

RESULT 415
 ABK01549
 ID ABK01549 standard; RNA; 17 BP.
 XX
 AC ABK01549;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO G-Cleaver #5.

Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200159103-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 XX WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.

Claim 88; Page 97; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNAzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with an RNA motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

XX PS Claim 88; Page 92; 200pp; English.

XX CC The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr

CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targeting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targeting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present

CC sequence is a G-cleaver molecule of the invention

XX SQ Sequence 17 BP; 5 A; 6 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1425

DB 1 CAGCAGCAGCAGCAUCA 17

RESULT 416

ABK02456

ID ABK02456 standard; RNA; 17 BP.

XX AC ABK02456;

XX DT 12-MAR-2002 (first entry)

XX DE Human NOGO Amberzyme #128.

XX KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

XX PN WO200159103-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004273.

XX PR 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

PI WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

XX central nervous system injury.

PS Claim 88; Page 133; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down

CC regulates expression of a neurite growth inhibitor gene (NOGO). The

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule

CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr

CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA

CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

CC Furthermore, it may be contacted with a cell to reduce CD20 activity of

CC the cell and treat a patient having a condition associated with the level

CC of CD20. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targeting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the CD20 targeting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the

CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

CC nucleic acid may be contacted with a cell to reduce NOGO activity of the

CC cell and treat a patient having a condition associated with the level of

CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targeting nucleic acid may be used to

CC treat central nervous system (CNS) injury and cerebrovascular accident

CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease

CC states which respond to the modulation of NOGO expression. The present

CC sequence is an amberzyme molecule of the invention

XX SQ Sequence 17 BP; 7 A; 5 C; 3 G; 0 T; 2 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 2.5e+02;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1700 CAAATGCAGATCAGCC 1716

DB 1 CAAAAGCAGAAUCUGCC 17

RESULT 417

ABL46974

ID ABL46974 standard; RNA; 17 BP.

XX AC ABL46974;

```
XX DT 27-JUN-2003 (first entry)
XX DE Human GRID zinzyme substrate oligonucleotide #58.
XX KW Human; Grb2-related with Insert Domain; GRID; T-cell;
XX KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
XX KW leukaemia; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200162911-A2.
XX PD 30-AUG-2001.
XX PF 23-FEB-2001; 2001WO-US005957.
XX PR 24-FEB-2000; 2000US-0184594P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (GLAX) GLAXO GROUP LTD.
XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX DR WPI; 2001-550088/61.
XX PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
XX PT (GRID) gene comprises using antisense and enzymatic nucleic acid
XX PT molecules such as hammerhead ribozymes.
XX PS Claim 4; Page 72; 108pp; English.
XX CC The present invention relates to oligonucleotides that downregulate the
XX CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
XX CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
XX CC for modulating the expression of GRID, to treat conditions such as
XX CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
XX CC administered in conjunction with other therapies such as radiation,
XX CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
XX CC used to illustrate the invention
XX SQ Sequence 17 BP; 4 A; 9 C; 3 G; 0 T; 1 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 983 CACGACGACGACGACCA 999
DB 1 CCCCUGCAGCAGCACCA 17
RESULT 418
ABL46825
ID ABL46825 standard; RNA; 17 BP.
XX AC ABL46825;
XX DT 27-JUN-2003 (first entry)
XX DE Human GRID NCH ribozyme substrate oligonucleotide #279.
XX KW Human; Grb2-related with Insert Domain; GRID; T-cell;
XX KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
XX KW leukaemia; cytostatic; ss.
XX OS Homo sapiens.
XX PN WO200162911-A2.
XX PD 30-AUG-2001.
XX PF 23-FEB-2001; 2001WO-US005957.
```

```
XX PR 24-FEB-2000; 2000US-0184594P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (GLAX) GLAXO GROUP LTD.
XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX DR WPI; 2001-550088/61.
XX PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
XX PT (GRID) gene comprises using antisense and enzymatic nucleic acid
XX PT molecules such as hammerhead ribozymes.
XX PS Claim 4; Page 68; 108pp; English.
XX CC The present invention relates to oligonucleotides that downregulate the
XX CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
XX CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
XX CC for modulating the expression of GRID, to treat conditions such as
XX CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
XX CC administered in conjunction with other therapies such as radiation,
XX CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
XX CC used to illustrate the invention
XX SQ Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2508 CACCAAACTGGGCTCT 2524
DB 1 CAACAAGCUGGGCCUCU 17
RESULT 419
ABA93692/c
ID ABA93692 standard; DNA; 17 BP.
XX AC ABA93692;
XX DT 29-APR-2002 (first entry)
XX DE GAPDH cDNA PCR primer #1.
XX KW Neomycin resistance; viral vector; plasmid; pSub201; CMV promoter;
XX KW reversed terminal repetitive sequence; polyclonal site; pRc/CMV;
XX KW cytomegalovirus promoter; GAPDH; PCR primer; ss.
XX OS Homo sapiens.
XX PN CN1322840-A.
XX PD 21-NOV-2001.
XX PF 20-JUN-2001; 2001CN-00118841.
XX PR 20-JUN-2001; 2001CN-00118841.
XX PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.
XX PI Zhu L, Shi G, Liu Y;
XX DR WPI; 2002-148632/20.
XX PT Glandular associated viral vector for mediating gene transfer, comprises
XX PT a reversed terminal repetitive sequence of plasmid pSub201.
XX PS Example 3; Page 16; 29pp; Chinese.
XX CC The present invention describes a viral vector as a 7146 base pair
XX CC plasmid including a reversed terminal repetitive sequence of plasmid
```

CC pSub201 and a CMV promoter, polyclonal site and neomycin resistance gene
 CC of plasmid pRC/CMV. A gene transferred by the vector of the present
 CC invention may be expressed stably in a host cell for a long period. The
 CC present sequence represents a PCR primer for GAPDH, which is used in an
 CC example from the present invention

XX
 SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 793 CCCCGCATCTCCATGG 809
 ||| |||||
 Db 17 CCCAGCTTCTCCATGG 1

RESULT 420
 ABN00672
 ID ABN00672 standard; DNA; 17 BP.
 XX
 AC ABN00672;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:664.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 XX WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1
 PT proteins, as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 664; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1

CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX
 SQ Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 664 TCAGCAAGCCAGAGGA 680
 |||||
 Db 1 TCAGCAAGCCAGAGAA 17

RESULT 421
 ABN10755
 ID ABN10755 standard; DNA; 17 BP.
 XX
 AC ABN10755;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10747.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 XX WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 XX Disclosure; SEQ ID NO 1872; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e-02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1022 CCTCTCTGCTGGACC 1038
 DB 1 CCTCTCTGCTGGACC 17
 RESULT 424
 ABN07810
 ID ABN07810 standard; DNA; 17 BP.
 XX
 AC ABN07810;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7802.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 OS
 PN WO200192524-A2.
 XX
 XX 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
 PA
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 XX Disclosure; SEQ ID NO 7802; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 6 A; 5 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e-02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1409 CAGCAGCAGCAGCAGCA 1425
 DB 1 CAGCAGCAGCAGCAGCA 17
 RESULT 425

ABN01881
ID ABN01881 standard; DNA; 17 BP.
AC ABN01881;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:1873.
XX
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 1873; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1023 CCTCCTCTGCTGGACCA 1039
DB 1 CCTCCTGAGCTGGACCA 17
RESULT 426
ABN10255
ID ABN10255 standard; DNA; 17 BP.
XX
AC ABN10255;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10247.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 10247; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1187 TCAGCCAGGCTGGGCA 1203
 Db 1 TCAGCCAAAGGTGGCA 17
 RESULT 427
 ABN02741
 ID ABN02741 standard; DNA; 17 BP.
 XX
 AC ABN02741;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2733.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 FI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 2733; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 765 CTCCTCAGCTGAGGCC 781
 Db 1 CTAGCGAGCTGAGGCC 17
 RESULT 428
 ABN07811
 ID ABN07811 standard; DNA; 17 BP.
 XX
 AC ABN07811;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7803.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 FI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI

XX WPI; 2002-179446/23.
XX
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX
PS Disclosure; SEQ ID NO 7803; 214pp; English.
XX
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 7 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCA 1441
Db 1 AGCAGCAGCTGAAGCA 17

RESULT 429
ABK25807/C
ID ABK25807 standard; DNA; 17 BP.
XX
XX AC ABK25807;
XX
XX 09-APR-2002 (first entry)
XX
XX
DE Stress tolerance conferring genome altering oligonucleotide #275.
XX
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; triazine resistance; disease resistance;
KW porphyrin herbicide resistance; sulphonylurea herbicide resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW increased stearate production; reduced palmitate production; albino plant;
KW photosynthetic process.
XX
XX Cucurbita sp.
OS Synthetic.
PN
PN WO2001192512-A2.
XX
XX 06-DEC-2001.
XX

PF 01-JUN-2001; 2001WO-US017672.
XX
XX
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
XX (UYDE) UNIV DELAWARE.
XX
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
XX creating plants with desired phenotypes, e.g. stress tolerance, improved
XX nutritional value, herbicide or disease resistance, or modified oil
XX production.
XX
XX Claim 7; Page 112; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
XX genetic sequence, which comprises a single-stranded oligonucleotide
XX having a DNA domain. The DNA domain has at least one mismatch with
XX respect to the genetic sequence to be altered and further comprises
XX chemical modifications of the oligonucleotide. The chemical modifications
XX consist of o-methyl modification, an LNA modification, two or more
XX phosphorothioate linkages on a terminus, or a combination of any two or
XX more of these modifications. The oligonucleotides are useful for
XX directing repair or alteration of plant genetic information. The
XX oligonucleotides are particularly useful for creating plants with desired
XX phenotypes, e.g. environmental or abiotic stress tolerance, improved
XX nutritional value (e.g. altering amino acid content of plants or
XX conferring amino acid over production), herbicide resistance (e.g.
XX glyphosate resistance, imidazolinone and sulphonylurea herbicide
XX resistance, porphyrin herbicide resistance or triazine resistance),
XX disease resistance, modified oil production, modified starch production
XX (e.g. increased starch or production of waxy starch), altered floral
XX morphology (e.g. male-sterile plants) or modified fatty acid content
XX (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
XX The oligonucleotides are also useful for producing albino mutants for the
XX analysis of photosynthetic processes. This sequence represents a genome
XX altering oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 CCAGCAGCTCAACAGA 944
Db 17 CCAGCTGCTCAACCGA 1

RESULT 430
ABK25808
ID ABK25808 standard; DNA; 17 BP.
XX
XX AC ABK25808;
XX
XX 09-APR-2002 (first entry)
XX
XX Stress tolerance conferring genome altering oligonucleotide #276.
XX
XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW

RESULT 432
ABK27199/c
ID ABK27199 standard; DNA; 17 BP.
XX
AC ABK27199;
XX
DT 09-APR-2002 (first entry)
XX
DE Reduced linolenic acid production genome altering oligonucleotide #95.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW o-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; herbicide resistance; disease resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Brassica napus.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US017672.
XX
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX
DR WPI; 2002-106307/14.
XX
PT New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
XX
PS Claim 7; Page 196; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
CC resistance, porphyrin herbicide resistance or triazine resistance),
CC disease resistance, modified oil production, modified starch production
CC (e.g. increased starch or production of waxy starch), altered floral
CC morphology (e.g. male-sterile plants) or modified fatty acid content
CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
CC The oligonucleotides are also useful for producing albino mutants for the
CC analysis of photosynthetic processes. This sequence represents a genome
CC altering oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 930 AGCAGCTCAAAACAGATA 946
DB 17 AGCAGCTCAAGCAGCTA 1
RESULT 433
ABK25787/c
ID ABK25787 standard; DNA; 17 BP.
XX
AC ABK25787;
XX
DT 09-APR-2002 (first entry)
XX
DE Stress tolerance conferring genome altering oligonucleotide #255.
XX
KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
KW c-methyl modification; LNA modification; phosphorothioate linkage;
KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
KW amino acid over production; herbicide resistance; glyphosate resistance;
KW imidazolinone herbicide resistance; herbicide resistance; disease resistance;
KW porphyrin herbicide resistance; triazine resistance; disease resistance;
KW modified oil production; modified starch production; waxy starch;
KW altered floral morphology; male-sterile plant; albino mutant;
KW modified fatty acid content; reduced palmitate production; albino plant;
KW increased stearate production; reduced linolenic acid production;
KW photosynthetic process.
XX
OS Cucumis sativus.
OS Synthetic.
XX
PN WO200192512-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US017672.
XX
PR 01-JUN-2000; 2000US-0208538P.
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX
PA (UYDE) UNIV DELAWARE.
XX
PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX
DR WPI; 2002-106307/14.
XX
PT New oligonucleotides with modified nuclease-resistant termini, useful for
PT creating plants with desired phenotypes, e.g. stress tolerance, improved
PT nutritional value, herbicide or disease resistance, or modified oil
PT production.
XX
PS Claim 7; Page 111; 220pp; English.
XX
CC The invention relates to an oligonucleotide for targeted alteration of a
CC genetic sequence, which comprises a single-stranded oligonucleotide
CC having a DNA domain. The DNA domain has at least one mismatch with
CC respect to the genetic sequence to be altered and further comprises
CC chemical modifications of the oligonucleotide. The chemical modifications
CC consist of o-methyl modification, an LNA modification, two or more
CC phosphorothioate linkages on a terminus, or a combination of any two or
CC more of these modifications. The oligonucleotides are useful for
CC directing repair or alteration of plant genetic information. The
CC oligonucleotides are particularly useful for creating plants with desired
CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
CC nutritional value (e.g. altering amino acid content of plants or
CC conferring amino acid over production), herbicide resistance (e.g.
CC glyphosate resistance, imidazolinone and sulphonylurea herbicide

CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention
 XX
 SQ Sequence 17 BP; 2 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 928 CCAGCAGCTCAACAGCA 944
 ||||| ||||| ||||| ||
 DB 17 CCAGCTGCTCAACCGA 1
 RESULT 434
 ID ABK25788 standard; DNA; 17 BP.
 XX
 AC ABK25788;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Stress tolerance conferring genome altering oligonucleotide #256.
 XX
 KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; LNA modification; phosphorothioate linkage;
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW modified fatty acid content; reduced palmitate production; albino plant;
 KW increased stearate production; reduced linolenic acid production;
 KW photosynthetic process.
 XX
 OS Cucumis sativus.
 OS Synthetic.
 XX
 PN WO200192512-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 01-JUN-2001; 2001WO-US017672.
 XX
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 PR 27-MAR-2001; 2001US-00818875.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 PI Kmiec EB, Gamper HB, Rice MC, Kim J;
 XX
 DR WPI; 2002-106307/14.
 XX
 PT New oligonucleotides with modified nuclease-resistant termini, useful for
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.
 XX
 PS Claim 7; Page 111; 220pp; English.
 XX
 CC The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises

CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention
 XX
 SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 928 CCAGCAGCTCAACAGCA 944
 ||||| ||||| ||||| ||
 DB 1 CCAGCTGCTCAACCGA 17
 RESULT 435
 ID ABN97699 standard; cDNA; 17 BP.
 XX
 AC ABN97699;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Human NEBD-1 scanning 17-mer sequence #209.
 XX
 KW NEBD-1; cytosstatic; human; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200226818-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 26-SEP-2001; 2001WO-US030287.
 XX
 PR 27-SEP-2000; 2000US-0236359P.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 01-JUN-2001; 2001US-00872462.
 XX
 PA (AEOM-) AEOMICA INT.
 XX
 PI Gu Y, Corrigan A;
 XX
 DR WPI; 2002-426011/45.
 XX
 PT Polynucleotide and polypeptide of human NEBD-1 useful for diagnosing,
 PT treating or preventing a disorder associated with decreased or increased
 PT expression or activity of the polypeptide.
 XX

PS Example 4; Page 159; 190pp; English.

XX This invention relates to an isolated polynucleotide encoding human NEDD-1, which is cytosolic in its action. The polynucleotide is useful for

CC diagnosing diseases caused by mutation in human NEDD-1, and for

CC diagnosing or monitoring diseases caused by altered expression of human

CC NEDD-1. Fragments of NEDD-1 are useful as hybridisation probes and

CC primers, and to direct expression or synthesis of epitopic or immunogenic

CC protein fragments. The proteins are useful as therapeutic supplement in

CC patients with specific deficiency in human NEDD-1 production, and for

CC treating subjects preferably with defects in NEDD-1. The present sequence

CC is a nucleotide sequence related to human NEDD-1

XX

SQ Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2676 AGTTACACACGAGTG 2692

Db 1 AGTTAGACCATCAGTG 17

RESULT 436

ABN97700

ID ABN97700 standard; cDNA; 17 BP.

XX

AC ABN97700;

XX

DT 30-JUL-2002 (first entry)

XX

DE Human NEDD-1 scanning 17-mer sequence #210.

XX

KW NEDD-1; cytosolic; human; ss.

XX

OS Homo sapiens.

XX

PN WO200226818-A2.

XX

PD 04-APR-2002.

XX

PF 26-SEP-2001; 2001WO-US030287.

XX

PR 27-SEP-2000; 2000US-0236359P.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 01-JUN-2001; 2001US-00872462.

XX

PA (AEOM-) AEOMICA INT.

XX

PI Gu Y, Corrigan A;

XX

PT WPI; 2002-426011/45.

XX

DR Polynucleotide and polypeptide of human NEDD-1 useful for diagnosing,

XX treating or preventing a disorder associated with decreased or increased

XX expression or activity of the polypeptide.

XX

PS Example 4; Page 159; 190pp; English.

XX This invention relates to an isolated polynucleotide encoding human NEDD-1, which is cytosolic in its action. The polynucleotide is useful for

CC diagnosing diseases caused by mutation in human NEDD-1, and for

CC diagnosing or monitoring diseases caused by altered expression of human

CC NEDD-1. Fragments of NEDD-1 are useful as hybridisation probes and

CC primers, and to direct expression or synthesis of epitopic or immunogenic

CC protein fragments. The proteins are useful as therapeutic supplement in

CC patients with specific deficiency in human NEDD-1 production, and for

CC treating subjects preferably with defects in NEDD-1. The present sequence

CC is a nucleotide sequence related to human NEDD-1

CC

CC NEDD-1. Fragments of NEDD-1 are useful as hybridisation probes and

CC primers, and to direct expression or synthesis of epitopic or immunogenic

CC protein fragments. The proteins are useful as therapeutic supplement in

CC patients with specific deficiency in human NEDD-1 production, and for

CC treating subjects preferably with defects in NEDD-1. The present sequence

CC is a nucleotide sequence related to human NEDD-1

XX

SQ Sequence 17 BP; 5 A; 4 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2677 GTTAACACACGAGTG 2693

Db 1 GTTAAGACCATCAGTG 17

RESULT 437

ABN97698

ID ABN97698 standard; cDNA; 17 BP.

XX

AC ABN97698;

XX

DT 30-JUL-2002 (first entry)

XX

DE Human NEDD-1 scanning 17-mer sequence #208.

XX

KW NEDD-1; cytosolic; human; ss.

XX

OS Homo sapiens.

XX

PN WO200226818-A2.

XX

PD 04-APR-2002.

XX

PF 26-SEP-2001; 2001WO-US030287.

XX

PR 27-SEP-2000; 2000US-0236359P.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 01-JUN-2001; 2001US-00872462.

XX

PA (AEOM-) AEOMICA INT.

XX

PI Gu Y, Corrigan A;

XX

PT WPI; 2002-426011/45.

XX

DR Polynucleotide and polypeptide of human NEDD-1 useful for diagnosing,

XX treating or preventing a disorder associated with decreased or increased

XX expression or activity of the polypeptide.

XX

PS Example 4; Page 159; 190pp; English.

XX This invention relates to an isolated polynucleotide encoding human NEDD-1, which is cytosolic in its action. The polynucleotide is useful for

CC diagnosing diseases caused by mutation in human NEDD-1, and for

CC diagnosing or monitoring diseases caused by altered expression of human

CC NEDD-1. Fragments of NEDD-1 are useful as hybridisation probes and

CC primers, and to direct expression or synthesis of epitopic or immunogenic

CC protein fragments. The proteins are useful as therapeutic supplement in

CC patients with specific deficiency in human NEDD-1 production, and for

CC treating subjects preferably with defects in NEDD-1. The present sequence

CC is a nucleotide sequence related to human NEDD-1

CC

```
XX SQ Sequence 17 BP; 6 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2675 CAGTTAACACCGAGT 2691
Db 1 CAGTTAAGACCATCATG 17

RESULT 438
ABN97696
ID ABN97696 standard; cDNA; 17 BP.
XX
AC ABN97696;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human NEDD-1 scanning 17-mer sequence #206.
XX
KW NEDD-1; cytosstatic; human; ss.
XX
OS Homo sapiens.
XX
PN WO200226818-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030287.
XX
PR 27-SEP-2000; 2000US-0236359P.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 01-JUN-2001; 2001US-00872462.
XX
PA (AEOM-) AEOMICA INT.
XX
PI Gu Y, Corrigan A;
XX
DR WPI; 2002-426011/45.
XX
PT Polynucleotide and polypeptide of human NEDD-1 useful for diagnosing,
PT treating or preventing a disorder associated with decreased or increased
PT expression or activity of the polypeptide.
XX
PS Example 4; Page 159; 190pp; English.
XX
CC This invention relates to an isolated polynucleotide encoding human NEDD-
CC 1, which is cytosstatic in its action. The polynucleotide is useful for
CC diagnosing diseases caused by mutation in human NEDD-1, and for
CC diagnosing or monitoring diseases caused by altered expression of human
CC NEDD-1. Fragments of NEDD-1 are useful as hybridisation probes and
CC primers, and to direct expression or synthesis of epitopic or immunogenic
CC protein fragments. The proteins are useful as therapeutic supplement in
CC patients with specific deficiency in human NEDD-1 production, and for
CC treating subjects preferably with defects in NEDD-1. The present sequence
CC is a nucleotide sequence related to human NEDD-1
XX
SQ Sequence 17 BP; 7 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2673 ACCAGTTAACACCGAGT 2689
Db 1 ACCAGTTAAGACCATCATG 17

RESULT 439
ABN97697
ID ABN97697 standard; cDNA; 17 BP.
XX
AC ABN97697;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human NEDD-1 scanning 17-mer sequence #207.
XX
KW NEDD-1; cytosstatic; human; ss.
XX
OS Homo sapiens.
XX
PN WO200226818-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030287.
XX
PR 27-SEP-2000; 2000US-0236359P.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 01-JUN-2001; 2001US-00872462.
XX
PA (AEOM-) AEOMICA INT.
XX
PI Gu Y, Corrigan A;
XX
DR WPI; 2002-426011/45.
XX
PT Polynucleotide and polypeptide of human NEDD-1 useful for diagnosing,
PT treating or preventing a disorder associated with decreased or increased
PT expression or activity of the polypeptide.
XX
PS Example 4; Page 159; 190pp; English.
XX
CC This invention relates to an isolated polynucleotide encoding human NEDD-
CC 1, which is cytosstatic in its action. The polynucleotide is useful for
CC diagnosing diseases caused by mutation in human NEDD-1, and for
CC diagnosing or monitoring diseases caused by altered expression of human
CC NEDD-1. Fragments of NEDD-1 are useful as hybridisation probes and
CC primers, and to direct expression or synthesis of epitopic or immunogenic
CC protein fragments. The proteins are useful as therapeutic supplement in
CC patients with specific deficiency in human NEDD-1 production, and for
CC treating subjects preferably with defects in NEDD-1. The present sequence
CC is a nucleotide sequence related to human NEDD-1
XX
SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2674 CCAGTTAACACCGAGT 2690
Db 1 CCAGTTAAGACCATCATG 17
```

RESULT 440
ABS74998
ID ABS74998 standard; DNA; 17 BP.
XX
XX
AC ABS74998;
XX
DT 24-DEC-2002 (first entry)
XX
DE Human PAPP-Ea associated 17-mer SEQ ID 524.
XX
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
XX
XX Homo sapiens.
OS
XX US2002102252-A1.
PN
XX 01-AUG-2002.
PD
XX 06-APR-2001; 2001US-00827998.
PF
XX 26-MAY-2000; 2000US-0207456P.
PR
XX (GUY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
XX Gu Y, Shannon ME;
PI
XX WPI; 2002-697817/75.
DR
XX New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.
PT
XX
PS Example 2; Page 144; 353pp; English.
XX
XX This invention describes a novel isolated nucleic acid that encodes one
CC of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention
XX
SQ Sequence 17 BP; 10 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 473 CAAATGACCCCAAGAGAA 489
Db 1 CAAAGGAACCAAGAGAA 17
|||||

RESULT 441
ABV90854/C
ID ABV90854 standard; DNA; 17 BP.
XX
AC ABV90854;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1567.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
DE

KW gene therapy; transgenic; ss.
XX
OS Homo sapiens.
XX
FN EPI2339051-A2.
XX
PD 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
PF
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
PA (ABOM-) AEOMICA INC.
XX
XX Shannon M;
PI
XX WPI; 2002-684061/74.
XX
DR Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
PS Example 2; SEQ ID NO 1567; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),
CC (S1) having 9% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 5 A; 6 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2211 TTCAGATATGGGATG 2227
Db 17 TTCGAAATGGGATG 1
|||||

RESULT 442
ABV89860
ID ABV89860 standard; DNA; 17 BP.
XX
AC ABV89860;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 573.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX Homo sapiens.
OS
PN EP1239051-A2.
XX
PD 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
PF 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M;
XX
XX WPI; 2002-684061/74.
XX
PT Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
PS Example 2; SEQ ID NO 573; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 4 A; 7 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2551 AGCCCTGACGCTGCGAG 2567
DB 1 ACCCCAGACGCTGCGAG 17
RESULT 443
ABV90268/c
ID ABV90268 standard; DNA; 17 BP.
XX
AC ABV90268;
XX

DT 23-DEC-2002 (first entry)
XX
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 981.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
OS Homo sapiens.
XX
XX EP1239051-A2.
XX
PD 11-SEP-2002.
XX
XX 28-JAN-2002; 2002EP-00001165.
XX
PF 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M;
XX
XX WPI; 2002-684061/74.
XX
PT Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
PS Example 2; SEQ ID NO 981; 60pp + Sequence Listing; English.
XX
CC The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
SQ Sequence 17 BP; 1 A; 5 C; 1 G; 10 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3090 AAAGAAGAAAGGGAAGA 3106
DB 17 AAACAAGATAGGGAAGA 1
RESULT 444
ABV98959
ID ABV98959 standard; DNA; 17 BP.

XX AC ABK55961;
XX DT 02-JUL-2002 (first entry)
XX DE Human CLCA1 gene enzymatic nucleic acid #332.
XX DE Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
XX KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
XX KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
XX KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
XX KW acetylcysteine.
XX OS Homo sapiens.
XX PN WO200211674-A2.
XX PD 14-FEB-2002.
XX PF 09-AUG-2001; 2001WO-US024970.
XX PR 09-AUG-2000; 2000US-0224383P.
XX PR (RIBO-) RIBOZYME PHARM INC.
XX PA (SYNT) SYNTAX USA LLC.
XX PA (THOM) THOMPSON J.
XX PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
XX PI Grupe A;
XX WPI; 2002-217145/27.
XX DR Enzymatic polynucleotide that down regulates expression of chloride
XX PT channel calcium activated gene, useful for treating Chronic obstructive
XX PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX PS Claim 4; Page 58; 152pp; English.
XX CC The invention relates to enzymatic nucleic acid molecules that down
XX CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
XX CC by cleaving RNA derived from the genes. The nucleic acid sequences are
XX CC useful as pharmaceutical agents for treating conditions such as chronic
XX CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
XX CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
XX CC that are related to or will respond to the levels of CLCA1 in a cell or
XX CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
XX CC hence, are useful for treatment of a patient having a condition
XX CC associated with the level of CLCA1, where the invention further comprises
XX CC the use of one or more therapies under conditions suitable for the
XX CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
XX CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
XX CC nucleic acids of the invention are also used as diagnostic tools to
XX CC examine genetic drift and mutations within diseased cells or to detect
XX CC the presence of CLCA1 RNA in a cell. This sequence represents an
XX CC enzymatic nucleic acid molecule of the invention
XX SQ Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.5e-02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1648 CCAGCGCTTGCTAAGGT 1664
DB 1 CCAGGCAUUGCUAAGGU 17
RESULT 447
AAD36054
ID AAD36054 standard; DNA; 17 BP.
XX AC AAD36054;
XX

DT 09-AUG-2002 (first entry)
XX DE Human cMLCK DNA amplifying primer 3.
XX KW Human; cardiac myosin light chain kinase; cMLCK; tricuspid valve;
XX KW cardiac dysfunction; systolic dysfunction; mitral valve prolapse;
XX KW diastolic dysfunction; cardiac hypertrophy; tricuspid insufficiency;
XX KW coronary heart disease; myocardial infarction; mitral insufficiency;
XX KW valvular heart disease; congestive heart failure; mitral valve;
XX KW cardiomyopathy; cardiac; PCR; primer; ss.
XX OS Homo sapiens.
XX PN WO200224899-A2.
XX PD 28-MAR-2002.
XX PF 12-SEP-2001; 2001WO-US028639.
XX PR 12-SEP-2000; 2000US-0232246P.
XX PR 13-SEP-2000; 2000US-0232456P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Epstein ND, Hassanzadeh S, Winitzky S, Davis JS;
XX DR WPI; 2002-394135/42.
XX PT New isolated cardiac myosin light chain kinase (cMLCK) protein, useful
XX PT for identifying cMLCK modulators that are used for treating cardiac
XX PT dysfunction e.g. systolic or diastolic dysfunction, myocardial
XX PS infarction.
XX PS Example 1; Page 31; 105pp; English.
XX CC The invention relates to cDNA, protein sequence and genomic structure of
XX CC the human cardiac isoform of myosin light chain kinase (cMLCK) and
XX CC mutations in cMLCK gene that are associated with cardiac dysfunction. The
XX CC invention also relates to methods for identifying agents that modulate
XX CC cMLCK activity. cMLCK is useful for detecting enhanced susceptibility of
XX CC a subject to cardiac dysfunction. cMLCK is useful for screening for an
XX CC agent that modulates its biological activity. The method is useful for
XX CC enhancing or preserving cardiac function in a subject having cardiac
XX CC dysfunction, and harbouring a mutation in cMLCK allele. The method is
XX CC useful for enhancing or preserving cardiac function in a subject having
XX CC cardiac dysfunction such as systolic dysfunction, diastolic dysfunction,
XX CC cardiac hypertrophy, cardiomyopathy, coronary heart disease, myocardial
XX CC infarction, or congestive heart failure, or for preserving cardiac
XX CC function, or cardiac dysfunction which comprises valvular heart disease
XX CC such as mitral valve disease, tricuspid valve disease, mitral
XX CC insufficiency, tricuspid insufficiency, or mitral valve prolapse. The
XX CC method is useful for treating cardiac dysfunction, e.g., systolic or
XX CC diastolic dysfunction, coronary heart disease, cardiac hypertrophy,
XX CC cardiomyopathy, myocardial infarction, or congestive heart failure. The
XX CC present sequence is a PCR primer used to amplify human cMLCK DNA
XX SQ Sequence 17 BP; 5 A; 8 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e-02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 845 TCAGTCCCTCAGAGCCA 861
DB 1 TCAGACCCCGAGAGCCA 17
RESULT 448
ACN03097/c
ID ACN03097 standard; RNA; 17 BP.
XX AC ACN03097;
XX

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DT 22-APR-2004 (first entry)
XX WNV Inozyme substrate SEQ ID NO 3100.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 3100; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 17 BP; 1 A; 3 C; 5 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 2698 GAGACCCATGAACCAA 2714
XX ||| ||||| ||||| |||||
XX 17 GAGCCACATGAACCAA 1
XX
XX
XX RESULT 449
XX ACN01188/c
XX ID ACN01188 standard; RNA; 17 BP.
XX
XX AC ACN01188;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1178.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;

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KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 1178; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 17 BP; 2 A; 3 C; 5 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 2700 GACCCATGAACCAAATG 2716
XX ||| ||||| ||||| |||||
XX 17 GCCACATGAACCAAATG 1
XX
XX
XX RESULT 450
XX ACN05943/c
XX ID ACN05943 standard; RNA; 17 BP.
XX
XX AC ACN05943;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV Amberzyme substrate SEQ ID NO 5946.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX

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PD 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 DR New nucleic acid molecule that modulates replication of West Nile Virus
 XX (WNV), useful for treating a condition related to WNV infection e.g.
 XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX Claim 23; SEQ ID NO 5946; 495pp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 4 A; 0 C; 8 G; 0 T; 5 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3704 CCACATCTCTACTTC 3720
 DB 17 CCAAAATCTCCACTTC 1
 RESULT 451
 ACN14376
 ID ACN14376 standard; RNA; 17 BP.
 AC ACN14376;
 XX 22-APR-2004 (first entry)
 DT WNV minus strand Amberzyme substrate SEQ ID NO 14379.
 DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS WO200268637-A2.
 PN 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.

PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 DR New nucleic acid molecule that modulates replication of West Nile Virus
 XX (WNV), useful for treating a condition related to WNV infection e.g.
 XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX Claim 23; SEQ ID NO 14379; 495pp; English.
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 XX Sequence 17 BP; 8 A; 5 C; 2 G; 0 T; 2 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. NO. 2.5e+02;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2699 AGACCCATGACCAAT 2715
 DB 1 AGCCACAUGAACCAAU 17
 RESULT 452
 ACN01465
 ID ACN01465 standard; RNA; 17 BP.
 XX ACN01465;
 XX 22-APR-2004 (first entry)
 DT WNV Inozyme substrate SEQ ID NO 1455.
 DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS WO200268637-A2.
 PN 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.

PT New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 1455; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX SQ Sequence 17 BP; 10 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2532 GAACAGCGAACAGCMA 2548

Db 1 GAACAAACAAACAGCGA 17

RESULT 453

ACN12785/C

ID ACN12785 standard; RNA; 17 BP.

AC ACN12785;

DT 22-APR-2004 (first entry)

XX WNV minus strand Zinzyme substrate SEQ ID NO 12788.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 12788; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX SQ Sequence 17 BP; 3 A; 5 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1212 TCCTCATGCGACAAAAG 1228

Db 17 TCCTCATGCGACGGAAG 1

RESULT 454

ACN02990

ID ACN02990 standard; RNA; 17 BP.

AC ACN02990;

XX 22-APR-2004 (first entry)

XX WNV Inozyme substrate SEQ ID NO 2993.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
 KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 2993; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

Sequence 17 BP; 8 A; 2 C; 4 G; 0 T; 3 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 70.6%; Pred. No. 2.5e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2813 TCAGAACACAGGTTGAA 2829
 :||| ||||| :|||
 Db 1 UCAGAGACAGGAUGAA 17

RESULT 455
 ACN05859/c
 ID ACN05859 standard; RNA; 17 BP.
 XX
 AC ACN05859;
 DT 22-APR-2004 (first entry)
 XX
 DE WNV Amberzyme substrate SEQ ID NO 5862.
 XX
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.
 XX WO200268637-A2.
 XX 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 XX (WNV), useful for treating a condition related to WNV infection e.g.
 XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX Claim 23; SEQ ID NO 5862; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 XX treating a condition related to WNV infection e.g. pancreatitis,
 XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 XX molecule is selected from the group of ribozymes consisting of
 XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 XX nucleic acid molecules further comprise at least five ribose residues, at
 XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 XX least three of the 5' terminal nucleotides and a 3' end modification of a
 XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 XX in the specification. The present sequence is that of a nucleic acid
 XX molecule of the invention

Sequence 17 BP; 3 A; 4 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2115 TGGCAACCCAGTTTCA 2131
 ||||| ||||| |||||
 Db 17 TGGCACACCCAGTTGTC A 1

RESULT 456
 ACN09716/c
 ID ACN09716 standard; RNA; 17 BP.
 XX
 AC ACN09716;
 DT 22-APR-2004 (first entry)
 XX
 DE WNV minus strand Inozyme substrate SEQ ID NO 9719.
 XX
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.
 XX WO200268637-A2.
 XX 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (BLAT/) BLATT L.
 XX (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
 XX (WNV), useful for treating a condition related to WNV infection e.g.
 XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX Claim 23; SEQ ID NO 9719; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
 XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 XX treating a condition related to WNV infection e.g. pancreatitis,
 XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 XX molecule is selected from the group of ribozymes consisting of
 XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 XX nucleic acid molecules further comprise at least five ribose residues, at
 XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 XX least three of the 5' terminal nucleotides and a 3' end modification of a
 XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 XX in the specification. The present sequence is that of a nucleic acid
 XX molecule of the invention

Sequence 17 BP; 3 A; 6 C; 1 G; 0 T; 7 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3040 TGACTGGATGAAAGACA 3056

```
Db      17 TGATGGATGGAGACA 1
|||||
ACN10151;
22-APR-2004 (first entry)
WNV minus strand Inozyme substrate SEQ ID NO 10154.
WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
virucide; neuroprotective; antibacterial; replication; pancreatitis;
encephalitis; myocarditis; meningitis; infection; hepatitis;
liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
Amberzyme; Zinzyme; ss.
West Nile Virus.
OS
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
(WNV), useful for treating a condition related to WNV infection e.g.
pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 10154; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
of the West Nile Virus (WNV). The nucleic acid molecules are useful for
treating a condition related to WNV infection e.g. pancreatitis,
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
molecule is selected from the group of ribozymes consisting of
Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
nucleic acid molecules further comprise at least five ribose residues, at
least ten 2'-O-methyl modifications, phosphorothioate linkages on at
least three of the 5' terminal nucleotides and a 3' end modification of a
3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
in the specification. The present sequence is that of a nucleic acid
molecule of the invention
XX
XX Sequence 17 BP; 2 A; 7 C; 0 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.5e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
QY 3666 TTTCTTCCCCATATTCA 3682
:::|||||:
Db 1 UUUUUUUUUUUUUUUUU 17
RESULT 458
ACN10151/c
ID ACN10151 standard; RNA; 17 BP.
Db      17 TGATGGATGGAGACA 1
|||||
ACN09847
22-APR-2004 (first entry)
WNV minus strand Inozyme substrate SEQ ID NO 9850.
WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
virucide; neuroprotective; antibacterial; replication; pancreatitis;
encephalitis; myocarditis; meningitis; infection; hepatitis;
liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
Amberzyme; Zinzyme; ss.
West Nile Virus.
OS
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
(WNV), useful for treating a condition related to WNV infection e.g.
pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 9850; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
of the West Nile Virus (WNV). The nucleic acid molecules are useful for
treating a condition related to WNV infection e.g. pancreatitis,
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
molecule is selected from the group of ribozymes consisting of
Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
nucleic acid molecules further comprise at least five ribose residues, at
least ten 2'-O-methyl modifications, phosphorothioate linkages on at
least three of the 5' terminal nucleotides and a 3' end modification of a
3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
in the specification. The present sequence is that of a nucleic acid
molecule of the invention
XX
XX Sequence 17 BP; 2 A; 7 C; 0 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 47.1%; Pred. No. 2.5e+02;
Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
QY 3666 TTTCTTCCCCATATTCA 3682
:::|||||:
Db 1 UUUUUUUUUUUUUUUUU 17
RESULT 459
ACN06089/c
ID ACN06089 standard; RNA; 17 BP.
XX
XX ACN06089;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV Amberzyme substrate SEQ ID NO 6092.
XX
```


KW WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 PI WPI; 2002-706994/76.
 DR
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 XX Claim 23; SEQ ID NO 6092; 495pp; English.
 PS
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 CC
 XX Sequence 17 BP; 2 A; 2 C; 5 G; 0 T; 8 U; 0 Other;
 SQ
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 617 ATCAATGCCACCATAAA 633
 Db 17 AACGATGCCACCATAAA 1
 |||||
 RESULT 460
 ACN07144/C
 ID ACN07144 standard; RNA; 17 BP.
 XX ACN07144;
 AC
 XX 22-APR-2004 (first entry)
 DT
 XX WNV Amberzyme substrate SEQ ID NO 7147.
 DE
 XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS

XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 PF
 XX 20-OCT-2000; 2000US-0242411P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 PI WPI; 2002-706994/76.
 DR
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 PT
 XX Claim 23; SEQ ID NO 7147; 495pp; English.
 PS
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 CC
 XX Sequence 17 BP; 8 A; 0 C; 7 G; 0 T; 2 U; 0 Other;
 SQ
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3656 TTTCTTCCCATATTCA 3682
 Db 17 TTTCTTCCCATTTCTCA 1
 |||||
 RESULT 461
 ACN01189/C
 ID ACN01189 standard; RNA; 17 BP.
 XX ACN01189;
 AC
 XX 22-APR-2004 (first entry)
 DT
 XX WNV Hammerhead Ribozyme substrate SEQ ID NO 1179.
 DE
 XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS
 XX WO200268637-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX
 XX 19-OCT-2001; 2001WO-US048350.
 PF

PR 20-OCT-2000; 2000US-0242411P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
PI WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 1179; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 17 BP; 2 A; 2 C; 5 G; 0 T; 8 U; 0 Other;
SQ

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2699 AGACCCATGACCAAT 2715
DB 17 AGCCACATGAACCAAT 1

RESULT 462
ACN11320
ID ACN11320 standard; RNA; 17 BP.
XX
XX ACN11320;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV minus strand Inozyme substrate SEQ ID NO 11323.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 11323; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyne. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 17 BP; 8 A; 5 C; 2 G; 0 T; 2 U; 0 Other;
SQ

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 617 ATCAATGCCACATAAA 633
DB 1 AACGAUGCCACCAUAAA 17

RESULT 463
ACN05400
ID ACN05400 standard; RNA; 17 BP.
XX
XX ACN05400;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV DNazyme substrate SEQ ID NO 5403.
XX
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX

PS Claim 23; SEQ ID NO 5403; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 17 BP; 7 A; 1 C; 6 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3039 ATGACTGCATGAAGAC 3055
Db 1 AUGAUGGAUGGAAGAC 17
|||:|||||
|:|:|:|:|:|

RESULT 464

ACN11532
ID ACN11532 standard; RNA; 17 BP.

XX ACN11532;

AC 22-APR-2004 (first entry)

DT WNV minus strand Inozyme substrate SEQ ID NO 11535.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyme; ss.

XX West Nile Virus.

OS WO200268637-A2.

PN 06-SEP-2002.

PD 19-OCT-2001; 2001WO-US048350.

PF 20-OCT-2000; 2000US-0242411P.

PR (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

PI WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 11535; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

XX Sequence 17 BP; 5 A; 8 C; 0 G; 0 T; 4 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3704 CCACAATCCTCTACTTC 3720
Db 1 CCAAAUCCUCCACUUC 17
|||:|||||
|:|:|:|:|:|

RESULT 465

ACN09448/C

ID ACN09448 standard; RNA; 17 BP.

XX ACN09448;

AC 22-APR-2004 (first entry)

DT WNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 9451.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic; virucide; neuroprotective; antibacterial; replication; pancreatitis; encephalitis; myocarditis; meningitis; infection; hepatitis; liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme; Amberzyme; Zinzyme; ss.

XX West Nile Virus.

OS WO200268637-A2.

PN 06-SEP-2002.

PD 19-OCT-2001; 2001WO-US048350.

PF 20-OCT-2000; 2000US-0242411P.

PR (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

PI WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 23; SEQ ID NO 9451; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication of the West Nile Virus (WNV). The nucleic acid molecules are useful for treating a condition related to WNV infection e.g. pancreatitis, encephalitis, myocarditis, meningitis, neurologic infection, hepatitis, liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid molecule is selected from the group of ribozymes consisting of Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The nucleic acid molecules further comprise at least five ribose residues, at least ten 2'-O-methyl modifications, phosphorothioate linkages on at least three of the 5' terminal nucleotides and a 3' end modification of a 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080 are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given in the specification. The present sequence is that of a nucleic acid molecule of the invention

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CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 0 A; 3 C; 4 G; 0 T; 10 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2532 GAACAAACACAGCA 2548
DB 17 GAACAAACACAGCA 1
RESULT 466
ACN11653
ID ACN11653 standard; RNA; 17 BP.
XX
AC ACN11653;
DT 22-APR-2004 (first entry)
XX
XX WNV minus strand Inozyme substrate SEQ ID NO 11656.
DE WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 11656; 495pp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, and zinzyne. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
SQ Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. NO. 2.5e+02;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2115 TGGCAAAACCCAGTTTCA 2131
DB 1 UGGCACACCCAGUGUCA 17
RESULT 467
ACD00549/C
ID ACD00549 standard; DNA; 17 BP.
XX
XX ACD00549;
AC
DT 28-JUL-2003 (first entry)
XX
XX G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #1022.
DE
XX
XX Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
XX Homo sapiens.
OS
XX WO2003031621-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032599.
XX
XX 12-OCT-2001; 2001US-0329000P.
XX
XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
XX
XX Zhang J;
XX
XX WPI; 2003-381720/36.
XX
XX New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT investigating and/or treating disorders associated with aberrant
PT expression or activity of GPCR-A-1, such as tumors and cancers.
XX
XX Example 2; SEQ ID NO 1046; 156pp; English.
XX
XX The invention describes an isolated nucleic acid encoding a G protein
CC coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC 409 residue amino acid sequence, all given in the specification, with or
CC without conservative amino acid substitutions, or complements of the
CC sequence of them. The encoding nucleic acid is not more than 100 kb in
CC length. The methods and compositions of the present invention are useful
CC for diagnosing, investigating and/or treating disorders associated with
CC aberrant expression or activity of GPCR-A-1, such as tumors and cancers.
CC This sequence represents an oligonucleotide used to analyse the gene
CC encoding human G-protein coupled receptor GPCR-A-1
XX
XX Sequence 17 BP; 4 A; 0 C; 3 G; 10 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2367 CAAGTAATAATAACAAT 2383
DB 17 CAATCATATAACAAT 1
RESULT 468
ABT37547/C
ID ABT37547 standard; DNA; 17 BP.
XX
XX ABT37547;
AC
XX
XX 12-JUN-2003 (first entry)
DT
XX

DE Tumour suppression related human fukutin oligo SEQ ID No 3184.
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX Homo sapiens.
 OS
 XX WO2003025175-A2.
 PN
 XX 27-MAR-2003.
 PD
 XX
 XX 17-SEP-2002; 2002WO-IB004208.
 XX
 PF 17-SEP-2001; 2001FR-00011978.
 XX
 PR 17-SEP-2001; 2001FR-00011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 XX WPI; 2003-313353/30.
 DR
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 PT
 XX
 XX Disclosure; Page 406; 720pp; French.
 PS
 XX
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 1 G; 10 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3417 AAAAAGGCTATAGAC 3433
 |||||
 DB 17 AAAAAGGTAAGAGATC 1
 RESULT 469
 ABT37040
 ID ABT37040 standard; DNA; 17 BP.
 XX
 AC ABT37040;
 XX
 XX 12-JUN-2003 (first entry)
 DT
 DE Tumour suppression related human fukutin oligo SEQ ID No 2677.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW human fukutin; ds.
 XX Homo sapiens.
 OS
 XX WO2003025175-A2.
 PN
 XX 27-MAR-2003.
 PD
 XX
 XX 17-SEP-2002; 2002WO-IB004208.
 XX
 PF 17-SEP-2001; 2001FR-00011978.
 XX
 PR 17-SEP-2001; 2001FR-00011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 XX WPI; 2003-313353/30.
 DR
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 PT
 XX
 XX Disclosure; Page 406; 720pp; French.
 PS
 XX
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 1 G; 10 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3417 AAAAAGGCTATAGAC 3433
 |||||
 DB 17 AAAAAGGTAAGAGATC 1
 RESULT 470
 ABT37508
 ID ABT37508 standard; DNA; 17 BP.
 XX
 AC ABT37508;
 XX
 XX 12-JUN-2003 (first entry)
 DT
 DE Tumour suppression related human fukutin oligo SEQ ID No 3145.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW human fukutin; ds.
 XX Homo sapiens.
 OS
 XX WO2003025175-A2.
 PN
 XX 27-MAR-2003.
 PD
 XX
 XX 17-SEP-2002; 2002WO-IB004208.
 XX
 PF 17-SEP-2001; 2001FR-00011978.
 XX
 PR 17-SEP-2001; 2001FR-00011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 XX WPI; 2003-313353/30.
 DR
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 PT
 XX
 XX Disclosure; Page 346; 720pp; French.
 PS
 XX
 XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 536 GATCCTGAGCTGCAGGA 552
 |||||
 DB 1 GATCCTGAGCTGCCGAA 17
 RESULT 470
 ABT37508
 ID ABT37508 standard; DNA; 17 BP.
 XX
 AC ABT37508;
 XX
 XX 12-JUN-2003 (first entry)
 DT
 DE Tumour suppression related human fukutin oligo SEQ ID No 3145.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;

```
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
XX
XX WO2003025175-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004208.
XX
XX 17-SEP-2001; 2001FR-00011978.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-313353/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX
XX Disclosure; Page 401; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX given in the specification, a sequence containing at least 15 consecutive
XX nucleotides from the 17 mer sequence, a sequence with, after optimal
XX alignment, at least 80 % identity to the 17 mer sequence, or the complement
XX hybridizes to them under highly stringent conditions, or the complement
XX of any of them, or the corresponding RNA. The novel isolated nucleic
XX acids of the invention are useful as probes and primers for detecting,
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX component of a gene chip, in vitro as (anti)sense reagents, and for
XX production of recombinant polypeptides. Any of the nucleic acids,
XX polypeptides, vectors containing the nucleic acids, cells containing the
XX vector or antibodies directed against the polypeptides are useful for
XX preparation of pharmaceuticals for prevention and/or treatment of viral
XX diseases that are characterised by development of tumours or cell
XX degeneration, specifically cancer but also Alzheimer's disease and
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX patient samples is useful for diagnosis and/or prognosis of these
XX diseases. The polypeptides can also be used to generate antibodies, and
XX both the polypeptide and antibodies are useful as components of protein
XX chips. The nucleic acid sequences of the invention can be used in gene
XX therapy. This polynucleotide sequence represents a tumour suppression
XX related human fukutin oligonucleotide of the invention
XX
XX Sequence 17 BP; 7 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1909 GATCATCGACAGAAAC 1925
XX ||||| ||||| |||||
XX 1 GATCCTGGACAGAAAC 17
XX
XX RESULT 471
XX ABT35272/c
XX ID ABT35272 standard; DNA; 17 BP.
XX
XX AC ABT35272;
XX
XX 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 909.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1747 ACAACAGACAGACAGATC 1763
XX ||||| ||||| |||||
XX 17 ACAACAGACATAGATC 1
XX
XX Db
XX
XX RESULT 472
XX ABT37737/c
XX ID ABT37737 standard; DNA; 17 BP.
XX
XX AC ABT37737;
XX
XX 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 3374.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1747 ACAACAGACAGACAGATC 1763
XX ||||| ||||| |||||
XX 17 ACAACAGACATAGATC 1
XX
XX Db
XX
XX RESULT 472
XX ABT37737/c
XX ID ABT37737 standard; DNA; 17 BP.
XX
XX AC ABT37737;
XX
XX 12-JUN-2003 (first entry)
XX
XX Tumour suppression related human fukutin oligo SEQ ID No 3374.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; protein chip; gene therapy; tumour suppression;
XX human fukutin; ds.
XX
XX Homo sapiens.
XX
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AC	ACA06547;	Query Match	0.4%;	Score 13.8;	DB 1;	Length 17;
XX	03-JUN-2003 (first entry)	Best Local Similarity	70.6%;	Pred. No. 2.5e+02;		
XX		Matches	12;	Conservative	3;	Mismatches 2;
XX						Indels 0;
XX						Gaps 0;
DE	NFKB sub-unit modulating inozyme substrate #366.					
XX		QV	1792	CCCCAGTCCCAAGTCCTA	1808	
XX	Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyne;	DB	1	CCCCUGUCCAGUCCUA	17	
KW	G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;					
KW	lung cancer; prostate cancer; colorectal cancer; brain cancer;					
KW	oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;					
KW	cervical cancer; head and neck cancer; ovarian cancer; melanoma;					
KW	lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;					
KW	chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;					
KW	cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;					
KW	gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;					
KW	rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;					
KW	gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;					
KW	transplant/graft rejection; reperfusion injury; glomerulonephritis;					
KW	allergic airway inflammation; inflammatory bowel disease; infection; ss.					
XX	Homo sapiens.					
OS						
PA	US2002177568-A1.					
PA						
PA						
PA						
PI	Stinchcomb DT, Mcswiggen J, Draper KG;					
XX	WPI; 2003-340953/32.					
XX						
XX	Novel enzymatic nucleic acid molecules which down regulates expression of					
XX	a sequence encoding a subunit of nuclear factor kappa B useful for					
XX	treating cancer, inflammatory disorders and autoimmune diseases.					
XX						
XX	Claim 3; Page 32; 72pp; English.					
XX						
XX	The invention describes an enzymatic nucleic acid molecule (I) which down					
XX	regulates expression of a sequence encoding a subunit of nuclear factor					
XX	kappa B (NFKB), where (I) is an inozyme, zinzyne, G-cleaver or amberyne					
XX	configuration. The enzymatic nucleic acid molecule is adapted to treat					
XX	cancer and is useful for down-regulating REL-A activity in a cell, for					
XX	treating a patient having a condition associated with the level of REL-A.					
XX	(I) is useful for cleaving RNA comprising a sequence of REL-A gene, in					
XX	the presence of a divalent cation, especially Mg ²⁺ . The enzymatic and					
XX	antisense nucleic acid molecules are useful for treating breast, lung,					
XX	prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,					
XX	cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or					
XX	multidrug resistant cancer. The method involves use of other drug					
XX	therapies such as monoclonal antibodies, REL-A-specific inhibitors or					
XX	chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,					
XX	cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,					
XX	gemcitabine or radiation therapy. The enzymatic and antisense nucleic					
XX	acid molecules are also useful for treating inflammatory disease such as					
XX	rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,					
XX	obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft					
XX	rejection, gene therapy applications, ischaemia/reperfusion injury					
XX	(central nervous system (CNS) and myocardial), glomerulonephritis,					
XX	sepsis, allergic airway inflammation, inflammatory bowel disease or					
XX	infection. This sequence represents the substrate of a novel enzymatic					
XX	nucleic acid molecule					
SQ	Sequence 17 BP; 2 A; 9 C; 2 G; 0 T; 4 U; 0 Other;					

Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2942 TTGACTTCTCAGCCA 2958
Db 17 TTGACTTCTCAGCCA 1
RESULT 479
ADB02404/C
ID ADB02404 standard; DNA; 17 BP.
XX AC ADB02404;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD24 scanning oligonucleotide SEQ ID 3390.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX Example 8; SEQ ID NO 3390; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

XX Example 8; SEQ ID NO 6958; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 4 A; 7 C; 1 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1664 TCACCTTCCCACTTCA 1680
Db 1 TCACCTTCCCACTTAA 17
RESULT 478
ADB00149/C
ID ADB00149 standard; DNA; 17 BP.
XX AC ADB00149;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD23 scanning oligonucleotide SEQ ID 1135.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX Example 8; SEQ ID NO 1135; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 976 GCACGACGACGACGACG 992
Db 17 GCTCCAGCACCAGCAGC 1
RESULT 480
ADA99981
ID ADA99981 standard; DNA; 17 BP.
XX
AC ADA99981;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD23 scanning oligonucleotide SEQ ID 970.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 970; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 5 A; 7 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 976 GCACGACGACGACGACG 992
Db 17 GCTCCAGCACCAGCAGC 1
RESULT 482
ADB00150/c

Qy 2578 CCCACACGGTACACCTG 2594
Db 1 CCCACACGGAGACCTG 17
RESULT 481
ADA99394/c
ID ADA99394 standard; DNA; 17 BP.
XX
AC ADA99394;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD23 scanning oligonucleotide SEQ ID 383.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 383; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 976 GCACGACGACGACGACG 992
Db 17 GCTCCAGCACCAGCAGC 1
RESULT 482
ADB00150/c

ID	ADB00150 standard; DNA; 17 BP.	
XX	ADB00150;	
AC	20-NOV-2003 (first entry)	
XX	Human MDZ3 scanning oligonucleotide SEQ ID 1136.	
DT		
XX		
DE		
XX	Cytostatic; immunostimulant; gene therapy; vaccine; human;	
KW	zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;	
XX	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;	
KW	developmental disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	EP1281758-A2.	
XX		
PD	05-FEB-2003.	
XX		
XX	30-JUL-2002; 2002EP-00016874.	
XX		
XX	02-AUG-2001; 2001US-00922181.	
OS	(AEOM-) AEOMICA INC.	
XX		
XX	Shannon M, Gu Y, Nguyen C;	
PI	WPI; 2003-423107/40.	
DR		
XX	New zinc finger-containing proteins and nucleic acids, useful in	
PT	manufacturing a medicament for treating or preventing a disorder	
XX	associated with decreased or increased expression or activity of MDZ3,	
XX	MDZ4, MDZ7 or MDZ12, e.g. cancer.	
XX	Example 8; SEQ ID NO 1136; 103pp; English.	
XX		
CC	The present invention relates to novel human zinc finger-containing	
CC	proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is	
CC	encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,	
CC	MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome	
CC	15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,	
CC	or in manufacturing a medicament for treating or preventing a disorder	
CC	associated with decreased or increased expression or activity of MDZ3,	
CC	MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic	
CC	acids and proteins are also useful for diagnosing or monitoring a disease	
CC	caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic	
CC	acids can also be used as probes to detect and characterize gross	
CC	alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are	
CC	useful in constructing microarrays for measuring gene expression. The	
CC	proteins are useful as therapeutic agents for gene therapy or as	
CC	vaccines. The present sequence was used to illustrate the invention.	
XX	Sequence 17 BP; 7 A; 4 C; 2 G; 2 T; 0 U; 0 Other;	
XX		
QY	2941 TTTTGACTTCTCTCAGCC 2957	
DB	17 TTTTGACTTCTCTCAGCC 1	
XX		
DE		
XX		
XX	RESULT 483	
ID	ADB00152/C	
XX	ADB00152 standard; DNA; 17 BP.	
XX		
AC	ADB00152;	
XX		
DT	20-NOV-2003 (first entry)	
XX		
XX	Human MDZ3 scanning oligonucleotide SEQ ID 1138.	
XX		
XX		
QY	Query Match 0.4%; Score 13.8; DB 1; Length 17;	
XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;	
XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
XX		
QY	2939 GCTTTTGACTTCTCTCAGC 2955	
DB	17 GCTTTTGACTTCTCTCAGC 1	
XX		
DE		
XX		
XX	RESULT 484	
ID	ADA93930/C	
XX	ADA93930 standard; DNA; 17 BP.	
XX		
AC	ADA93930;	
XX		
DT	20-NOV-2003 (first entry)	
XX		
XX	Human MDZ3 scanning oligonucleotide SEQ ID 379.	
XX		
XX	Cytostatic; immunostimulant; gene therapy; vaccine; human;	
KW	zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;	
KW	chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;	
XX	developmental disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
XX	EP1281758-A2.	

```
XX PD 05-FEB-2003.
XX XX
XX PF 30-JUL-2002; 2002EP-00016874.
XX XX
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX XX
XX PI Shannon M, Gu Y, Nguyen C;
XX DR WPI; 2003-423107/40.
XX XX
XX PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX XX
XX PS Example 8; SEQ ID NO 379; 103pp; English.
XX XX
XX CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX XX
XX SQ Sequence 17 BP; 1 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 980 CAGCACCAGCAGCAGCA 996
DB 17 CAGCACCAGCAGCTCCA 1
RESULT 495
ADB02405/c
ID ADB02405 standard; DNA; 17 BP.
XX
XX AC ADB02405;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Human MD24 scanning oligonucleotide SEQ ID 3391.
XX
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1281758-A2.
XX
XX PD 05-FEB-2003.
XX
XX PF 30-JUL-2002; 2002EP-00016874.
XX
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
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XX PI Shannon M, Gu Y, Nguyen C;
XX XX
XX DR WPI; 2003-423107/40.
XX XX
XX PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX XX
XX PS Example 8; SEQ ID NO 3391; 103pp; English.
XX XX
XX CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX XX
XX SQ Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 975 TGCACGACGACGACGAG 991
DB 17 TGCTCCGACGACGACGAG 1
RESULT 486
ADA99395/c
ID ADA99395 standard; DNA; 17 BP.
XX
XX AC ADA99395;
XX
XX DT 20-NOV-2003 (first entry)
XX
XX DE Human MD23 scanning oligonucleotide SEQ ID 384.
XX
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1281758-A2.
XX
XX PD 05-FEB-2003.
XX
XX PF 30-JUL-2002; 2002EP-00016874.
XX
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX
XX PI Shannon M, Gu Y, Nguyen C;
XX XX
XX DR WPI; 2003-423107/40.
XX XX
XX PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
```

PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 384; 103pp; English.
XX
The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 2 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 975 TGCAGCAGCAGCAGCAG 991
DB 17 TGCTCCAGCAGCAGCAG 1
RESULT 487
ABZ61649/C
ID ABZ61649 standard; RNA; 17 BP.
XX
AC ABZ61649;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human H-Ras DNazyme target #440.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
FN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 58; Page 119; 185pp; English.
PS
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic

CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 6 A; 4 C; 2 G; 0 T; 5 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 237 TCMAAAGAAATTCGTGTT 253
DB 17 TCMAAAGAACTTGGTGTT 1
RESULT 488
ACDS1476/C
ID ACDS1476 standard; RNA; 17 BP.
XX
AC ACDS1476;
XX
DT 23-SEP-2003 (first entry)
XX
DE HBV hammerhead ribozyme substrate sequence #585.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis B virus.
XX
FN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEEF/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Example 1; Page 147; 387pp; English.
PS

XX The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberszymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HBV
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberszyme sequences
 CC disclosed in the present invention
 XX
 SQ Sequence 17 BP; 6 A; 2 C; 2 G; 0 T; 7 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1154 GTAATGGCTAACTACAT 1170
 DB 17 GTAATGATTAATACAT 1
 ||||| |||||
 ||||| |||||
 17 GTAATGATTAATACAT 1
 RESULT 489
 ACID61082/c
 ID ACID61082 standard; RNA; 17 BP.
 XX
 AC ACID61082;
 XX
 DT 24-SEP-2003 (first entry)
 XX
 DE HCV DNazyme substrate sequence #2156.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberszyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 XX 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.
 PR 05-DEC-2001; 2001US-0337055P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MACE/) MACEJAK D.
 PA (MCSW/) MCSWIGGEN J.
 PA (MORR/) MORRISSEY D.
 PA (PAVC/) PAVCO P.
 PA (LEEF/) LEE P.
 PA (DRAP/) DRAPER K.
 PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX
 DR WPI; 2003-229207/22.
 XX
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX
 PS Claim 1; Page 272; 387pp; English.
 XX
 CC The present invention relates to nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
 CC inozymes, zinzymes, amberszymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNazyme or minus strand DNazyme sequences disclosed in the present
 CC invention
 XX
 SQ Sequence 17 BP; 4 A; 2 C; 6 G; 0 T; 5 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 693 CCTCCTTACCCTGGAG 709
 DB 17 CATCCTTACCCTAGAG 1
 ||||| |||||
 ||||| |||||
 17 CATCCTTACCCTAGAG 1
 RESULT 490
 ACID54845/c
 ID ACID54845 standard; RNA; 17 BP.
 XX
 AC ACID54845;
 XX
 DT 24-SEP-2003 (first entry)
 XX
 DE HBV DNazyme substrate sequence #149.
 XX
 KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
 KW amberszyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200281494-A1.
 XX
 PD 17-OCT-2002.
 XX
 XX 26-MAR-2002; 2002WO-US009187.
 XX
 PR 26-MAR-2001; 2001US-00817879.
 PR 08-JUN-2001; 2001US-00877478.
 PR 08-JUN-2001; 2001US-0296876P.
 PR 24-OCT-2001; 2001US-0335059P.

PR	05-DEC-2001; 2001US-0337055P.
XX	(RIBO-) RIBOZYME PHARM INC.
PPA	(BLAT/) BLATT L.
PPA	(MACE/) MACEJAK D.
PPA	(MCSW/) MCSWIGGEN J.
PPA	(MORR/) MORRISSEY D.
PPA	(PAVC/) PAVCO P.
PPA	(LEEP/) LEE P.
PPA	(DRAP/) DRAPER K.
PPA	(ROBE/) ROBERTS E.
XX	
PPI	Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PPI	Draper K, Roberts E;
XX	WPI; 2003-229207/22.
XX	
PPT	Novel compound useful for treating cirrhosis, liver failure,
PPT	Hepatocellular carcinoma, or condition associated with hepatitis C virus
PT	infection.
XX	
PS	Example 1; Page 189; 387pp; English.
XX	
CC	The present invention relates to nucleic acid molecules which modulate
CC	the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC	Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC	and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC	inozymes, zinyzmes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC	are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC	transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC	as oligonucleotides that specifically bind the Enhancer I region of HBV
CC	DNA. The nucleic acids may be used to modulate the expression of HBV
CC	genes and HBV viral replication. Also disclosed is a method for screening
CC	compounds and/or potential therapies directed against HBV, and compounds
CC	that modulate the expression and/or replication of HCV. The compounds and
CC	methods of the invention are useful for the treatment of degenerative and
CC	disease states related to HBV and HCV infection, replication and gene
CC	expression such as cirrhosis, liver failure, and hepatocellular
CC	carcinoma. The present sequence represents a substrate for one of the HBV
CC	ribozyme, inozyme, G-cleaver, zinyzyme, DNazyme or amberzyme sequences
CC	disclosed in the present invention
XX	
SQ	Sequence 17 BP; 5 A; 2 C; 2 G; 0 T; 8 U; 0 Other;
	Query Match 0.4%; Score 13.8; DB 1; Length 17;
	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY	1153 AGTAATGGCTAACTACA 1169
Db	17 AGTAATGATTAACACTACA 1
RESULT	491
ACC73351	
ID	ACC73351 standard; DNA; 17 BP.
XX	
AC	ACC73351;
XX	
DT	15-JUL-2003 (first entry)
XX	
DE	Mycobacterium gastrii specific probe GAS-01.
XX	
KW	Microarray; probe; Mycobacterium; antibiotic-resistance; genotyping; ss.
XX	
OS	Mycobacterium gastrii.
XX	
FN	WO2003031654-A1.
XX	
PD	17-APR-2003.
PF	
XX	09-OCT-2002; 2002WO-KR001885.
XX	

CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 7 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3013 TTTATTGAAGACAGAC 3029
 DB 17 TTTATTGAAGTCAGATC 1

RESULT 493
 ACC65076
 ID ACC65076 standard; DNA; 17 BP.
 XX
 AC ACC65076;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2323.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 302; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 6 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2756 GGTCTGAATCTCAGACC 2772
 DB 1 GATCTGAATCTCAGAAC 17

RESULT 494
 ACC65169
 ID ACC65169 standard; DNA; 17 BP.
 XX
 AC ACC65169;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2416.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 313; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 8 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1982 GATCAGATAAACCGACA 1998
 DB 1 GATCAGATAAACCATCA 17

RESULT 495
 ACC65958/C
 ID ACC65958 standard; DNA; 17 BP.
 XX
 AC ACC65958;
 XX

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DT 01-JUL-2003 (first entry)
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 3205.
DE
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
XX
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004210.
XX
XX 17-SEP-2001; 2001FR-00011979.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX
XX Disclosure; Page 405; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC6806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 1 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1222 GCAGAGCCCTCAGGATC 1238
Db 17 GGAAAGCCCCCAGGATC 1

RESULT 496
ACC68010
ID ACC68010 standard; DNA; 17 BP.
XX
XX ACC68010;
AC
XX
XX 01-JUL-2003 (first entry)
XX
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 5257.
DE
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
XX
XX 27-MAR-2003.
PD

```

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XX 17-SEP-2002; 2002WO-IB004210.
PP
XX
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT
XX
XX Disclosure; Page 645; 738pp; French.
PS
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC6806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 6 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1909 GATCATGGAGCAGAAAC 1925
Db 1 GATCATGGAGCAGAAAC 17

RESULT 497
ACC65917/c
ID ACC65917 standard; DNA; 17 BP.
XX
XX ACC65917;
AC
XX
XX 01-JUL-2003 (first entry)
XX
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 3164.
DE
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
XX
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004210.
XX
XX 17-SEP-2001; 2001FR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PT

```

XX Disclosure; Page 400; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-ACC68806), which are associated with tumour suppression, tumour CC reversal, apoptosis and virus resistance. The oligonucleotides are CC useful as (1) as probes and primers for detecting, identifying, CC quantifying and/or amplifying nucleic acid, e.g. as one component of a CC gene chip; in vitro as (anti)sense reagents; and (2) for production of CC recombinant polypeptides. The oligonucleotides are useful for preparation CC of pharmaceuticals for prevention and/or treatment of viral diseases that CC are characterised by development of tumours or cell degeneration, CC specifically cancer but also Alzheimer's disease and schizophrenia.

XX Sequence 17 BP; 2 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 998 CAGCCTACCACTGTC 1014
Db 17 CAGCCAACCACTGATC 1

RESULT 498
ADAL5895
ID ADAL5895 standard; DNA; 17 BP.
AC ADAL5895;
XX
XX 20-NOV-2003 (first entry)
XX
XX Primer for amplification of GAPDH DNA #SEQ ID 74.
XX Human; beta-actin; GAPDH; loop-mediated isothermal amplification; LAMP;
KW Glyceraldehyde-3-phosphate dehydrogenase; cancer; metastasis;
KW genetic engineering; PCR; primer; ss.
XX Homo sapiens.
OS
XX WO2003070935-A1.
PN
XX 28-AUG-2003.
PD
XX 13-FEB-2003; 2003WO-JP001474.
PF
XX 20-FEB-2002; 2002JP-00043866.
PR
XX 20-FEB-2002; 2002JP-00043867.
XX (SYSM-) SYSMEX CORP.
PA
XX Tada S;
PI
XX WPI; 2003-679880/64.
DR
XX Primers for nucleic acid amplification in detecting housekeeping gene
PT mRNAs to confirm amplification of beta-actin and glyceraldehyde-3-
PT phosphate dehydrogenase useful in diagnosis of cancer.
XX Claim 5; Page 26; 90pp; Japanese.

XX The invention relates to primers for nucleic acid amplification for
CC detecting a housekeeping gene and/or a housekeeping gene-related mRNA by
CC the Loop-mediated isothermal amplification (LAMP) method. Particularly
CC referred to are primers for the amplification of beta-actin or GAPDH. The
CC primers of the invention are for nucleic acid amplification in detecting
CC housekeeping gene mRNAs, e.g. to confirm amplification of beta-actin and
CC glyceraldehyde-3-phosphate dehydrogenase (GAPDH), which are useful in
CC diagnosis of cancer and metastasis. By applying such primers, the
CC amplification of beta-actin and GAPDH can be used to confirm the presence
CC or absence of a tumour marker, e.g. cytokeratin, which can be used in the
CC control of data correction in the LAMP method, particularly in genetic

CC engineering, molecular biology and clinical medicine including disease
CC diagnosis. Using this method, diagnosis is fast (within 15 minutes) and
CC highly reliable. The required primers were designed based upon the gene
CC domain of e.g. beta-actin. After reaction by the reverse transcriptase-
CC loop-mediated isothermal amplification (RT-LAMP) method, the
CC amplification product was detected to confirm amplification of beta-actin
CC in the samples. The current sequence represents a primer for the
CC amplification of human GAPDH.

XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 793 CCCGCGATTCTCCATGG 809
Db 1 CCCAGCCTCTCCATGG 17

RESULT 499
ADB43213
ID ADB43213 standard; DNA; 17 BP.
XX
AC ADB43213;
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
XX Tumour suppression/reversion associated nucleotide #3536.
DE
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX WO2003040369-A2.
PN
XX 15-MAY-2003.
PD
XX 17-SEP-2002; 2002WO-IB004219.
PF
XX 17-SEP-2001; 2001FR-00011981.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-441574/41.
DR
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
XX Disclosure; Page 445; 771pp; French.

XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2966 GATAACATGGGCCCTGC 2982
DB 1 GATCACTTGGGCCCTGC 17
RESULT 500
ADB41766
ID ADB41766 standard; DNA; 17 BP.
XX
AC ADB41766;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #2089.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 276; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.

CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX Sequence 17 BP; 7 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1909 GATCATGGAGAGAAAC 1925
DB 1 GATCATGGAGATGAAC 17
RESULT 501
ADB40208/C
ID ADB40208 standard; DNA; 17 BP.
XX
AC ADB40208;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #531.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 94; 771pp; French.
XX
CC The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.

SQ Sequence 17 BP; 6 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2756 GGTCTGAATCTCAGACC 2772
 DB 17 GTTCTGAATCTCAGATC 1

RESULT 502
 ADB41665/c
 ID ADB41665 standard; DNA; 17 BP.
 XX AC ADB41665;
 XX DT 18-DEC-2003 (revised)
 XX DT 04-DEC-2003 (first entry)
 XX DE Tumour suppression/reversion associated nucleotide #1988.
 XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX OS Homo sapiens.
 XX PN WO2003040369-A2.
 XX PD 15-MAY-2003.
 XX PF 17-SEP-2002; 2002WO-IB004219.
 XX PR 17-SEP-2001; 2001PR-00011981.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX DR WPI; 2003-441574/41.
 XX PT New nucleic acid encoding human prostate membrane-specific antigen,
 XX useful e.g. for treatment of tumors and viral infection, also related
 XX polypeptide and antibodies.
 XX PS Disclosure; Page 264; 771pp; French.
 XX CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX SQ Sequence 17 BP; 3 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

SQ Sequence 17 BP; 6 A; 1 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 503
 ADB43678/c
 ID ADB43678 standard; DNA; 17 BP.
 XX AC ADB43678;
 XX DT 18-DEC-2003 (revised)
 XX DT 04-DEC-2003 (first entry)
 XX DE Tumour suppression/reversion associated nucleotide #4001.
 XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX OS Homo sapiens.
 XX PN WO2003040369-A2.
 XX PD 15-MAY-2003.
 XX PF 17-SEP-2002; 2002WO-IB004219.
 XX PR 17-SEP-2001; 2001PR-00011981.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX DR WPI; 2003-441574/41.
 XX PT New nucleic acid encoding human prostate membrane-specific antigen,
 XX useful e.g. for treatment of tumors and viral infection, also related
 XX polypeptide and antibodies.
 XX PS Disclosure; Page 499; 771pp; French.
 XX CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX SQ Sequence 17 BP; 6 A; 1 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 3486 AACTCCTTAATTGCTC 3502
DB 17 AACTCCTTAATATGATC 1

RESULT 504
ADB42015
ID ADB42015 standard; DNA; 17 BP.
XX
AC ADB42015;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #2338.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
XX
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX
XX Disclosure; Page 305; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
XX
XX Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 536 GATCCTGAGCTGCAGGA 552
DB 1 GATCCTGAGCTGCCGAA 17
```

```
RESULT 505
ADC70444/C
ID ADC70444 standard; DNA; 17 BP.
XX
XX ADC70444;
XX
XX 18-DEC-2003 (first entry)
XX
DE Tn3O-T PCR primer used to amplify target sequences of known mutants.
XX
XX Tn3O-T; PCR; primer; ss; transposon; mutant; parallel screening;
XX microbial; medical; industrial; agricultural; plate screen.
XX
XX Unidentified.
XX
XX US6528257-B1.
XX
XX 04-MAR-2003.
XX
XX 07-JUL-2000; 2000US-00612555.
XX
XX 07-JUL-2000; 2000US-00612555.
XX
XX (COUL ) COUNCIL SCI & IND RES.
XX
XX Sharma VM, Ganesan K;
XX WPI; 2003-695435/66.
XX
XX Simultaneously monitoring of the abundance of individual mutants of a
XX microbe in mixed populations, comprises generating a population of
XX mutants of a microbe having a genome by the random insertion of a known
XX transposon in the genome.
XX
XX Example 4; SEQ ID NO 13; 10pp; English.
XX
XX This invention relates to an improved and efficient method for
XX simultaneous monitoring of the abundance of individual mutants of a
XX microbe in mixed populations. Specifically, it comprises the random
XX insertion of a known transposon into the genome and quantitatively
XX tracing the abundance of identified mutants to follow their fitness under
XX various environmental conditions. The present invention describes a
XX method useful for parallel screening of large number of mutated genes and
XX for discovering the functions of microbial genes that have medical,
XX industrial and/ or agricultural importance. This improved method is
XX easier and faster, and furthermore is able to detect subtle differences
XX in phenotype to allow the isolation of mutants without a plate screen.
XX This oligonucleotide sequence is the PCR primer Tn3O-T used to amplify
XX the target sequences of known mutants in an exemplification of the
XX invention.
XX
XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2753 AGGGGCTCTGAATCTCAG 2769
DB 17 AGGGGCTCTGACGCTCAG 1

RESULT 506
ADC38460
ID ADC38460 standard; DNA; 17 BP.
XX
XX ADC38460;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human AMLP1b scanning 17-mer oligonucleotide SEQ ID NO:809.
XX
XX
```

XX human; angiominotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1b; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX WO2003037931-A2.
 PN
 XX 08-MAY-2003.
 PD
 XX
 XX 01-NOV-2002; 2002WO-US035129.
 PF
 XX
 XX 01-NOV-2001; 2001US-0334773P.
 PR
 XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 PA
 XX Shannon M, Phan T;
 PI
 XX WPI; 2003-430501/40.
 DR
 XX New isolated nucleic acid molecule encoding a human angiominotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 XX Example 2; SEQ ID NO 809; 172pp; English.
 PS
 XX The present invention describes the human angiominotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1b, which is used in an example from the
 CC present invention.
 XX
 XX . Sequence 17 BP; 7 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 150 GTTCTTGAAGAAAA 166
 DB 1 GTTCTTGAAGAAAA 17

RESULT 507
 ADB44767
 ID ADB44767 standard; DNA; 17 BP.
 XX
 AC ADB44767;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #5090.
 XX
 KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 XX 17-SEP-2002; 2002WO-IB004219.
 PF
 XX 17-SEP-2001; 2001FR-00011981.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA

XX Telerman A, Amson R, Tuijnder M;
 PI WPI; 2003-441574/41.
 XX
 XX New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX
 XX Disclosure; Page 627; 771pp; French.
 PS
 XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 GATCGCGCTGCACAAATC 71
 DB 1 GATCGCTGCACAAACC 17

RESULT 508
 ADB45671
 ID ADB45671 standard; DNA; 17 BP.
 XX
 AC ADB45671;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #5994.
 XX
 KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 XX 17-SEP-2002; 2002WO-IB004219.
 PF
 XX 17-SEP-2001; 2001FR-00011981.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA
 XX Telerman A, Amson R, Tuijnder M;
 PI WPI; 2003-441574/41.
 XX

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XX  New nucleic acid encoding human prostate membrane-specific antigen.
PT  useful e.g. for treatment of tumors and viral infection, also related
PT  polypeptide and antibodies.
XX
XX  Disclosure; Page 732; 771pp; French.
XX
CC  The invention relates to the isolation of 6327 nucleotide sequences,
CC  fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC  sequence having at least 80% identity, after optimal alignment, with the
CC  nucleotides, a sequence that hybridizes under stringent conditions with
CC  the nucleotides, or the complement, or corresponding RNA, of the
CC  nucleotides. The nucleotides are used as probes or primers for detecting,
CC  identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC  sense and antisense sequences, of nucleotides involved in tumour
CC  suppression or reversion, apoptosis and or viral resistance, to produce
CC  recombinant polypeptides, and to prepare transgenic animals, as
CC  experimental models. The nucleotides (also vectors containing them and
CC  cells containing the vectors), the encoded polypeptides and antibodies
CC  (Ab) against the polypeptide are useful for prevention and/or treatment
CC  of viral infections or diseases characterized by development of tumours
CC  or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC  Analysis of the expression of the nucleotides can be used for diagnosis
CC  and/or prognosis of these diseases. The nucleotides and polypeptides can
CC  also be used to screen for their specific interactive molecules,
CC  potentially useful for treating diseases associated with abnormal
CC  expression of the nucleotides.
XX
SQ  Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
      Query Match      0.4%; Score 13.8; DB 1; Length 17;
      Best Local Similarity 88.2%; Pred. No. 2.5e+02;
      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2898 GTTCCAGGGCCTTTCAA 2914
Db  1 GATCCAGGGCCTTTCAA 17

RESULT 509
ADB45324/C
ID  ADB45324 standard; DNA; 17 BP.
XX
AC  ADB45324;
XX
DT  18-DEC-2003 (first entry)
XX
DE  Tumour suppression/reversion associated nucleotide #5647.
XX
KW  cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW  primer; probe; tumour suppression; tumour reversion; apoptosis;
KW  virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW  diagnosis.
XX
OS  Homo sapiens.
XX
PN  WO2003040369-A2.
XX
PD  15-MAY-2003.
XX
PF  17-SEP-2002; 2002WO-IB004219.
XX
PR  17-SEP-2001; 2001PR-00011981.
XX
PA  (MOLE-) MOLECULAR ENGINES LAB.
XX
PI  Telerman A, Amson R, Tuijnder M;
XX  WPI; 2003-441574/41.
XX
PT  New nucleic acid encoding human prostate membrane-specific antigen,
PT  useful e.g. for treatment of tumors and viral infection, also related
PT  polypeptide and antibodies.
XX
XX  Disclosure; Page 712; 771pp; French.
XX
CC  The invention relates to the isolation of 6327 nucleotide sequences,

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XX  Disclosure; Page 692; 771pp; French.
XX
CC  The invention relates to the isolation of 6327 nucleotide sequences,
CC  fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC  sequence having at least 80% identity, after optimal alignment, with the
CC  nucleotides, a sequence that hybridizes under stringent conditions with
CC  the nucleotides, or the complement, or corresponding RNA, of the
CC  nucleotides. The nucleotides are used as probes or primers for detecting,
CC  identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC  sense and antisense sequences, of nucleotides involved in tumour
CC  suppression or reversion, apoptosis and or viral resistance, to produce
CC  recombinant polypeptides, and to prepare transgenic animals, as
CC  experimental models. The nucleotides (also vectors containing them and
CC  cells containing the vectors), the encoded polypeptides and antibodies
CC  (Ab) against the polypeptide are useful for prevention and/or treatment
CC  of viral infections or diseases characterized by development of tumours
CC  or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC  Analysis of the expression of the nucleotides can be used for diagnosis
CC  and/or prognosis of these diseases. The nucleotides and polypeptides can
CC  also be used to screen for their specific interactive molecules,
CC  potentially useful for treating diseases associated with abnormal
CC  expression of the nucleotides.
XX
SQ  Sequence 17 BP; 5 A; 1 C; 5 G; 6 T; 0 U; 0 Other;
      Query Match      0.4%; Score 13.8; DB 1; Length 17;
      Best Local Similarity 88.2%; Pred. No. 2.5e+02;
      Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3335 ATTTATCCAAACAGAAC 3351
Db  17 ATTTCTCCAAACAGATC 1

RESULT 510
ADB45499/C
ID  ADB45499 standard; DNA; 17 BP.
XX
AC  ADB45499;
XX
DT  18-DEC-2003 (first entry)
XX
DE  Tumour suppression/reversion associated nucleotide #5822.
XX
KW  cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW  primer; probe; tumour suppression; tumour reversion; apoptosis;
KW  virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW  diagnosis.
XX
OS  Homo sapiens.
XX
PN  WO2003040369-A2.
XX
PD  15-MAY-2003.
XX
PF  17-SEP-2002; 2002WO-IB004219.
XX
PR  17-SEP-2001; 2001PR-00011981.
XX
PA  (MOLE-) MOLECULAR ENGINES LAB.
XX
PI  Telerman A, Amson R, Tuijnder M;
XX  WPI; 2003-441574/41.
XX
PT  New nucleic acid encoding human prostate membrane-specific antigen,
PT  useful e.g. for treatment of tumors and viral infection, also related
PT  polypeptide and antibodies.
XX
XX  Disclosure; Page 712; 771pp; French.
XX
CC  The invention relates to the isolation of 6327 nucleotide sequences,

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CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules.
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

XX
 SQ Sequence 17 BP; 1 A; 4 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1918 GCAGAAACAGCAACTTC 1934
 |||||
 Db 17 GCAGAAACAGCAAGATC 1

RESULT 511
 ADD69451
 ID ADD69451 standard; DNA; 17 BP.
 AC ADD69451;
 XX
 DT 15-JAN-2004 (first entry)
 DE 5' anchored (ISSR)-PCR primer - SEQ ID 9.
 XX
 KW inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
 KW animal; Basmati rice; ss.
 XX
 OS Synthetic.
 XX
 PN WO2003085133-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 09-JAN-2003; 2003WO-IB0000041.
 XX
 PR 08-APR-2002; 2002IN-CH000260.
 XX
 PA (DNAF-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
 XX
 PI Nagaraju JG;
 XX
 DR WPI; 2003-804317/75.
 XX
 PT New set of inter-simple sequence repeats (ISSR)-PCR primers for
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
 PT animal systems.
 XX
 PS Claim 1; SEQ ID NO 9; 60pp; English.
 XX
 CC The invention relates to a novel set of inter-simple sequence repeats
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
 CC invention may be useful for genotyping diverse genomes of plant and
 CC animal systems, in particular for distinguishing Basmati rice varieties
 CC from non-Basmati rice varieties and traditional Basmati rice varieties
 CC from evolved Basmati rice varieties. The current sequence is that of the
 CC 5' anchored (ISSR)-PCR primer of the invention.

XX
 SQ Sequence 17 BP; 8 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1554 AACCAACAGCAGCAGCAG 1570
 |||||
 Db 1 AAATACAGCAGCAGCAG 17
 RESULT 512
 ADD44223/c
 ID ADD44223 standard; DNA; 17 BP.
 XX
 AC ADD44223;
 XX
 DT 15-JAN-2004 (first entry)
 DE Carboxypeptidase G2 (CPG2) enzyme mutagenic oligonucleotide OL588.
 XX
 KW bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;
 KW immunogenic; T-cell epitope; MHC class II binding ligand;
 KW immunostimulant; enzyme therapy; immune response;
 KW gene directed enzyme produg strategy; vaccine; enzyme; EC 3.4.17.11;
 KW mutagenic; ss.
 XX
 OS Synthetic.
 OS Pseudomonas sp. RS-16.
 XX
 PN WO2003045426-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 27-NOV-2002; 2002WO-EP013351.
 XX
 PR 29-NOV-2001; 2001EP-00128519.
 PR 25-JAN-2002; 2002EP-00001778.
 PR 13-SEP-2002; 2002EP-00020634.
 XX
 PA (MERE) MERCK PATENT GMBH.
 XX
 PI Heilendoorn K, Baker M, Williams S, Carr FJ;
 DR WPI; 2003-513617/48.
 XX
 PT New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
 PT substantially non-immunogenic or less immunogenic than any non-modified
 PT CPG2, useful for inducing an immune response in a human host.
 XX
 PS Example 4; Page 37; 52pp; English.
 XX
 CC The invention relates to a novel modified bacterial enzyme
 CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
 CC proteins that are substantially non-immunogenic or less immunogenic than
 CC any non-modified CPG2 having essentially the same biological specificity
 CC when used in vivo, and comprising specific amino acid residues having
 CC alterations compared with the non-modified parochial enzyme. The
 CC alterations cause a reduction or an elimination of one or more of T-cell
 CC epitope sequences, which act in the parental enzyme as MHC class II
 CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
 CC CPG2 proteins have immunostimulant activity and may be used in enzyme
 CC therapy. The modified CPG2 enzyme may be used to induce an immune
 CC response in a human host, or as a therapeutic entity such as the gene
 CC directed enzyme produg strategy. The peptide is useful for the
 CC manufacture of a modified CPG2 enzyme having substantially no or less
 CC immunogenicity than any non-modified parental enzyme when used in vivo,
 CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
 CC This polynucleotide sequence represents a mutagenic oligonucleotide used
 CC in the production of a modified CPG2 gene of the invention.
 XX
 SQ Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match		0.4%;	Score 13.8;	DB 1;	Length 17;										
Best Local Similarity		88.2%;	Pred. No. 2.5e+02;												
Matches 15;		Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;									
QY	3590	TTGTTTGGAGTAACCAA	3606												
DB	1	TTCTTTGGAGTAAGCAA	17												
RESULT 513															
ID	ADD44239	standard; DNA; 17 BP.													
XX	AC														
XX	ADD44239;														
XX	15-JAN-2004	(first entry)													
XX	Carboxypeptidase G2 (CPG2)	enzyme mutagenic oligonucleotide OL604.													
XX	bacterial enzyme;	carboxypeptidase G2; CPG2; non-immunogenic;													
KW	immunogenic;	T-cell epitope; MHC class II binding ligand;													
KW	immunostimulant;	enzyme therapy; immune response;													
KW	gene directed enzyme prod	rug strategy; vaccine; enzyme; EC 3.4.17.11;													
KW	mutagenic; ss.														
XX	Synthetic.														
OS	Pseudomonas sp.	RS-16.													
XX	WO2003045426-A1.														
XX	05-JUN-2003.														
XX	27-NOV-2002;	2002WO-EP013351.													
XX	29-NOV-2001;	2001EP-00128519.													
PR	25-JAN-2002;	2002EP-00001778.													
PR	13-SEP-2002;	2002EP-00020634.													
XX	(MERE)	MERCK PATENT GMBH.													
PA	Hellendoorn K, Baker M, Williams S, Carr FJ;														
PI	WPI;	2003-513617/48.													
XX	New modified bacterial enzyme carboxypeptidase G2 (CPG2) having	substantially non-immunogenic or less immunogenic than any non-modified CPG2, useful for inducing an immune response in a human host.													
XX	Example 4; Page 38; 52pp; English.														
PS	The invention relates to a novel modified bacterial enzyme	carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2 proteins that are substantially non-immunogenic or less immunogenic than any non-modified CPG2 having essentially the same biological specificity when used in vivo, and comprising specific amino acid residues having alterations compared with the non-modified parochial enzyme. The alterations cause a reduction or an elimination of one or more of T-cell epitope sequences, which act in the parental enzyme as MHC class II binding ligands and stimulate T-cells. The modified CPG2 enzyme and the CPG2 proteins have immunostimulant activity and may be used in enzyme therapy. The modified CPG2 enzyme may be used to induce an immune response in a human host, or as a therapeutic entity such as the gene directed enzyme prodrg strategy. The peptide is useful for the manufacture of a modified CPG2 enzyme having substantially no or less immunogenicity than any non-modified parental enzyme when used in vivo, and for vaccination of patients to reduce immunogenicity to CPG2 in vivo. This polynucleotide sequence represents a mutagenic oligonucleotide used in the production of a modified CPG2 gene of the invention.													
XX	Sequence 17 BP; 5 A; 2 C; 4 G; 6 T; 0 U; 0 Other;														
Query Match		0.4%;	Score 13.8;					DB 1;	Length 17;						
Best Local Similarity		88.2%;	Pred. No. 2.5e+02;												
Matches 15;		Conservative	0;					Mismatches 2;	Indels 0;	Gaps 0;					
QY	3590	TTGTTTGGAGTAACCAA	3606												
DB	1	TTCTTTGGAGTAAGCAA	17												
RESULT 514															
ID	ADF64073	standard; DNA; 17 BP.													
XX	AC														
XX	ADF64073;														
XX	12-FEB-2004	(first entry)													
XX	Human PCCP1	DNA fragment SEQ ID 8-directed probe - SEQ ID 1977.													
DE	chromatin organisation modifier;	CHROMO domain; cytostatic; PCCP1;													
KW	prostate cancer candidate protein 1;	tumour; gene therapy; vaccine;													
KW	human; ss; probe.														
XX	Homo sapiens.														
OS	WO2003050284-A1.														
XX	19-JUN-2003.														
XX	22-NOV-2002;	2002WO-US037506.													
PF	10-DEC-2001;	2001US-0339764P.													
XX	(AMSH)	AMERSHAM BIOSCIENCES SV CORP.													
PA	Guo J;														
PI	WPI;	2003-532916/50.													
XX	New prostate cancer candidate protein 1 (PCCP1),	useful for preparing a composition for treating or preventing a disorder associated with decreased or increased expression or activity of PCCP1 e.g., tumor.													
XX	Example 2; SEQ ID NO 1977; 164pp; English.														
PS	The invention relates to a novel isolated nucleic acid that encodes a protein with a chromatin organisation modifier (CHROMO) domain. The polynucleotide of the invention demonstrates cytostatic activity and may be useful for preparing a composition for treating or preventing a disorder associated with decreased or increased expression or activity of PCCP1, such as a tumour, as well as during gene therapy and vaccine production procedures. The current sequence is that of the human PCCP1-related DNA fragment SEQ ID 8-directed probe of the invention. Note: The current sequence is not shown within the specification per se but was retrieved from the Wipoweb database.														
XX	Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 U; 0 Other;														
Query Match		0.4%;	Score 13.8;	DB 1;	Length 17;										
Best Local Similarity		88.2%;	Pred. No. 2.5e+02;												
Matches 15;		Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;									
QY	1772	GTGCTAGGCGCAGAACAC	1788												
DB	17	GTGCTAGGCGCAGAACAC	1												
RESULT 515															
ID	ADI43470	standard; DNA; 17 BP.													
XX	AC														
XX	ADI43470;														

XX 17-SEP-2001; 2001FR-00011980.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX
 XX Disclosure; SEQ ID NO 4307; 30pp; French.
 XX
 XX This invention relates to novel isolated nucleic acid sequences involved
 XX in the phenomena of tumour suppression, tumour reversion, apoptosis
 XX and/or resistance to viruses. The invention may be useful for the
 XX development of compounds with a cytostatic, virucide, neuroprotective,
 XX neurotropic or neuroleptic activity. The DNA sequences may be useful as
 XX probes and primers for detecting, identifying, quantifying and/or
 XX amplifying nucleic acid, for example as one component of a gene chip, in
 XX vitro as antisense reagents and for production of recombinant
 XX polypeptides. The invention may therefore be useful for preparation of
 XX pharmaceuticals for prevention and/or treatment of viral diseases that
 XX are characterised by development of tumours or cell degeneration. The
 XX specifically cancer but also Alzheimer's disease and schizophrenia. The
 XX present sequence is that of a nucleic acid sequence of the invention.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/publishedpct_sequences
 XX
 XX Sequence 17 BP; 3 A; 7 C; 2 G; 5 T; 0 U; 0 Other;
 XX
 XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
 XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 1662 GGTCACTTTCACGAA 1703
 XX | | | | | | | | | | | | | | | | | |
 XX DB 1 GATCCTACTTCAGAAA 17
 XX
 XX RESULT 518
 XX ADI49729
 XX ID ADI49729 standard; DNA; 17 BP.
 XX AC ADI49729;
 XX DT 15-APR-2004 (first entry)
 XX DE Human tumour suppression/reversion-related DNA sequence SeqID2232.
 XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 XX cytosatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 XX primer; PCR; gene chip; antisense; viral disease; tumour;
 XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX OS Homo sapiens.
 XX PN WO2003025177-A2.
 XX PD 27-MAR-2003.
 XX PF 17-SEP-2002; 2002WO-IB004523.
 XX PR 17-SEP-2001; 2001FR-00011980.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX
 XX Disclosure; SEQ ID NO 1893; 30pp; French.
 XX
 XX This invention relates to novel isolated nucleic acid sequences involved

XX 17-SEP-2001; 2001FR-00011980.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX
 XX Disclosure; SEQ ID NO 4307; 30pp; French.
 XX
 XX This invention relates to novel isolated nucleic acid sequences involved
 XX in the phenomena of tumour suppression, tumour reversion, apoptosis
 XX and/or resistance to viruses. The invention may be useful for the
 XX development of compounds with a cytostatic, virucide, neuroprotective,
 XX neurotropic or neuroleptic activity. The DNA sequences may be useful as
 XX probes and primers for detecting, identifying, quantifying and/or
 XX amplifying nucleic acid, for example as one component of a gene chip, in
 XX vitro as antisense reagents and for production of recombinant
 XX polypeptides. The invention may therefore be useful for preparation of
 XX pharmaceuticals for prevention and/or treatment of viral diseases that
 XX are characterised by development of tumours or cell degeneration. The
 XX specifically cancer but also Alzheimer's disease and schizophrenia. The
 XX present sequence is that of a nucleic acid sequence of the invention.
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/publishedpct_sequences
 XX
 XX Sequence 17 BP; 7 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
 XX
 XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
 XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX QY 1687 GCTCCTACTTCAGAAA 1703
 XX | | | | | | | | | | | | | | | | | |
 XX DB 1 GATCCTACTTCAGAAA 17
 XX
 XX RESULT 518
 XX ADI49729
 XX ID ADI49729 standard; DNA; 17 BP.
 XX AC ADI49729;
 XX DT 15-APR-2004 (first entry)
 XX DE Human tumour suppression/reversion-related DNA sequence SeqID2232.
 XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 XX cytosatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 XX primer; PCR; gene chip; antisense; viral disease; tumour;
 XX cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX OS Homo sapiens.
 XX PN WO2003025177-A2.
 XX PD 27-MAR-2003.
 XX PF 17-SEP-2002; 2002WO-IB004523.
 XX PR 17-SEP-2001; 2001FR-00011980.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-313354/30.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 XX with tumors and cell degeneration, also related polypeptides, antibodies
 XX and transfected cells.
 XX
 XX Disclosure; SEQ ID NO 1893; 30pp; French.
 XX
 XX This invention relates to novel isolated nucleic acid sequences involved

CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences

XX
 SQ Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1108 GAGCTCCCCCATGCTG 1124
 |||||
 Db 1 GATCTCTCCCATGCTG 17

RESULT 520
 ADI49542
 ID ADI49542 standard; DNA; 17 BP.
 AC ADI49542;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID2045.
 DE
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosolic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004523.
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313354/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 2045; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of

CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences

XX
 SQ Sequence 17 BP; 1 A; 4 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1339 GATGCTTCTGTTTTCG 1355
 |||||
 Db 1 GATCCTTCTGTTTTCG 17

RESULT 521
 ADI49656/c
 ID ADI49656 standard; DNA; 17 BP.
 AC ADI49656;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Human tumour suppression/reversion-related DNA sequence SeqID2159.
 DE
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosolic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025177-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004523.
 XX
 PR 17-SEP-2001; 2001FR-00011980.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313354/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; SEQ ID NO 2159; 30pp; French.
 XX
 CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences

Tue Aug 16 13:09:33 2005

vivlemore-10-698-070-1.rng

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SQ Sequence 17 BP; 6 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
  Query Match      0.4%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 2.5e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3066 ATGAAATCTTGGGGAAC 3082
    ||||| ||||| ||||| |||||
DB 17 ATGATATCTTGGGGATC 1

RESULT 522
ADI49672
ID ADI49672 standard; DNA; 17 BP.
XX AC ADI49672;
XX DT 15-APR-2004 (first entry)
XX DE Human tumour suppression/reversion-related DNA sequence SeqID2175.
XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
XX KW primer; PCR; gene chip; antisense; viral disease; tumour;
XX KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX OS Homo sapiens.
XX PN WO2003025177-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004523.
XX PR 17-SEP-2001; 2001FR-00011980.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-313354/30.
XX KW New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; SEQ ID NO 2175; 30pp; French.
XX CC This invention relates to novel isolated nucleic acid sequences involved
XX CC in the phenomena of tumour suppression, tumour reversion, apoptosis
XX CC and/or resistance to viruses. The invention may be useful for the
XX CC development of compounds with a cytostatic, virucide, neuroprotective,
XX CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
XX CC probes and primers for detecting, identifying, quantifying and/or
XX CC amplifying nucleic acid, for example as one component of a gene chip, in
XX CC vitro as antisense reagents and for production of recombinant
XX CC polypeptides. The invention may therefore be useful for preparation of
XX CC pharmaceuticals for prevention and/or treatment of viral diseases that
XX CC are characterised by development of tumours or cell degeneration,
XX CC specifically cancer but also Alzheimer's disease and schizophrenia. The
XX CC present sequence is that of a nucleic acid sequence of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/publishedpct_sequences
XX SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match      0.4%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 2.5e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2898 GTTCCAGGCGCTTTCAA 2914
    ||||| ||||| ||||| |||||
DB 17 ATGATATCTTGGGGATC 1

RESULT 524
ADI47871/c
ID ADI47871 standard; DNA; 17 BP.
XX AC ADI47871;
XX AC ADI47871;

Db 1 GATCCAGGCGCTTTCAA 17

RESULT 523
ADI52660/c
ID ADI52660 standard; DNA; 17 BP.
XX AC ADI52660;
XX DT 15-APR-2004 (first entry)
XX DE Human tumour suppression/reversion-related DNA sequence SeqID5163.
XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KW cytostatic; virucide; neuroprotective; neurotropic; neuroleptic; probe;
XX KW primer; PCR; gene chip; antisense; viral disease; tumour;
XX KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX OS Homo sapiens.
XX PN WO2003025177-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004523.
XX PR 17-SEP-2001; 2001FR-00011980.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-313354/30.
XX KW New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; SEQ ID NO 5163; 30pp; French.
XX CC This invention relates to novel isolated nucleic acid sequences involved
XX CC in the phenomena of tumour suppression, tumour reversion, apoptosis
XX CC and/or resistance to viruses. The invention may be useful for the
XX CC development of compounds with a cytostatic, virucide, neuroprotective,
XX CC neurotropic or neuroleptic activity. The DNA sequences may be useful as
XX CC probes and primers for detecting, identifying, quantifying and/or
XX CC amplifying nucleic acid, for example as one component of a gene chip, in
XX CC vitro as antisense reagents and for production of recombinant
XX CC polypeptides. The invention may therefore be useful for preparation of
XX CC pharmaceuticals for prevention and/or treatment of viral diseases that
XX CC are characterised by development of tumours or cell degeneration,
XX CC specifically cancer but also Alzheimer's disease and schizophrenia. The
XX CC present sequence is that of a nucleic acid sequence of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/publishedpct_sequences
XX SQ Sequence 17 BP; 1 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

  Query Match      0.4%; Score 13.8; DB 1; Length 17;
  Best Local Similarity 88.2%; Pred. No. 2.5e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1918 GCAGAAACAGCAACTTC 1934
    ||||| ||||| ||||| |||||
DB 17 GCAGAAACAGCAAGATC 1

RESULT 524
ADI47871/c
ID ADI47871 standard; DNA; 17 BP.
XX AC ADI47871;
XX AC ADI47871;
```

XX 15-APR-2004 (first entry)
XX Human tumour suppression/reversion-related DNA sequence SeqID374.
XX
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
DE cytostatic; virucide; neuroprotective; nontropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
XX Homo sapiens.
XX WO2003025177-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002WO-IB004523.
XX
XX 17-SEP-2001; 2001FR-00011980.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313354/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; SEQ ID NO 374; 30pp; French.
XX
XX This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nontropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/publishedpet_sequences
XX
XX Sequence 17 BP; 4 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 523 AGACAACTGATGGATC 539
XX |||||||
Db 17 AGCACAACTGTTGGATC 1
XX
XX RESULT 525
XX ACC54207
XX ID ACC54207 standard; DNA; 17 BP.
XX
XX ACC54207;
XX
XX 27-JUN-2003 (first entry)
XX
XX Human tumour suppressor sequence #2974.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.

XX Homo sapiens.
XX OS
XX PN FR2826373-A1.
XX
XX PD. 27-DEC-2002.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX
XX Tuijnder M, Telerman A, Amson R;
XX WPI; 2003-250498/25.
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.
XX
XX Claim 1; Page 727; 798pp; French.
XX
XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration
XX
XX Sequence 17 BP; 3 A; 2 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 3348 GAACCTGGTGTGCTCAATG 3364
XX |||||||
Db 1 GATCTGTGTGCTCAATG 17
XX
XX RESULT 526
XX ACC51702
XX ID ACC51702 standard; DNA; 17 BP.
XX
XX ACC51702;
XX
XX 27-JUN-2003 (first entry)
XX
XX Human tumour suppressor sequence #469.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
XX Homo sapiens.
XX
XX PN FR2826373-A1.
XX
XX PD. 27-DEC-2002.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX
XX Tuijnder M, Telerman A, Amson R;
XX WPI; 2003-250498/25.
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
PT tumour regression; apoptosis; virus resistance; diagnosis;
XX cellular degeneration.

PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 148; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated
 CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration

XX Sequence 17 BP; 9 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1982 GATCAGATTAACGACA 1998
 ||||| ||||| ||||| |||||
 Db 1 GATCAGAGAACAGACA 17

RESULT 527
 ADL51684/C
 ID ADL51684 standard; RNA; 17 BP.

XX ADL51684;

DT 20-MAY-2004 (first entry)

XX Human PTGDR substrate sequence #803.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PTGDR;
 KW substrate; ds.

XX Unidentified.

XX WO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

XX 29-MAY-2001; 2001US-0294412P.

XX 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite

PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or

PT protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 161; SEQ ID NO 5217; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)

CC that down regulate the expression or inhibit the function of a receptor

CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, glomerulonephritis, sepsis, and allergic
 CC ischaemia/reperfusion injury, allergic rhinitis or atopic dermatitis). The
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.

XX Sequence 17 BP; 1 A; 4 C; 7 G; 0 T; 5 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 977 CAGCAGCACCAGCAGCA 993
 ||||| ||||| ||||| |||||
 Db 17 CATCAGCGCCAGCAGCA 1

RESULT 528

ADL48748/C

ID ADL48748 standard; RNA; 17 BP.

XX ADL48748;

DT 20-MAY-2004 (first entry)

XX Human IKK-gamma substrate sequence #1258.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; Human IKK-gamma;
 KW substrate; ds.

XX Unidentified.

XX WO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

XX 29-MAY-2001; 2001US-0294412P.

XX 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fosnaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite

PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or

PT protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 59; SEQ ID NO 2281; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)

CC that down regulate the expression or inhibit the function of a receptor

CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human IKK-
 CC gamma substrate sequence.

XX
 SQ Sequence 17 BP; 5 A; 5 C; 4 G; 0 T; 3 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2230 TGGAAATCTGCCTTGTA 2246
 ||||| || |||||
 Db 17 TGGAGTCCGCTTGTA 1

RESULT 529
 ADL49592/c
 ID ADL49592 standard; RNA; 17 BP.
 AC ADL49592;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PKR substrate sequence #706.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; human PKR;
 KW substrate; ds.
 XX
 OS Unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fossnaugh K;
 XX
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 59; SEQ ID NO 3125; 317pp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC substrate sequence.

XX
 SQ Sequence 17 BP; 1 A; 4 C; 5 G; 0 T; 7 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 672 GCCAGAGGAGCACACCT 688
 ||||| |||||
 Db 17 GCCAGAGAGGACACCT 1

RESULT 530
 ADL46971/c
 ID ADL46971 standard; RNA; 17 BP.
 AC ADL46971;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human NOGO receptor inozyme substrate sequence #404.
 XX
 KW antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; IkappaB kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis;
 KW NOGO receptor inozyme; substrate; ds.
 XX
 OS Unidentified.
 XX
 PN WO200281628-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010512.
 XX
 PR 05-APR-2001; 2001US-00827395.
 PR 29-MAY-2001; 2001US-0294412P.
 PR 28-AUG-2001; 2001US-0315315P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Chowrira B, Haerberli P, Mcswiggen J, Fossnaugh K;
 XX
 DR WPI; 2003-058513/05.
 XX
 PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, IkappaB kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX
 PS Claim 9; SEQ ID NO 504; 317pp; English.
 XX
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC IkappaB kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
 CC contacting the cell with the novel nucleic acid molecule, an expression
 CC vector comprising a nucleic acid sequence (encoding at least the novel
 CC nucleic acid molecule in a manner that allows its expression), a
 CC mammalian cell including the expression vector and an enzymatic nucleic
 CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
 CC molecule is useful for treating a condition associated with the level of
 CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
 CC a target region for the enzymatic nucleic acids of the invention.

SQ Sequence 17 BP; 4 A; 6 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 70.6%; Pred. No. 2.5e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2508 CACCAACTGGGCTCT 2524
 |||||:|||||:
 Db 1 CAACAGCGGGCCUCU 17

RESULT 533
 ADM54088
 ID ADM54088 standard; mRNA; 17 BP.
 XX
 AC ADM54088;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human GRID mRNA substrate sequence #363.

Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
 NCH ribozyme; G-cleaver ribozyme; Zinzyne; DNazyme; Inozyme;
 hairpin ribozyme; tissue rejection; graft rejection; leukaemia.

OS Homo sapiens.

XX US2003134806-A1.

PN 17-JUL-2003.

XX 23-FEB-2001; 2001US-00792818.

XX 10-FEB-2000; 2000US-0181594P.

(JARV/) JARVIS T.
 (CARL/) CARLOWITZ I V.
 (MCSW/) MCSWIGGEN J.
 (HAMB/) HAMBLIN P A.
 (ELLI/) ELLIS J H.

Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
 WPI; 2003-829646/77.

New nucleic acid molecule that down-regulates expression of Grb2-related
 with insert domain (GRID) gene, useful for treating a condition
 associated with the level of GRID, e.g. tissue/graft rejection and
 leukemia.

Claim 4; SEQ ID NO 363; 74pp; English.

The invention relates to a nucleic acid molecule that down-regulates
 expression of Grb2-related with insert domain (GRID) gene, e.g. a
 hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyne, DNazyme,
 amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
 including the novel nucleic acid molecule, reducing GRID activity in a
 cell by contacting the cell with the novel nucleic acid molecule,
 treating a patient having a condition associated with the level of GRID
 (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
 the novel nucleic acid molecule, cleaving RNA of a GRID gene by
 contacting the cell with the novel nucleic acid molecule, an expression
 vector comprising a nucleic acid sequence (encoding at least the novel

CC nucleic acid molecule in a manner that allows its expression), a
 CC mammalian cell including the expression vector and an enzymatic nucleic
 CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
 CC molecule is useful for treating a condition associated with the level of
 CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
 CC a target region for the enzymatic nucleic acids of the invention.

SQ Sequence 17 BP; 5 A; 9 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 979 GCAGCACCAGCAGCAGC 995
 |||||:|||||:
 Db 1 GCACCACCAGCACCAGC 17

RESULT 534
 ADM54297
 ID ADM54297 standard; mRNA; 17 BP.

XX ADM54297;

AC ADM54297;
 XX
 DT 03-JUN-2004 (first entry)

XX Human GRID mRNA substrate sequence #607.

Human; ss; GRID; Grb2-related with insert domain; hammerhead ribozyme;
 NCH ribozyme; G-cleaver ribozyme; Zinzyne; DNazyme; amberzyme; Inozyme;
 hairpin ribozyme; tissue rejection; graft rejection; leukaemia.

OS Homo sapiens.

XX US2003134806-A1.

PN 17-JUL-2003.

XX 23-FEB-2001; 2001US-00792818.

XX 10-FEB-2000; 2000US-0181594P.

(JARV/) JARVIS T.
 (CARL/) CARLOWITZ I V.
 (MCSW/) MCSWIGGEN J.
 (HAMB/) HAMBLIN P A.
 (ELLI/) ELLIS J H.

Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
 WPI; 2003-829646/77.

New nucleic acid molecule that down-regulates expression of Grb2-related
 with insert domain (GRID) gene, useful for treating a condition
 associated with the level of GRID, e.g. tissue/graft rejection and
 leukemia.

Claim 4; SEQ ID NO 607; 74pp; English.

The invention relates to a nucleic acid molecule that down-regulates
 expression of Grb2-related with insert domain (GRID) gene, e.g. a
 hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyne, DNazyme,
 amberzyme, Inozyme or hairpin ribozyme. Also include are a mammalian cell
 including the novel nucleic acid molecule, reducing GRID activity in a
 cell by contacting the cell with the novel nucleic acid molecule,
 treating a patient having a condition associated with the level of GRID
 (e.g. tissue/graft rejection or leukaemia) by contacting the cell with
 the novel nucleic acid molecule, cleaving RNA of a GRID gene by
 contacting the cell with the novel nucleic acid molecule, an expression
 vector comprising a nucleic acid sequence (encoding at least the novel
 nucleic acid molecule in a manner that allows its expression), a
 mammalian cell including the expression vector and an enzymatic nucleic
 acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid

CC molecule is useful for treating a condition associated with the level of
CC GRID, e.g. tissue/graft rejection and leukaemia. The present sequence is
CC a target region for the enzymatic nucleic acids of the invention.
XX
SQ Sequence 17 BP; 4 A; 9 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 983 CACCAGCAGCAGCACCA 999
Db 1 CCCCUGCAGCAGCACCA 17

RESULT 535
ADM43565
ID ADM43565 standard; cDNA; 17 BP.
XX
AC ADM43565;
XX
DT 03-JUN-2004 (first entry)
XX
DE Signature sequence from human gene suppressed by cholesterol #17.
XX
KW Signature sequence; Human; ss; MPSS;
KW massively parallel signature sequencing; cholesterol homeostasis;
KW atherosclerosis; heart disease.
XX
OS Homo sapiens.
XX
PN US2003170700-A1.
XX
PD 11-SEP-2003.
XX
PF 08-JAN-2003; 2003US-00340192.
XX
PR 09-JAN-2002; 2002US-0347396P.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Shang J, Bowen BA;
XX
WPI; 2003-811493/76.
XX
PT New polypeptides encoded by polynucleotides suppressed or induced by
PT cholesterol useful for treating responses to alterations in cholesterol
PT levels in cells, tissues or organisms e.g. atherosclerosis or heart
PT disease.
XX
PS Claim 1; SEQ ID NO 17; 45pp; English.
XX
CC The invention relates to isolated or recombinant polypeptides encoded by
CC polynucleotides suppressed or induced by cholesterol. The polypeptides
CC comprise at least one sequence encoded by a polynucleotide as follows:
CC having at least 70% identity to one of ADM43549-ADM43636; having sequence
CC complementary/hybridising under stringent conditions to one of the 88
CC sequences; hybridising to a polynucleotide that is physically linked in
CC human genome to a polynucleotide as in (i) or (ii); or comprising at
CC least 10 contiguous nucleotides of one of the 88 sequences or a
CC complementary sequence. The 88 sequences are signature sequences from
CC cDNAs up- or downregulated in response to cholesterol. Also included are
CC polynucleotide compositions comprising at least one expression vector
CC comprising a polynucleotide as above, cells comprising a polynucleotide
CC expression vector as above, labelled probes comprising a polynucleotide
CC as above, an antibody (optionally monoclonal antibody/polyclonal serum)
CC specific for polypeptide, a marker set for evaluating a
CC condition/characteristic associated with altered cholesterol levels and
CC arrays of two or more labelled probes or two or more polypeptides, or
CC comprising marker. The polypeptides can be administered therapeutically
CC to patients to treat responses to alterations of cholesterol levels e.g.
CC atherosclerosis or heart disease. They can be included with a (preferably
CC pharmaceutical) excipient in compositions which can be similarly

CC administered. They can also be used to modulate physiological or
CC pathological responses to alterations in cholesterol levels (especially
CC atherosclerosis or heart disease) in cells (e.g. liver cells), tissues or
CC organisms by modulating polypeptide expression or activity. They are also
CC useful to evaluate conditions/ characteristics associated with
CC alterations in cholesterol levels in subjects e.g. by using marker sets
CC or arrays. Polynucleotide compositions (optionally comprising a
CC pharmaceutical excipient) may be administered therapeutically to treat
CC responses to alterations of cholesterol levels as above. The
CC polynucleotides are also useful to modulate physiological/pathological
CC responses to alterations in cholesterol levels by modulating polypeptide
CC expression/activity as above. They may also be used to detect altered
CC expression/activity of expression product e.g. in response to
CC pharmaceuticals administration or diet. The polynucleotides can also be
CC used to evaluate conditions/characteristic associated with alterations in
CC cholesterol levels (especially elevated levels) as above.
CC Polynucleotides, polynucleotide compositions and probes can be used to
CC identify genes capable of altering physiological/pathological responses
CC to alterations in cholesterol level, especially in response to
CC pharmaceuticals administration or diet. The present sequence is a
CC signature sequence from a gene whose expression is suppressed in response
CC to cholesterol.
XX
SQ Sequence 17 BP; 3 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3348 GAACGTGGTGTGCAATG 3364
Db 1 GATCTGTGTGCAATG 17

RESULT 536
ADK96182
ID ADK96182 standard; DNA; 17 BP.
XX
AC ADK96182;
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer of the invention #1902.
XX
KW human; single nucleotide polymorphism; SNP; ss; primer.
XX
OS Synthetic.
XX
PN JP2003259875-A.
XX
PD 16-SEP-2003.
XX
PF 08-MAR-2002; 2002JP-00064373.
XX
PR 08-MAR-2002; 2002JP-00064373.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2004-093977/10.
XX
PT Novel polynucleotide useful for PCR amplification along with two DNA
PT fragment from another set of sequences, or for detecting single
PT nucleotide polymorphism in human gene.
XX
PS Claim 2; SEQ ID NO 5211; 2627pp; Japanese.
XX
CC The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
XX
SQ Sequence 17 BP; 4 A; 4 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 960 AGCAGCATGCCGGATG 976
|||||
Db 1 AGCAGCATGCTGGAGG 17

RESULT 537
ADM60003/c
ID ADM60003 standard; RNA; 17 BP.
XX
AC ADM60003;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #2137.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW Hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US2004054156-A1.
XX
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX
DR WPI; 2004-247781/23.
XX
PT Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 2137; 122pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 5 A; 2 C; 2 G; 0 T; 8 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1153 AGTAATGCTAACTACA 1169
|||||
Db 17 AGTAATGATTAACTACA 1

RESULT 538
ADM58484/c
ID ADM58484 standard; RNA; 17 BP.
XX
AC ADM58484;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis B virus (HBV) RNA target sequence #618.
XX
KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
KW Hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
KW virucide; hepatotropic; antiinflammatory; cytostatic.
XX
OS Hepatitis B virus.
XX
PN US2004054156-A1.
XX
PD 18-MAR-2004.
XX
PF 15-JAN-2003; 2003US-00342902.
XX
PR 14-MAY-1992; 92US-00882712.
PR 07-FEB-1994; 94US-00193627.
PR 08-NOV-1999; 99US-00436430.
PR 20-MAR-2000; 2000US-00531025.
PR 09-AUG-2000; 2000US-00636385.
PR 24-OCT-2000; 2000US-00696347.
PR 08-JUN-2001; 2001US-00877478.
XX
PA (DRAP/) DRAPER K.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (MORR/) MORRISSEY D.
XX
PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
XX
DR WPI; 2004-247781/23.
XX
PT Novel enzymatic nucleic acid molecule such as DNazymes and inozymes
PT specifically cleaving RNA derived from hepatitis B virus and comprising
PT one or more binding arms, useful for treating hepatitis and cirrhosis.
XX
PS Disclosure; SEQ ID NO 618; 122pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule that
CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
CC comprising one or more binding arms, without requiring the presence of a
CC 2'-OH group within the molecule for activity. The nucleic acids are
CC useful for treating hepatitis B virus infection, hepatitis,
CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
CC combination with other therapies such as lamivudine and interferons. The
CC nucleic acids are useful as diagnostic tools to examine genetic drift and
CC mutations within diseased cells, for detecting the presence of HBV RNA in
CC a cell, for the study of RNA and for down-regulating gene expression of
CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
CC sequence represents an HBV RNA target sequence, used in the scope of the
CC invention. Note: The sequence data for this patent is also available in
CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 17 BP; 6 A; 2 C; 2 G; 0 T; 7 U; 0 Other;

Best Local Similarity 88.2%; Pred. No. 2.5e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1154 GTAATGGCTAACTACAT 1170
DB 17 GTAATGATTAACAT 1

RESULT 539
ADN45890/c
ID ADN45890 standard; DNA; 17 BP.
XX
AC ADN45890;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mutant cell identification-related mutagenic oligonucleotide SeqID2559.
XX
KW cell identification; oligonucleotide-directed sequence alteration;
KW selectable phenotype; transgenic plant; herbicide resistance;
KW sterile plant; abiotic stress tolerance; albino plant;
KW amino acid production; ss.
XX
OS Brassica napus.
OS Synthetic.
XX
PN WO2004033708-A2.
XX
PD 22-APR-2004.
XX
PF 07-OCT-2003; 2003WO-US031862.
XX
PR 07-OCT-2002; 2002US-0416983P.
PR 07-MAR-2003; 2003US-0453360P.
XX
XX
XX (UYDE) UNIV DELAWARE.
PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
XX
PI Kmiec EB, Van Brabant A;
XX
XX WPI; 2004-340941/31.
XX
XX
XX Identifying a cell with a desired oligonucleotide-directed sequence alteration at a nucleic acid target site within the cell by identifying the desired sequence alteration in cells selected for the presence of a selectable phenotype.
XX
XX Example 29; SEQ ID NO 2559; 303pp; English.
XX
XX This invention relates to a novel method of identifying a cell having a desired oligonucleotide-directed sequence alteration at a first nucleic acid target site within the cell. The method comprises identifying the desired sequence alteration in cells that have been selected for the presence of a selectable phenotype conferred by a concurrent oligonucleotide-directed sequence alteration at a second nucleic acid target site within the cells. The method is useful in identifying a cell having a desired oligonucleotide-directed sequence alteration at a first nucleic acid target site within the cell. The method may be useful for the production of plants with herbicide resistance, male or female sterile plants, abiotic stress tolerance, albino plants or plants with altered amino acid production as well as for use in mammalian cell lines. The present sequence is that of a mutagenic oligonucleotide which was used in the exemplification of the invention.
XX
XX Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 AGCAGCTCAACAGATA 946
DB 17 AGCAGCTCAACAGCTA 1

RESULT 541
ADN44479
ID ADN44479 standard; DNA; 17 BP.
XX

RESULT 540
ADN45391
ID ADN45891 standard; DNA; 17 BP.
XX
AC ADN45891;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mutant cell identification-related mutagenic oligonucleotide SeqID2560.
XX
KW cell identification; oligonucleotide-directed sequence alteration;
KW selectable phenotype; transgenic plant; herbicide resistance;
KW sterile plant; abiotic stress tolerance; albino plant;
KW amino acid production; ss.
XX
OS Brassica napus.
OS Synthetic.
XX
PN WO2004033708-A2.
XX
PD 22-APR-2004.
XX
PF 07-OCT-2003; 2003WO-US031862.
XX
PR 07-OCT-2002; 2002US-0416983P.
PR 07-MAR-2003; 2003US-0453360P.
XX
XX
XX (UYDE) UNIV DELAWARE.
PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
XX
PI Kmiec EB, Van Brabant A;
XX
XX WPI; 2004-340941/31.
XX
XX
XX Identifying a cell with a desired oligonucleotide-directed sequence alteration at a nucleic acid target site within the cell by identifying the desired sequence alteration in cells selected for the presence of a selectable phenotype.
XX
XX Example 29; SEQ ID NO 2560; 303pp; English.
XX
XX This invention relates to a novel method of identifying a cell having a desired oligonucleotide-directed sequence alteration at a first nucleic acid target site within the cell. The method comprises identifying the desired sequence alteration in cells that have been selected for the presence of a selectable phenotype conferred by a concurrent oligonucleotide-directed sequence alteration at a second nucleic acid target site within the cells. The method is useful in identifying a cell having a desired oligonucleotide-directed sequence alteration at a first nucleic acid target site within the cell. The method may be useful for the production of plants with herbicide resistance, male or female sterile plants, abiotic stress tolerance, albino plants or plants with altered amino acid production as well as for use in mammalian cell lines. The present sequence is that of a mutagenic oligonucleotide which was used in the exemplification of the invention.
XX
XX Sequence 17 BP; 6 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 930 AGCAGCTCAACAGATA 946
DB 1 AGCAGCTCAACAGCTA 17

RESULT 541
ADN44479
ID ADN44479 standard; DNA; 17 BP.
XX

AC ADN44479;
 XX 15-JUL-2004 (first entry)
 DT
 XX Mutant cell identification-related mutagenic oligonucleotide SeqID1148.
 DE
 XX cell identification; oligonucleotide-directed sequence alteration;
 XX selectable phenotype; transgenic plant; herbicide resistance;
 KW sterile plant; abiotic stress tolerance; albino plant;
 KW amino acid production; ss.
 XX
 XX Cucumis sativus.
 OS Synthetic.
 XX WO2004033708-A2.
 FN
 XX 22-APR-2004.
 PD
 XX 07-OCT-2003; 2003WO-US031862.
 PF
 XX 07-OCT-2002; 2002US-0416983P.
 PR
 XX 07-MAR-2003; 2003US-0453360P.
 PR
 XX (UYDE) UNIV DELAWARE.
 PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
 XX Kmiec EB, Van Brabant A;
 FI
 XX WPI; 2004-340941/31.
 DR
 XX Identifying a cell with a desired oligonucleotide-directed sequence
 PT alteration at a nucleic acid target site within the cell by identifying
 PT the desired sequence alteration in cells selected for the presence of a
 PT selectable phenotype.
 PS Example 25; SEQ ID NO 1148; 303pp; English.
 XX This invention relates to a novel method of identifying a cell having a
 CC desired oligonucleotide-directed sequence alteration at a first nucleic
 CC acid target site within the cell. The method comprises identifying the
 CC desired sequence alteration in cells that have been selected for the
 CC presence of a selectable phenotype conferred by a concurrent
 CC oligonucleotide-directed sequence alteration at a second nucleic acid
 CC target site within the cells. The method is useful in identifying a cell
 CC having a desired oligonucleotide-directed sequence alteration at a first
 CC nucleic acid target site within the cell. The method may be useful for
 CC the production of plants with herbicide resistance, male or female
 CC sterile plants, abiotic stress tolerance, albino plants or plants with
 CC altered amino acid production as well as for use in mammalian cell lines.
 CC The present sequence is that of a mutagenic oligonucleotide which was
 CC used in the exemplification of the invention.
 XX SQ Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 928 CCAGCAGCTCAACAGCAGA 944
 DB 1 CCAGCTGCTCAACCCGA 17
 RESULT 542
 ADN44498/C
 ID ADN44498 standard; DNA; 17 BP.
 XX AC ADN44498;
 XX 15-JUL-2004 (first entry)
 DT
 XX Mutant cell identification-related mutagenic oligonucleotide SeqID1167.
 DE
 XX cell identification; oligonucleotide-directed sequence alteration;
 XX selectable phenotype; transgenic plant; herbicide resistance;
 KW sterile plant; abiotic stress tolerance; albino plant;
 KW amino acid production; ss.
 XX
 XX Cucumis sativus.

KW cell identification; oligonucleotide-directed sequence alteration;
 KW selectable phenotype; transgenic plant; herbicide resistance;
 KW sterile plant; abiotic stress tolerance; albino plant;
 KW amino acid production; ss.
 XX Cucurbita.
 OS Synthetic.
 XX WO2004033708-A2.
 FN
 XX 22-APR-2004.
 PD
 XX 07-OCT-2003; 2003WO-US031862.
 PF
 XX 07-OCT-2002; 2002US-0416983P.
 PR
 XX 07-MAR-2003; 2003US-0453360P.
 PR
 XX (UYDE) UNIV DELAWARE.
 PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
 XX Kmiec EB, Van Brabant A;
 FI
 XX WPI; 2004-340941/31.
 DR
 XX Identifying a cell with a desired oligonucleotide-directed sequence
 PT alteration at a nucleic acid target site within the cell by identifying
 PT the desired sequence alteration in cells selected for the presence of a
 PT selectable phenotype.
 PS Example 25; SEQ ID NO 1167; 303pp; English.
 XX This invention relates to a novel method of identifying a cell having a
 CC desired oligonucleotide-directed sequence alteration at a first nucleic
 CC acid target site within the cell. The method comprises identifying the
 CC desired sequence alteration in cells that have been selected for the
 CC presence of a selectable phenotype conferred by a concurrent
 CC oligonucleotide-directed sequence alteration at a second nucleic acid
 CC target site within the cells. The method is useful in identifying a cell
 CC having a desired oligonucleotide-directed sequence alteration at a first
 CC nucleic acid target site within the cell. The method may be useful for
 CC the production of plants with herbicide resistance, male or female
 CC sterile plants, abiotic stress tolerance, albino plants or plants with
 CC altered amino acid production as well as for use in mammalian cell lines.
 CC The present sequence is that of a mutagenic oligonucleotide which was
 CC used in the exemplification of the invention.
 XX SQ Sequence 17 BP; 2 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 928 CCAGCAGCTCAACAGCAGA 944
 DB 17 CCAGCTGCTCAACCCGA 1
 RESULT 543
 ADN44478/C
 ID ADN44478 standard; DNA; 17 BP.
 XX AC ADN44478;
 XX 15-JUL-2004 (first entry)
 DT
 XX Mutant cell identification-related mutagenic oligonucleotide SeqID1147.
 DE
 XX cell identification; oligonucleotide-directed sequence alteration;
 XX selectable phenotype; transgenic plant; herbicide resistance;
 KW sterile plant; abiotic stress tolerance; albino plant;
 KW amino acid production; ss.
 XX
 XX Cucumis sativus.

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OS Synthetic.
XX WO2004033708-A2.
XX PD 22-APR-2004.
XX PF 07-OCT-2003; 2003WO-US031862.
XX PF 07-OCT-2002; 2002US-0416983P.
XX PR 07-MAR-2003; 2003US-0453360P.
XX XX
XX (UYDE ) UNIV DELAWARE.
XX PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
XX PI Kmiec EB, Van Brabant A;
XX DR WPI; 2004-340941/31.
XX XX
XX Identifying a cell with a desired oligonucleotide-directed sequence
PT alteration at a nucleic acid target site within the cell by identifying
PT the desired sequence alteration in cells selected for the presence of a
PT selectable phenotype.
XX
XX Example 25; SEQ ID NO 1147; 303pp; English.
XX
XX This invention relates to a novel method of identifying a cell having a
CC desired oligonucleotide-directed sequence alteration at a first nucleic
CC acid target site within the cell. The method comprises identifying the
CC desired sequence alteration in cells that have been selected for the
CC presence of a selectable phenotype conferred by a concurrent
CC oligonucleotide-directed sequence alteration at a second nucleic acid
CC target site within the cells. The method is useful in identifying a cell
CC having a desired oligonucleotide-directed sequence alteration at a first
CC nucleic acid target site within the cell. The method may be useful for
CC the production of plants with herbicide resistance, male or female
CC sterile plants, abiotic stress tolerance, albino plants or plants with
CC altered amino acid production as well as for use in mammalian cell lines.
CC The present sequence is that of a mutagenic oligonucleotide which was
CC used in the exemplification of the invention.
XX
XX Sequence 17 BP; 2 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 CCAGCAGCTCAACAGCA 944
Db 17 CCAGCTGCTCAACCGA 1

RESULT 544
ADN44499
ID ADN44499 standard; DNA; 17 BP.
XX
XX ADN44499;
XX
XX 15-JUL-2004 (first entry)
XX
XX Mutant cell identification-related mutagenic oligonucleotide SeqID1168.
XX
XX cell identification; oligonucleotide-directed sequence alteration;
XX selectable phenotype; transgenic plant; herbicide resistance;
XX sterile plant; abiotic stress tolerance; albino plant;
XX amino acid production; ss.
XX
XX Cucurbita.
XX Synthetic.
XX
XX WO2004033708-A2.
XX
XX 22-APR-2004.
XX
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PF 07-OCT-2003; 2003WO-US031862.
XX
XX 07-OCT-2002; 2002US-0416983P.
XX PR 07-MAR-2003; 2003US-0453360P.
XX XX
XX (UYDE ) UNIV DELAWARE.
XX PA (NAPR-) NAPRO BIO THERAPEUTICS INC.
XX PI Kmiec EB, Van Brabant A;
XX DR WPI; 2004-340941/31.
XX XX
XX Identifying a cell with a desired oligonucleotide-directed sequence
PT alteration at a nucleic acid target site within the cell by identifying
PT the desired sequence alteration in cells selected for the presence of a
PT selectable phenotype.
XX
XX Example 25; SEQ ID NO 1169; 303pp; English.
XX
XX This invention relates to a novel method of identifying a cell having a
CC desired oligonucleotide-directed sequence alteration at a first nucleic
CC acid target site within the cell. The method comprises identifying the
CC desired sequence alteration in cells that have been selected for the
CC presence of a selectable phenotype conferred by a concurrent
CC oligonucleotide-directed sequence alteration at a second nucleic acid
CC target site within the cells. The method is useful in identifying a cell
CC having a desired oligonucleotide-directed sequence alteration at a first
CC nucleic acid target site within the cell. The method may be useful for
CC the production of plants with herbicide resistance, male or female
CC sterile plants, abiotic stress tolerance, albino plants or plants with
CC altered amino acid production as well as for use in mammalian cell lines.
CC The present sequence is that of a mutagenic oligonucleotide which was
CC used in the exemplification of the invention.
XX
XX Sequence 17 BP; 5 A; 7 C; 3 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 928 CCAGCAGCTCAACAGCA 944
Db 1 CCAGCTGCTCAACCGA 17

RESULT 545
ACN64970
ID ACN64970 standard; DNA; 17 BP.
XX
XX ACN64970;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human GDMPLP-1 probe SEQ ID NO:1872.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
XX hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
XX skeletal muscle function.
XX
XX Homo sapiens.
XX
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX
XX 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX
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PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 1872; Opp; English.
XX
CC The invention relates to a novel polypeptide (1) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63102
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1022 CCCTCCTCTGCTGGACC 1038
Db 1 CCCTCCTGAGCTGGACC 17
RESULT 546
ACN70900
ID ACN70900 standard; DNA; 17 BP.
XX
AC ACN70900;
XX
XX 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:7802.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
XX skeletal muscle function.
XX
OS Homo sapiens.
XX
XX US2004137589-A1.
XX
XX 15-JUL-2004.
XX

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PF 26-NOV-2003; 2003US-00723361.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0236487P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 7802; Opp; English.
XX
CC The invention relates to a novel polypeptide (1) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
SQ Sequence 17 BP; 6 A; 5 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1409 CAGCAGCAGCAGCAGCA 1425.
Db 1 CAGCAGCAGCTGAGCA 17
RESULT 547
ACN65831
ID ACN65831 standard; DNA; 17 BP.
XX
AC ACN65831;
XX
XX 02-DEC-2004 (first entry)
XX
DE Human GDMLP-1 probe SEQ ID NO:2733.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;

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KW	skeletal muscle function.	AC	ACN63763;
XX		XX	
OS	Homo sapiens.	DT	
XX		XX	
XX	US2004137589-A1.	DE	02-DEC-2004 (first entry)
XX		XX	
PD	15-JUL-2004.	XX	Human GDMPLP-1 probe SEQ ID NO:665.
XX		KW	Human; se; probe; myosin-like protein-1; hGDMPLP-1;
XX		KW	hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
PF	26-NOV-2003; 2003US-00723361.	KW	skeletal muscle function.
XX		XX	
XX	26-MAY-2000; 2000US-0207456P.	OS	Homo sapiens.
PR	21-SEP-2000; 2000US-0234687P.	XX	
PR	27-SEP-2000; 2000US-0236359P.	XX	US2004137589-A1.
PR	04-OCT-2000; 2000GB-00024263.	XX	
PR	30-JAN-2001; 2001WO-US000661.	PD	15-JUL-2004.
PR	30-JAN-2001; 2001WO-US000662.	XX	
PR	30-JAN-2001; 2001WO-US000663.	XX	26-NOV-2003; 2003US-00723361.
PR	30-JAN-2001; 2001WO-US000664.	XX	
PR	30-JAN-2001; 2001WO-US000665.	XX	26-MAY-2000; 2000US-0207456P.
PR	30-JAN-2001; 2001WO-US000666.	PR	21-SEP-2000; 2000US-0234687P.
PR	30-JAN-2001; 2001WO-US000667.	PR	27-SEP-2000; 2000US-0236359P.
PR	30-JAN-2001; 2001WO-US000668.	PR	04-OCT-2000; 2000GB-00024263.
PR	30-JAN-2001; 2001WO-US000669.	PR	30-JAN-2001; 2001WO-US000661.
PR	30-JAN-2001; 2001WO-US000670.	PR	30-JAN-2001; 2001WO-US000662.
PR	05-FEB-2001; 2001US-0266860P.	PR	30-JAN-2001; 2001WO-US000663.
PR	25-MAY-2001; 2001US-00866108.	PR	30-JAN-2001; 2001WO-US000664.
XX		PR	30-JAN-2001; 2001WO-US000665.
PA	(GUYV/) GU Y.	PR	30-JAN-2001; 2001WO-US000666.
PA	(JIYY/) JI Y.	PR	30-JAN-2001; 2001WO-US000667.
PA	(PENN/) PENN S G.	PR	30-JAN-2001; 2001WO-US000668.
PA	(HANZ/) HANZEL D K.	PR	30-JAN-2001; 2001WO-US000669.
PA	(RANK/) RANK D.	PR	30-JAN-2001; 2001WO-US000670.
PA	(CHEN/) CHEN W.	PR	05-FEB-2001; 2001US-0266860P.
PA	(SHAN/) SHANNON M E.	PR	25-MAY-2001; 2001US-00866108.
XX		XX	
PI	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;	XX	
XX		XX	(GUYV/) GU Y.
XX		XX	(JIYY/) JI Y.
XX		XX	(PENN/) PENN S G.
XX		XX	(HANZ/) HANZEL D K.
XX		XX	(RANK/) RANK D.
XX		XX	(CHEN/) CHEN W.
XX		XX	(SHAN/) SHANNON M E.
XX		PI	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX		XX	
XX		XX	WPI; 2004-533378/51.
XX		XX	
XX		XX	Novel myosin-like protein-1, useful for treating or preventing disorder
XX		XX	associated with decreased expression or activity of human genome-derived
XX		XX	myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX		XX	function.
XX		XX	
XX		XX	Disclosure; SEQ ID NO 2733; Opp; English.
XX		XX	
XX		XX	The invention relates to a novel polypeptide (I) comprising a sequence
XX		XX	(S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
XX		XX	defined in the specification, a fragment of at least 8 amino acids of
XX		XX	(S1), 95% deviation from (S1) which are conservative substitutions, and
XX		XX	65% identity to (S1). A polypeptide of the invention acts as an agonist or
XX		XX	antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
XX		XX	pharmaceutical composition of the invention is useful for treating or
XX		XX	preventing a disorder associated with decreased expression or activity of
XX		XX	hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
XX		XX	The present sequence represents a 17-mer nucleotide, used in the
XX		XX	invention for scanning the sequence represented in ACN63102
XX		XX	
XX		XX	Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	765 CTCCTCAGCTGAGGCC 781	QY	665 CAGCAAAGCCGAGGAG 681
Db	1 CTACGAGCTGAGGCC 17	XX	
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX		XX	Sequence 17 BP; 7 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
XX		XX	
XX		XX	Query Match 0.4%; Score 13.8; DB 1; Length 17;
XX		XX	Best Local Similarity 88.2%; Pred. No. 2.5e+02;
XX		XX	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX		XX	
XX			

CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63102
 XX
 SQ Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 664 TCAGCAAGCCAGAGGA 680
 Db 1 TCAGCCAGCCAGAGAA 17
 RESULT 551
 ACN73845
 ID ACN73845 standard; DNA; 17 BP.
 XX AC ACN73845;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human GDMPLP-1 probe SEQ ID NO:10747.
 XX
 KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 OS Homo sapiens.
 XX
 PN US2004137589-A1.
 XX
 XX 15-JUL-2004.
 XX
 PF 26-NOV-2003; 2003US-00723361.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001WO-US000670.
 PR 25-MAY-2001; 2001US-0266860P.
 XX
 XX (GUIY/) GU Y.
 PA (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 PI WPI; 2004-533378/51.
 XX
 DR Novel myosin-like protein-1, useful for treating or preventing disorder
 XX associated with decreased expression or activity of human genome-derived
 PT

PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX
 PS Disclosure; SEQ ID NO 10747; Opp; English.
 XX
 CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 SQ Sequence 17 BP; 3 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1771 TGTGCTAGCCAGAAC 1787
 Db 1 TGTGCTAGCCAGAAC 17
 RESULT 552
 ACN64971
 ID ACN64971 standard; DNA; 17 BP.
 XX AC ACN64971;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human GDMPLP-1 probe SEQ ID NO:1873.
 XX
 KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 OS Homo sapiens.
 XX
 PN US2004137589-A1.
 XX
 XX 15-JUL-2004.
 XX
 PF 26-NOV-2003; 2003US-00723361.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001WO-US000670.
 PR 25-MAY-2001; 2001US-00866108.
 XX
 XX (GUIY/) GU Y.
 PA (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.

PA (SHAN/) SHANNON M E.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 DR Novel myosin-like protein-1, useful for treating or preventing disorder
 XX associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX Disclosure; SEQ ID NO 1873; Opp; English.
 PS The invention relates to a novel polypeptide (I) comprising a sequence
 XX (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63102
 XX
 SQ Sequence 17 BP; 3-A; 7 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1023 CCTCTCTGCTGGACCA 1039
 DB 1 CCTCTGAGTGGACCA 17
 RESULT 553
 ACN73345
 ID ACN73345 standard; DNA; 17 BP.
 AC ACN73345;
 XX
 XX 02-DEC-2004 (first entry)
 DT Human GDMLP-1 probe SEQ ID NO:10247.
 DE
 DE Human; ss; probe; myosin-like protein-1; hGDMLP-1;
 KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 OS Homo sapiens.
 XX
 XX US2004137589-A1.
 PN
 XX 15-JUL-2004.
 PD
 XX 26-NOV-2003; 2003US-00723361.
 PF
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.

PR 25-MAY-2001; 2001US-00866108.

XX (GUY/) GU Y.
 PA (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 DR

XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX Disclosure; SEQ ID NO 10247; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 SQ Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1187 TCAGCCCGAGGTGGGCA 1203
 DB 1 TCAGCCAAAGGTGGGCA 17

Search completed: August 16, 2005, 12:54:22
 Job time : 26 secs

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OM nucleic - nucleic search, using sw model

Run on: August 16, 2005, 12:48:29 ; Search time 14 Seconds
(without alignments)
3.358 Million cell updates/sec

Title: US-10-698-070-1
Perfect score: 3763
Sequence: 1 aggtggcgcgagagatgg.....taacaaataatagagctg 3763

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 337 seqs, 6247 residues

Total number of hits satisfying chosen parameters: 674

Minimum DB seq length: 17
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 346 summaries

Database : fetchrge.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	32	0.9	33	1	AR084540
C 2	30.4	0.8	33	1	AR241963
C 3	30	0.8	30	1	AR084541
C 4	30	0.8	30	1	AR165925
C 5	30	0.8	30	1	E34522
C 6	30	0.8	30	1	I84405
C 7	30	0.8	30	1	I84410
C 8	30	0.8	31	1	AR078304
C 9	29	0.8	31	1	AX249451
C 10	24	0.6	24	1	AR084605
C 11	23	0.6	23	1	BD183252
C 12	22	0.6	22	1	BD183253
C 13	22	0.6	25	1	AX754188
C 14	22	0.6	25	1	AX754189
C 15	22	0.6	25	1	AX754190
C 16	22	0.6	25	1	AX754191
C 17	21.2	0.6	26	1	BD174259
C 18	21.2	0.6	26	1	AX486861
C 19	21	0.6	21	1	AR053160
C 20	21	0.6	21	1	AR084539
C 21	21	0.6	21	1	AR084551
C 22	21	0.6	21	1	AR084571
C 23	21	0.6	21	1	AR084577
C 24	21	0.6	21	1	AR084580
C 25	21	0.6	21	1	AR084598
C 26	21	0.6	21	1	AX104588
C 27	21	0.6	21	1	AX55212
C 28	21	0.6	21	1	AX547641
C 29	21	0.6	25	1	AX754187
C 30	21	0.6	25	1	AX754192
C 31	20.8	0.6	24	1	BD169605
C 32	20.8	0.6	24	1	BD182475
C 33	20.8	0.6	24	1	BD102725

C 34	20.4	0.5	25	1	A27144
C 35	20.2	0.5	25	1	A27143
C 36	20	0.5	20	1	AX487367
C 37	20	0.5	20	1	AX488408
C 38	20	0.5	25	1	AX754186
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C 41	19.4	0.5	22	1	AX088799
C 42	19	0.5	20	1	AR315939
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C 44	18.8	0.5	22	1	AX360164
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C 47	18.4	0.5	20	1	AR036870
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C 50	18.4	0.5	20	1	AX053091
C 51	18.4	0.5	20	1	AX317754
C 52	18.4	0.5	20	1	AX546302
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C 54	18.4	0.5	21	1	AR084546
C 55	18.4	0.5	21	1	AR084558
C 56	18.4	0.5	21	1	AR084600
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C 58	18	0.5	18	1	AR084528
C 59	18	0.5	18	1	BD274822
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C 61	18	0.5	18	1	AX598368
C 62	18	0.5	20	1	AR271209
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C 64	17.8	0.5	21	1	AR084588
C 65	17.4	0.5	19	1	AR038671
C 66	17.4	0.5	20	1	AR428075
C 67	17.4	0.5	20	1	AX053083
C 68	17.4	0.5	20	1	AX053092
C 69	17.4	0.5	20	1	AX149057
C 70	17.4	0.5	20	1	AX546303
C 71	17.4	0.5	20	1	AX546393
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C 73	17.4	0.5	21	1	CQ821171
C 74	17.4	0.5	21	1	AX146085
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C 92	16.4	0.4	18	1	AR121115
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C 98	16.4	0.4	20	1	AX764066
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C 100	16	0.4	17	1	AX753819
C 101	16	0.4	17	1	AX753826
C 102	16	0.4	20	1	AR224718
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C 105	15.6	0.4	33	1	AR241963
C 106	15.4	0.4	17	1	AR190113

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ACCESSION	AR084541
VERSION	AR084541.1 GI:10011312
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 30)
AUTHORS	Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE	Oligonucleotide repeat arrays
JOURNAL	Patent: US 5981185-A 30 09-NOV-1999;
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ACCESSION	AR165925
VERSION	AR165925.1 GI:16241014
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 30)
AUTHORS	Ranum,L.P.W., Koob,M.D., Moseley-Allredge,M.L. and Benzow,K.A.
TITLE	SCA7 gene and method of use
JOURNAL	Patent: US 6280938-A 4 28-AUG-2001;
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ACCESSION	E34522
VERSION	E34522.1 GI:13018890
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SOURCE	Homo sapiens (human)
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ACCESSION	E34522
VERSION	E34522.1 GI:13018890
KEYWORDS	JP 1999206393-A/4.
SOURCE	Homo sapiens (human)

Unclassified.
1 (bases 1 to 30)
Schalling, M., Hudson, T.J. and Housman, D.E.
TITLE Direct detection of expanded nucleotide repeats in the human genome
JOURNAL Patent: US 5695933-A 11 09-DEC-1997;
FEATURES Location/Qualifiers
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RESULT 8
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LOCUS AR078304 31 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 14 from patent US 5962332.
ACCESSION AR078304
VERSION AR078304.1 GI:10005050
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS Singer, R.H. and Taneja, K.L.
TITLE Detection of trinucleotide repeats by in situ hybridization
JOURNAL Patent: US 5962332-A 14 05-OCT-1999;
FEATURES Location/Qualifiers
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QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAG 1438
Db 1 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 30

RESULT 9
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LOCUS AX249451 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1530 from Patent WO0166800.
ACCESSION AX249451
VERSION AX249451.1 GI:15864074
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1530 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES Location/Qualifiers
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QY 1561 GCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 1591
Db 1 GCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 31

RESULT 10
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DEFINITION Sequence 94 from patent US 5981185.
ACCESSION AR084605
VERSION AR084605.1 GI:10011376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 94 09-NOV-1999;
FEATURES Location/Qualifiers
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QY 1411 GCAGCAGCAGCAGCAGCAGCAGCAGCA 1434
Db 1 GCAGCAGCAGCAGCAGCAGCAGCAGCA 24

RESULT 11
BD183252
LOCUS BD183252 23 bp DNA linear PAT 17-JUN-2003
DEFINITION Marker for genealogical diagnosis.
ACCESSION BD183252
VERSION BD183252.1 GI:31875452
KEYWORDS JP 2002360268-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
AUTHORS Ohara, O., Nagase, T., Oishi, M., Yokota, H. and Isono, M.
TITLE Marker for genealogical diagnosis
JOURNAL Patent: JP 2002360268-A 6 17-DEC-2002;
KAZUSA DNA RESEARCH INSTITUTE, DAIICHI PHARMACEUTICAL CO LTD
COMMENT OS Artificial Sequence
PN JP 2002360268-A/6
PF 17-DEC-2002
PI 03-AUG-2001 JP 2001236788
PI OSAMU OHARA, TAKAHIRO NAGASE, MICHIO OISHI, HIROSHI YOKOTA, MICHIO ISONO
PC C12N15/09, A61K35/12, A61K35/64, A61K35/72, A61K35/74, A61K35/76,
PC A61K39/395, A61K39/395, A61K45/00, A61K48/00, A61P25/28, C07K14/47,
PC C07K16/18,
PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/02, C12Q1/68, G01N33/15,
PC G01N33/53, G01N33/53, G01N33/53, G01N33/56, C12N15/00, C12N5/00,
PC A61K37/02
CC Description of Artificial Sequence: Designed polynucleotide CC based on the base sequence of the sequence No.1 in the present sequence

CC base sequence of the sequence No.1 in the present sequence CC
FH Key listing Location/Qualifiers
FT source 1..23
/organism="Artificial Sequence".
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/organism="synthetic construct"
/mol_type="genomic DNA"


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Query Match      0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
Db 2 GCAGCAGCAGCAACAGCAGCAG 23

RESULT 16
AX754191
LOCUS AX754191 25 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 538 from Patent WO03037931.
ACCESSION AX754191
VERSION AX754191.1 GI:32166888
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 538 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAGCAGCAG 1450
Db 1 GCAGCAGCAGCAACAGCAGCAG 22

RESULT 17
BD174259/c
LOCUS BD174259 26 bp DNA linear PAT 18-FEB-2003
DEFINITION Novel physiological active peptide and its use.
ACCESSION BD174259
VERSION BD174259.1 GI:28415598
KEYWORDS WO 02062944-A/6.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Otaki,T., Masuda,Y., Takatsu,Y., Watanabe,T., Terao,Y., Shintani,Y.
and Hinuma,S.
TITLE Novel physiological active peptide and its use
JOURNAL Patent: WO 02062944-A 6 15-AUG-2002;
TAKEDA CHEMICAL INDUSTRIES LTD,TETSUYA OTAKI,YASUSHI MASUDA,
YOSHIIRO TAKATSU,TAKUYA WATANABE,YASUKO TERAU,YASUSHI SHINTANI,
SHUJI HINUMA
COMMENT OS Artificial Sequence
PN WO 02062944-A/6
PD 15-AUG-2002
PF 01-FEB-2002 WO 2002JP000852
PR 02-FEB-2001 JP 01P 026820
PI TETSUYA OTAKI,YASUSHI MASUDA,YOSHIIRO TAKATSU,TAKUYA
WATANABE,
PI YASUKO TERAU,YASUSHI SHINTANI,SHUJI HINUMA
PC C07K14/47,C07K14/705,C12N15/12,C12P21/02,C07K16/18,A61K67/027,
PC C12N5/10,
PC G01N33/15,G01N33/50,A61P1/00
CC DNA primer, hBv8-F1 primer
FH Key
FT source
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/organism="synthetic construct"
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Best Local Similarity 88.5%; Pred. No. 70;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1407 AACAGCAGCAGCAGCAGCAGCAG 1432
Db 26 AACAGCAGCGGCAGCAGCAGAAAGTAG 1

RESULT 18
AX486861/c
LOCUS AX486861 26 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 4161 from Patent WO02053728.
ACCESSION AX486861
VERSION AX486861.1 GI:22321009
KEYWORDS Candida albicans
SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE 1
AUTHORS Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 4161 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
source
1. .26
/organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"

Query Match      0.6%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 70;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1568 CAGCAGCAACACACAGCAGCAACA 1593
Db 26 CAACAACAACACACACACACACACA 1

RESULT 19
AR053160/c
LOCUS AR053160 21 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 66 from patent US 5834183.
ACCESSION AR053160
VERSION AR053160.1 GI:5978022
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE Gene sequence for spinocerebellar ataxia type 1 and method for
diagnosis
JOURNAL Patent: US 5834183-A 66 10-NOV-1998;
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Query Match      0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AGCAGCAGCAGCAGCAGCAGCAGC 1430
Db 21 AGCAGCAGCAGCAGCAGCAGCAGC 1
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PAT 01-SEP-2000

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ACCESSION AR084598
VERSION AR084598.1 GI:10011369
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 87 09-NOV-1999;
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Query Match      0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAGCA 1431
Db 21 GCAGCAGCAGCAGCAGCAGCA 1

RESULT 26
AX104588/c
LOCUS AX104588 21 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 780 from Patent WO0122972.
ACCESSION AX104588
VERSION AX104588.1 GI:13920785
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 780 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"

Query Match      0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 27
AX355212/c
LOCUS AX355212 21 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 240 from Patent WO0197843.
ACCESSION AX355212
VERSION AX355212.1 GI:18619879
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL cancer
PATENT: WO 0197843-A 240 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
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Query Match      0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
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QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 28
AX547641/c
LOCUS AX547641 21 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 780 from Patent WO02053141.
ACCESSION AX547641
VERSION AX547641.1 GI:25812785
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 780 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic Sequence"

Query Match      0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCAGCAG 1429
Db 21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 29
AX754187
LOCUS AX754187 25 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 534 from Patent WO03037931.
ACCESSION AX754187
VERSION AX754187.1 GI:32166884
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 534 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
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Query Match      0.6%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 67;
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QY 1429 GCAGCAGCAGCAACAGCAGCA 1449
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20-JUN-2001 WO 2001JP005257 06-SEP-2000 JP 00P  
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21-JUN-2000 TB 00P 131089
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13-APR-2001 JP 01P 116000
PI MASAAKI MORI, YUKIO SHIMOMURA, MIOKO HARADA, MIKA KURIHARA, CHIEKO
KITADA,
PI TAIJI ASAMI, YOSHIO MATSUMOTO, YUKA ADACHI, TAKUYA WATANABE, PI
TSUKASA SUGO,
PI MICHIO ASE
PC C12N15/12, C07K14/47, C12N1/21, C07K16/18, G01N33/53, G01N33/50, PC
G01N33/15,
PC C12P21/02, C12P21/08, A61K31/711, A61K38/17, A01K67/027, A61P1/14,
PC A61P3/04
CC Primer
FH Key
FT source Location/Qualifiers
FT 1..24
FT Location/Qualifiers
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FT /organism="Artificial Sequence".
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.6%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 65;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1418 CAGCAGCAGCAGCAGCAGCA 1441
Db 1 CAGCGGCAGCAGCAGCAGCAGTAA 24
RESULT 34
A27144/c
LOCUS 25 bp DNA linear PAT 22-AUG-1996
DEFINITION synthetic leader.
ACCESSION A27144
VERSION A27144.1 GI:1931892
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 78;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1420 GCAGCAGCAGCAGCAGCAGCA 1441
Db 25 GGAGCAGCAGCAGCAGCAGCA 4
RESULT 35
A27143
LOCUS 25 bp DNA linear PAT 22-AUG-1996
DEFINITION synthetic leader.
ACCESSION A27143
VERSION A27143.1 GI:1831891
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
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Patent: CA 1306208-A 1 11-AUG-1992;
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 82;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1407 AACAGCAGCAGCAGCAGCAGCA 1431
Db 1 AATTGGAGCAGCAGCAGCAGCA 25
RESULT 36
AX487367/c
LOCUS 20 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 4667 from Patent WO02053728.
ACCESSION AX487367
VERSION AX487367.1 GI:22321515
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
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Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1553 CAACACAGCAGCAGCAGCA 1572
Db 20 CAACACAGCAGCAGCAGCA 1
RESULT 37
AX488408/c
LOCUS 20 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 5708 from Patent WO02053728.
ACCESSION AX488408
VERSION AX488408.1 GI:22322488
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
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/organism="Candida albicans"
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Query Match 0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1555 ACAACAGCAGCAGCAGCAGC 1574
Db 20 ACAACAGCAGCAGCAGCAGC 1
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RESULT 38
AX754186
LOCUS AX754186 25 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 533 from Patent WO03037931.
ACCESSION AX754186
VERSION AX754186.1 GI:32166893
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M. and Phan, T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 533 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 0.5%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAACAGCAGC 1448
DB 6 GCAGCAGCAGCAACAGCAGC 25

RESULT 39
AX754193
LOCUS AX754193 25 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 540 from Patent WO03037931.
ACCESSION AX754193
VERSION AX754193.1 GI:32166890
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M. and Phan, T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 540 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.5%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1431 AGCAGCAGCAACAGCAGCAG 1450
DB 1 AGCAGCAGCAACAGCAGCAG 20

RESULT 40
BD105783/c
LOCUS BD105783 24 bp DNA linear PAT 27-AUG-2002
DEFINITION Conjugates of biologically stable polymers and polynucleotides for
treating systemic lupus erythematosus.
ACCESSION BD105783
VERSION BD105783.1 GI:22651357
KEYWORDS JP 2001354569-A/8.
SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Conrad, M. J. and Coutts, S.
TITLE Conjugates of biologically stable polymers and polynucleotides for
treating systemic lupus erythematosus
JOURNAL Patent: JP 2001354569-A 8 25-DEC-2001;
LA JOLLA PHARMACEUTICAL CO
COMMENT OS Artificial Sequence
PN JP 2001354569-A/8
PD 25-DEC-2001
PF 04-APR-2001 JP 2001106534
PR 16-JAN-1990 US 466138, 13-MAR-1990 US 494118 PI
MICHAEL J CONRAD, STEPHEN COUTTS
PC A61K31/7088, A61K47/48, A61P37/02, C07K14/00, C12N15/00, C12N15/00
CC Synthetic Construct
CQ Key Location/Qualifiers
FT source 1..24
FT /organism="Artificial Sequence".
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 83;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1571 CAGCAACAACAACAGCAACAACA 1593
DB 24 CAACAACAACAACAACAACAACA 2

RESULT 41
AX088799
LOCUS AX088799 22 bp DNA linear PAT 17-MAR-2001
DEFINITION Sequence 125 from Patent WO0114416.
ACCESSION AX088799
VERSION AX088799.1 GI:13397595
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Neepser, M. P., McClements, W. L., Jansen, K. U., Schultz, L. D., Chen, L.
and Wang, X. M.
TITLE Synthetic human papillomavirus genes
JOURNAL Patent: WO 0114416-A 125 01-MAR-2001;
Merck & Co., Inc. (US)
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source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Codon-Optimized HPV6 E2 fragment"
Query Match 0.5%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1497 CTCACAACAACAGCAACAGCAGC 1517
DB 2 CGCAACAACAACAGCAACAGCAGC 22

RESULT 42
AR315939/c
LOCUS AR315939 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6476 from patent US 6559294.
ACCESSION AR315939
VERSION AR315939.1 GI:31709365
KEYWORDS
SOURCE

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SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalfe, B.J., Peek, J.A.,
            Sankaran, B., and Fletcher, L.D.
TITLE       Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL     Patent: US 6559294-A 6476 06-MAY-2003;
FEATURES    Location/Qualifiers
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Query Match
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QY 1454 CAGCAACAGCAACGAGCAAC 1472
Db 19 CAGCAACAGCAACGAGCAAC 1

RESULT 43
LOCUS      AX088798/c
DEFINITION Sequence 124 from Patent WO0114416.
ACCESSION  AX088798
VERSION     AX088798.1 GI:13397594
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Neepser, M.P., McClements, W.L., Jansen, K.U., Schultz, L.D., Chen, L.
            and Wang, X.M.
TITLE       Synthetic human papillomavirus genes
JOURNAL     Patent: WO 0114416-A 124 01-MAR-2001;
            Merck & Co., Inc. (US)
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /note="Codon-Optimized HPV6 E2 fragment"

Query Match
Best Local Similarity 0.5%; Score 19; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1499 CAACAACAGCAACGAGCAGC 1517
Db 22 CAACAACAGCAACGAGCAGC 4

RESULT 44
LOCUS      AX360164/c
DEFINITION Sequence 120 from Patent WO0200860.
ACCESSION  AX360164
VERSION     AX360164.1 GI:18675731
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Sheppard, P.O., Baindur, N. and Bishop, P.D.
TITLE       Mammalian adhesion protease peptides
JOURNAL     Patent: WO 0109293-A 24 08-FEB-2001;
            ZymoGenetics, Inc. (US)
FEATURES    Location/Qualifiers
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            /db_xref="taxon:32630"
            /note="ologonucleotide ZC21.076"

Query Match
Best Local Similarity 0.5%; Score 18.8; DB 1; Length 23;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1421 CAGCAGCAGCAGCAGCAGCAAC 1442
Db 23 CAGTAGTAGCAGCAGCAGCAAC 2

RESULT 45
LOCUS      AR219249/c
DEFINITION Sequence 24 from patent US 6420154.
ACCESSION  AR219249
VERSION     AR219249.1 GI:23320207
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 23)
AUTHORS     Sheppard, P.O., Baindur, N. and Bishop, P.D.
TITLE       Mammalian adhesion protease peptides
JOURNAL     Patent: US 6420154-A 24 16-JUL-2002;
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Query Match
Best Local Similarity 0.5%; Score 18.8; DB 1; Length 23;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1421 CAGCAGCAGCAGCAGCAGCAAC 1442
Db 23 CAGTAGTAGCAGCAGCAGCAAC 2

RESULT 46
LOCUS      AX082174/c
DEFINITION Sequence 24 from Patent WO0109293.
ACCESSION  AX082174
VERSION     AX082174.1 GI:13170970
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Sheppard, P.O., Baindur, N. and Bishop, P.D.
TITLE       Mammalian adhesion protease peptides
JOURNAL     Patent: WO 0109293-A 24 08-FEB-2001;
            ZymoGenetics, Inc. (US)
FEATURES    Location/Qualifiers
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Query Match
Best Local Similarity 0.5%; Score 18.8; DB 1; Length 23;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1421 CAGCAGCAGCAGCAGCAGCAAC 1442
Db 23 CAGTAGTAGCAGCAGCAGCAAC 2

RESULT 47
LOCUS      AR219249/c
DEFINITION Sequence 24 from patent US 6420154.
ACCESSION  AR219249
VERSION     AR219249.1 GI:23320207
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 23)
AUTHORS     Sheppard, P.O., Baindur, N. and Bishop, P.D.
TITLE       Mammalian adhesion protease peptides
JOURNAL     Patent: US 6420154-A 24 16-JUL-2002;
            Location/Qualifiers
            1..23
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.5%; Score 18.8; DB 1; Length 23;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1421 CAGCAGCAGCAGCAGCAGCAAC 1442
Db 23 CAGTAGTAGCAGCAGCAGCAAC 2

RESULT 47

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AR036870/c
LOCUS          AR036870          20 bp      DNA          linear          PAT 29-SEP-1999
DEFINITION     Sequence 1 from patent US 5800990.
ACCESSION      AR036870
VERSION        AR036870.1  GI:5954726
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Raynolds,M.V. and Perryman,M.Benjamin.
TITLE         Angiotensin-converting enzyme genetic variant screens
JOURNAL       Patent: US 5800990-A 1 01-SEP-1998;
FEATURES      Location/Qualifiers
                source
                1..20
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match    0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1402 GCAGCAACAGCAGCAGCAGC 1421
Db 20 GCAGCAACAGCAGCAGCAGC 1

RESULT 48
BD244919/c
LOCUS          BD244919          20 bp      DNA          linear          PAT 17-JUL-2003
DEFINITION     Modulation of gene expression by combination therapy.
ACCESSION      BD244919
VERSION        BD244919.1  GI:33054689
KEYWORDS       JP 2002528391-A/47.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE         Modulation of gene expression by combination therapy
JOURNAL       Patent: JP 2002528391-A 47 03-SEP-2002;
COMMENT        METHYLENE INC
                OS Artificial Sequence
                PN JP 2002528391-A/47
                PD 03-SEP-2002
                PF 19-OCT-1999 JP 2000576885
                PR 19-OCT-1998 US 60/104804
                PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
                A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
                706.
                A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
                09//
                PC C12N5/10,C12N15/00,C12N5/00
                CC antisense
                FH Key
                FT source
                FT source
                Location/Qualifiers
                1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
Query Match    0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 49
AR053082/c
LOCUS          AR053082          20 bp      DNA          linear          PAT 12-JAN-2001
DEFINITION     Sequence 6 from Patent WO0071703.
ACCESSION      AR053082
VERSION        AR053082.1  GI:12227139
KEYWORDS       synthetic construct
SOURCE         other sequences; artificial sequences.
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS       Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE         Inhibition of histone deacetylase
JOURNAL       Patent: WO 0071703-A 6 30-NOV-2000;
FEATURES      Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="synthetic oligonucleotide"
Query Match    0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 50
AR053091/c
LOCUS          AR053091          20 bp      DNA          linear          PAT 12-JAN-2001
DEFINITION     Sequence 15 from Patent WO0071703.
ACCESSION      AR053091
VERSION        AR053091.1  GI:12227148
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS       Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE         Inhibition of histone deacetylase
JOURNAL       Patent: WO 0071703-A 15 30-NOV-2000;
FEATURES      Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Description of Combined DNA/RNA Molecule: Positions
                1-4 and 17-20 are 2'-methoxyribose substituted
                nucleotides; positions 5-16 are deoxyribonucleotides"
Query Match    0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 51
AR317754/c
LOCUS          AR317754          20 bp      DNA          linear          PAT 14-DEC-2001
DEFINITION     Sequence 15 from Patent WO0190313.
ACCESSION      AR317754
VERSION        AR317754.1  GI:17900639
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
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AR036870/c
LOCUS          AR036870          20 bp      DNA          linear          PAT 29-SEP-1999
DEFINITION     Sequence 1 from patent US 5800990.
ACCESSION      AR036870
VERSION        AR036870.1  GI:5954726
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Raynolds,M.V. and Perryman,M.Benjamin.
TITLE         Angiotensin-converting enzyme genetic variant screens
JOURNAL       Patent: US 5800990-A 1 01-SEP-1998;
FEATURES      Location/Qualifiers
                source
                1..20
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match    0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1402 GCAGCAACAGCAGCAGCAGC 1421
Db 20 GCAGCAACAGCAGCAGCAGC 1

RESULT 48
BD244919/c
LOCUS          BD244919          20 bp      DNA          linear          PAT 17-JUL-2003
DEFINITION     Modulation of gene expression by combination therapy.
ACCESSION      BD244919
VERSION        BD244919.1  GI:33054689
KEYWORDS       JP 2002528391-A/47.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS       Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE         Modulation of gene expression by combination therapy
JOURNAL       Patent: JP 2002528391-A 47 03-SEP-2002;
COMMENT        METHYLENE INC
                OS Artificial Sequence
                PN JP 2002528391-A/47
                PD 03-SEP-2002
                PF 19-OCT-1999 JP 2000576885
                PR 19-OCT-1998 US 60/104804
                PI JEFFREY M BESTERMAN,ALAN ROBERT MACLEOD,WILLIAM M SIDERS PC
                A61K48/00,A61K31/165,A61K31/19,A61K31/513,A61K31/517,A61K31/ PC
                706.
                A61K31/7068,A61K31/7088,A61K31/7125,A61K45/00,A61P35/00,C12N15/ PC
                09//
                PC C12N5/10,C12N15/00,C12N5/00
                CC antisense
                FH Key
                FT source
                FT source
                Location/Qualifiers
                1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
Query Match    0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 49
AR053082/c
LOCUS          AR053082          20 bp      DNA          linear          PAT 12-JAN-2001
DEFINITION     Sequence 6 from Patent WO0071703.
ACCESSION      AR053082
VERSION        AR053082.1  GI:12227139
KEYWORDS       synthetic construct
SOURCE         other sequences; artificial sequences.
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS       Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE         Inhibition of histone deacetylase
JOURNAL       Patent: WO 0071703-A 6 30-NOV-2000;
FEATURES      Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="synthetic oligonucleotide"
Query Match    0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 50
AR053091/c
LOCUS          AR053091          20 bp      DNA          linear          PAT 12-JAN-2001
DEFINITION     Sequence 15 from Patent WO0071703.
ACCESSION      AR053091
VERSION        AR053091.1  GI:12227148
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS       Macleod,A.R., Li,Z. and Besterman,J.M.
TITLE         Inhibition of histone deacetylase
JOURNAL       Patent: WO 0071703-A 15 30-NOV-2000;
FEATURES      Location/Qualifiers
                source
                1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Description of Combined DNA/RNA Molecule: Positions
                1-4 and 17-20 are 2'-methoxyribose substituted
                nucleotides; positions 5-16 are deoxyribonucleotides"
Query Match    0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1409 CAGCAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCAGCA 1

RESULT 51
AR317754/c
LOCUS          AR317754          20 bp      DNA          linear          PAT 14-DEC-2001
DEFINITION     Sequence 15 from Patent WO0190313.
ACCESSION      AR317754
VERSION        AR317754.1  GI:17900639
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS      Feinberg,A.T., Strichman-Almashanu,L.T. and Jiang,S.C.
TITLE        Methods for assaying gene imprinting and methylated cpg islands
JOURNAL      Patent: WO 0190313-A 15 29-NOV-2001;
              The Johns Hopkins University (US)
FEATURES     source
              1..20
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1430 CAGCAGCAGCAGCAGCA 1449
Db 20 CAGTAGCAGCAACAGCAGCA 1

RESULT 52
AX546302/c
LOCUS          AX546302
DEFINITION     Sequence 51 from Patent EP1243290.
ACCESSION      AX546302
VERSION        AX546302.1 GI:25811493
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE          Modulation of gene expression by combination therapy
JOURNAL        Patent: EP 1243290-A 51 25-SEP-2002;
              Methylgene, Inc. (CA)
FEATURES     source
              1..20
              /organism="synthetic construct"
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              /db_xref="taxon:32630"
              /note="oligonucleotide"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCA 1

RESULT 53
AX546392/c
LOCUS          AX546392
DEFINITION     Sequence 51 from Patent EP1243289.
ACCESSION      AX546392
VERSION        AX546392.1 GI:25811583
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE          Modulation of gene expression by combination therapy
JOURNAL        Patent: EP 1243289-A 51 25-SEP-2002;
              Methylgene, Inc. (CA)
FEATURES     source
              1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"

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/note="oligonucleotide"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 80;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1428
Db 20 CGGCAGCAGCAGCAGCA 1

RESULT 54
AR084546
LOCUS          AR084546
DEFINITION     Sequence 35 from patent US 5981185.
ACCESSION      AR084546
VERSION        AR084546.1 GI:10011371
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE          Oligonucleotide repeat arrays
JOURNAL        Patent: US 5981185-A 35 09-NOV-1999;
              Location/Qualifiers
FEATURES     source
              1..21
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACAACAACAGCAACA 1593
Db 2 CAACAACAACAACAACA 21

RESULT 55
AR084558
LOCUS          AR084558
DEFINITION     Sequence 47 from patent US 5981185.
ACCESSION      AR084558
VERSION        AR084558.1 GI:10011329
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE          Oligonucleotide repeat arrays
JOURNAL        Patent: US 5981185-A 47 09-NOV-1999;
              Location/Qualifiers
FEATURES     source
              1..21
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACAACAACAGCAACA 1593
Db 1 CAACAACAACAACAACA 20

RESULT 56
AR084600/c
LOCUS          AR084600
DEFINITION     Sequence 89 from patent US 5981185.
ACCESSION      AR084600
VERSION        AR084600.1 GI:10011371

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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 9 09-NOV-1999;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACAACAACAGCAACA 1593
Db 20 CAACAACAACAGCAACA 1

RESULT 57
AR084603/c
LOCUS AR084603 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 92 from patent US 5981185.
ACCESSION AR084603
VERSION AR084603.1 GI:10011374
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 9 09-NOV-1999;
FEATURES Location/Qualifiers
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1. .21
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACAACAACAGCAACA 1593
Db 21 CAACAACAACAGCAACA 2

RESULT 58
AR084528/c
LOCUS AR084528 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 17 from patent US 5981185.
ACCESSION AR084528
VERSION AR084528.1 GI:10011299
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 17 09-NOV-1999;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428
Db 18 GCAGCAGCAGCAGCAGCA 1

RESULT 59
BD274822/c
LOCUS BD274822 18 bp DNA linear PAT 17-JUL-2003
DEFINITION CANCER CELL VACCINE.
ACCESSION BD274822
VERSION BD274822.1 GI:33084590
KEYWORDS JP 2002531582-A/47.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kusu,M., Qiu,G. and Hunfreese,R.
TITLE CANCER CELL VACCINE
JOURNAL Patent: JP 2002531582-A 47 24-SEP-2002;
COMMENT ANTIGEN EXPRESS INC
OS Artificial Sequence
PN JP 2002531582-A/47
PD 24-SEP-2002 JP 200585901
PF 24-NOV-1999 JP 200585901
PI 04-DEC-1998 US 09/205995
PT minzhen kusu,gang qiu,robert hunfreese
CC Description of Artificial Sequence: antisense oligonucleotide
CC corresponding
CC to a specific region of the mouse Ii gene.
FH Key Location/Qualifiers
FEATURES Location/Qualifiers
source
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAG 1417
Db 18 CAGCAGCAACAGCAGCAG 1

RESULT 60
AR205288/c
LOCUS AR205288 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 48 from patent US 6368855.
ACCESSION AR205288
VERSION AR205288.1 GI:21502833
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Xu,M., Qiu,G. and Humphreys,R.
TITLE MHC class II antigen presenting cells containing oligonucleotides
JOURNAL Patent: US 6368855-A 48 09-APR-2002;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAG 1417
Db 18 CAGCAGCAACAGCAGCAG 1

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RESULT 61
AX598368
LOCUS AX598368 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 642 from Patent WO0244994.
ACCESSION AX598368
VERSION AX598368.1 GI:28398544
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Brower,A., Brow,M.A., Cracauer,R.F., Fors,L., Granske,R., de arruda
Indig,M., Kurensky,D., Luedtke,C., Lukowiak,A., Lyamichev,V.,
Neri,B.P., Reiner,N.D., Roeven,R.T., Skrzypczynski,Z., Ziarno,W.A.,
Comerford,J., Stump,S. and Wiegut,D.D.
TITLE Systems and method for detection assay production and sale
JOURNAL Patent: WO 0244994-A 642 06-JUN-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCA 1428
Db 1 GCAGCAGCAGCAGCAGCA 18

RESULT 62
AR271209/c
LOCUS AR271209 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 152 from patent US 6503152.
ACCESSION AR271209
VERSION AR271209.1 GI:29702512
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Pelz,D.T.
TITLE Putting trainer
JOURNAL Patent: US 6503152-A 152 07-JAN-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1602 AGCAGCAGCAACCAACCAT 1619
Db 20 AGCAGCAGCAACCAACCAT 3

RESULT 63
AR084525
LOCUS AR084525 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 14 from patent US 5981185.
ACCESSION AR084525
VERSION AR084525.1 GI:10011296
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)

AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 14 09-NOV-1999;
FEATURES
source
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1572 AGCAACAACAACGACCAAC 1592
Db 1 AACACAACAACAACAACAAC 21

RESULT 64
AR084588/c
LOCUS AR084588 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 77 from patent US 5981185.
ACCESSION AR084588
VERSION AR084588.1 GI:10011359
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 77 09-NOV-1999;
FEATURES
source
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1572 AGCAACAACAACGACCAAC 1592
Db 21 AACACAACAACAACAACAAC 1

RESULT 65
AR038671
LOCUS AR038671 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5807678.
ACCESSION AR038671
VERSION AR038671.1 GI:5958034
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Miller,W.L., Lin,D. and Strauss,J.F. III.
TITLE Identification of gene mutations associated with congenital lipoid
adrenal hyperplasia
JOURNAL Patent: US 5807678-A 5 15-SEP-1998;
FEATURES
source
Location/Qualifiers
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 92;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
Db 1 GCAGCAGCAGCAGCAGCAG 19

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RESULT 66
LOCUS       AR428075                     20 bp    DNA          linear    PAT 18-DEC-2003
DEFINITION   Sequence 5 from patent US 6641818.
ACCESSION   AR428075
VERSION     AR428075.1 GI:40187443
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Spear, P.G., Warner, M.S., Geraghty, R.J., Martinez, W.M.,
            Montgomery, R.I., Cohen, G.H., Eisenberg, R.J., Whitbeck, C.J. and
            Kruppenacher, C.
TITLE      Cellular proteins which mediate herpesvirus entry
JOURNAL     Patent: US 6641818-A 5 04-NOV-2003;
FEATURES    Location/Qualifiers
             source
               1..20
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 973 GATGCGAGCGACCCAGCAG 991
      ||||||||||||||||
DB 2 GAAGCAGCAGCACCAGCAG 20

RESULT 67
AX053083/c
LOCUS       AX053083                     20 bp    DNA          linear    PAT 12-JAN-2001
DEFINITION   Sequence 7 from Patent WO0071703.
ACCESSION   AX053083
VERSION     AX053083.1 GI:12227140
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct; other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Macleod, A.R., Li, Z. and Besterman, J.M.
TITLE      Inhibition of histone deacetylase
JOURNAL     Patent: WO 0071703-A 7 30-NOV-2000;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
             source
               1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="synthetic oligonucleotide"

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAG 1429
      ||||||||||||||||
DB 20 GCAGCAGCAGCAGCAGGAG 2

RESULT 68
AX053092/c
LOCUS       AX053092                     20 bp    DNA          linear    PAT 12-JAN-2001
DEFINITION   Sequence 16 from Patent WO0071703.
ACCESSION   AX053092
VERSION     AX053092.1 GI:12227149
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct; other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Besterman, J.M., Macleod, A.R. and Siders, W.M.
TITLE      Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243290-A 52 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
             source
               1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"

AUTHORS    Macleod, A.R., Li, Z. and Besterman, J.M.
TITLE      Inhibition of histone deacetylase
JOURNAL     Patent: WO 0071703-A 16 30-NOV-2000;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
             source
               1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Antisense oligonucleotide"

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1456 GCAACAGCACACGCAACAG 1474
      ||||||||||||||||
DB 19 GAAACAGCAACAGCAACAG 1

RESULT 70
AX546303/c
LOCUS       AX546303                     20 bp    DNA          linear    PAT 26-NOV-2002
DEFINITION   Sequence 52 from Patent EP1243290.
ACCESSION   AX546303
VERSION     AX546303.1 GI:25811494
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct; other sequences; artificial sequences.
REFERENCE   1
AUTHORS    Besterman, J.M., Macleod, A.R. and Siders, W.M.
TITLE      Modulation of gene expression by combination therapy
JOURNAL     Patent: EP 1243290-A 52 25-SEP-2002;
            Methylgene, Inc. (CA)
FEATURES    Location/Qualifiers
             source
               1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
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/db_xref="taxon:32630"
/notes="oligonucleotide"

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAGCAG 1429
    |||||
Db 20 GCAGCAGCAGCAGCAGCAGCAG 2

RESULT 71
AX546393/c
LOCUS
DEFINITION
Sequence 52 from Patent EP1243289.
ACCESSION
AX546393
VERSION
AX546393.1 GI:25811584
KEYWORDS
synthetic construct
SOURCE
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Besterman,J.M., Macleod,A.R. and Siders,W.M.
TITLE
Modulation of gene expression by combination therapy
JOURNAL
Patent: EP 1243289-A 52 25-SEP-2002;
Methylgene, Inc. (CA)
FEATURES
Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="oligonucleotide"

Query Match      0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAGCAG 1429
    |||||
Db 20 GCAGCAGCAGCAGCAGCAGCAG 2

RESULT 72
BD266062
LOCUS
DEFINITION
Universal arrays.
ACCESSION
BD266062
VERSION
BD266062.1 GI:33075830
KEYWORDS
JP 2002539849-A/62.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 21)
AUTHORS
Fan,J.B., Hirschhorn,J.N., Huang,X., Kaplan,P., Lander,E.S.,
Lockhart,D.J., Ryder,T. and Sklar,P.
TITLE
Universal arrays
JOURNAL
Patent: JP 2002539849-A 62 26-NOV-2002;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH,AFFYMETRIX INC
COMMENT
OS Homo sapiens (human)
PN JP 2002539849-A/62
PD 26-NOV-2002
PF 27-MAR-2000 JP 2000608794
PR 26-MAR-1999 US 60/126473,23-JUN-1999 US 60/140359 PI
JIAN BING FAN,JOEL N HIRSCHORN,XIAOHUA
HUANG,PAUL KAPLAN,ERIC
PI S LANDER,
PC DAVID J LOCKHART,THOMAS RYDER,PAMELA SKLAR
G01N33/566,
PC C12Q1/68,C12M1/00,C12N15/09,C12N15/09,G01N33/53, PC
G01N33/566,
CC G01N37/00,C12N15/00,C12N15/00,C12N15/00
variation
/note="n' represents a polymorphic base"

PH Key Location/Qualifiers
FT source 1..21
/organism='Homo sapiens (human)'

FEATURES
source
1..21
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1404 AGCAACAGCAGCAGCAGCAGCAGC 1424
    |||||
Db 1 AGCAACAGCAGCAGCAGCAGCAGC 21

RESULT 73
CQ821171/c
LOCUS
DEFINITION
Sequence 1 from Patent WO2004046377.
ACCESSION
CQ821171
VERSION
CQ821171.1 GI:48715855
KEYWORDS
synthetic construct
SOURCE
ORGANISM
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Casari,G., de Fusco,M. and Marconi,R.
TITLE
Diagnostic and therapeutic means for pathologies associated with
alpha 2 subunit of the na, k pump
JOURNAL
Patent: WO 2004046377-A 1 03-JUN-2004;
FONDAZIONE CENTRO SAN ROMANELLO DEL MONTE TABOR (IT)
FEATURES
Location/Qualifiers
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2296 ACAGAGAAACCCAAAGCAA 2314
    |||||
Db 21 ACAGAGAAACCCAAAGCAA 3

RESULT 74
AX146085
LOCUS
DEFINITION
Sequence 276 from Patent WO0134840.
ACCESSION
AX146085
VERSION
AX146085.1 GI:14284603
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Au,K.G., Chen,J.G., Patil,N. and Thomas,D.
TITLE
Genetic compositions and methods
JOURNAL
Patent: WO 0134840-A 276 17-MAY-2001;
GLAXO GROUP LIMITED (GB) ; Affymetrix, Inc. (US)
FEATURES
Location/Qualifiers
source
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

variation
/note="n' represents a polymorphic base"

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Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1440 AACAGCAGCAGCAGCA 1459
|||||
Db 2 AACAGCAGCAGCAGCCA 21

RESULT 75
AX697037/c
LOCUS AX697037 21 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 105 from Patent WO0078961.
ACCESSION AX697037
VERSION AX697037.1 GI:29498021
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,
Eaton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,
Godowski, P.J., Gurney, A.L., Smith, V., Tumas, D., Wood, W.I.,
Grimaldi, C.J., Hillian, K.J., Paoni, N.F., Roy, M.A. and Watanabe, C.K.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0078961-A 105 28-DEC-2000;
Genentech Inc. (US)
FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCAGC 1418
|||
Db 20 CAGGAGCAACAGCAGCAGC 2

RESULT 76
AX753820
LOCUS AX753820 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 167 from Patent WO03037931.
ACCESSION AX753820
VERSION AX753820.1 GI:32166517
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Shannon, M. and Phan, T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 167 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAGCAGC 1445
|||||
Db 1 GCAGCAGCAGCAGCAGC 17

RESULT 77
AX753821
LOCUS AX753821 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 168 from Patent WO03037931.
ACCESSION AX753821
VERSION AX753821.1 GI:32166518
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Shannon, M. and Phan, T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 168 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1430 CAGCAGCAGCAACAGCA 1446
|||||
Db 1 CAGCAGCAGCAACAGCA 17

RESULT 78
AX753822
LOCUS AX753822 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 169 from Patent WO03037931.
ACCESSION AX753822
VERSION AX753822.1 GI:32166519
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
Shannon, M. and Phan, T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 169 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1431 AGCAGCAGCAACAGCAGC 1447
|||||
Db 1 AGCAGCAGCAACAGCAGC 17

RESULT 79
AX753823
LOCUS AX753823 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 170 from Patent WO03037931.
ACCESSION AX753823
VERSION AX753823.1 GI:32166520
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 170 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1432 GCAGCAGCAACAGCAGC 1448
Db 1 GCAGCAGCAACAGCAGC 17

RESULT 80
AX753824
LOCUS AX753824 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 171 from Patent WO03037931.
ACCESSION AX753824
VERSION AX753824.1 GI:32166521
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 171 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1400 CAGCAGCAACAGCAGCA 1416
Db 1 CAGCAGCAACAGCAGCA 17

RESULT 81
AX753825
LOCUS AX753825 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 172 from Patent WO03037931.
ACCESSION AX753825
VERSION AX753825.1 GI:32166522
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 172 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 170 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1401 AGCAGCAACAGCAGCAG 1417
Db 1 AGCAGCAACAGCAGCAG 17

RESULT 82
AR083088
LOCUS AR083088 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 2 from patent US 5976803.
ACCESSION AR083088
VERSION AR083088.1 GI:10009878
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Meek,K.D.
TITLE Genetic test for equine severe combined immunodeficiency disease
JOURNAL Patent: US 5976803-A 2 02-NOV-1999;
FEATURES
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GGGAGAATCTCTCTGCA 271
Db 1 GGGAGAATCTCTCTGCA 17

RESULT 83
AR139665/c
LOCUS AR139665/c 21 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 3 from patent US 6207390.
ACCESSION AR139665
VERSION AR139665.1 GI:14482161
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cantor,C.R. and Sano,T.
TITLE Methods for the use of reduced affinity streptavidin
JOURNAL Patent: US 6207390-A 3 27-MAR-2001;
FEATURES
source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1425 AGCAGCAGCAGCAGCAA 1441
Db 19 AGCAGCAGCAGCAGCAA 3

RESULT 84
AR159548
LOCUS AR159548 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6251589.
ACCESSION AR159548
VERSION AR159548.1 GI:16222233
KEYWORDS
```

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tsuchi, S. and Sanpei, K.
TITLE Method for diagnosing spinocerebellar ataxia type 2 and primers therefor
JOURNAL Patent: US 6251589-A 8 26-JUN-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1448 CAGCAGCAGCAACAGCAACA 1467
|||||
Db 1 CACCACGACAGCAACA 20
RESULT 85
LOCUS BD177753 20 bp DNA linear PAT 16-APR-2003
DEFINITION A method for snp typing.
ACCESSION BD177753
VERSION BD177753.1 GI:30015016
KEYWORDS JP 2002300894-A/43.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakamura, Y., Tanaka, T., Onishi, Y., Ozaki, K. and Yamada, A.
TITLE A method for snp typing
JOURNAL Patent: JP 2002300894-A 43 15-OCT-2002;
COMMENT THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
OS Artificial Sequence
PN JP 2002300894-A/43
PD 15-OCT-2002
PF 29-JAN-2002 JP 2002019752
PI YUSUKE NAKAMURA, TOSHIHIRO TANAKA, YOZO ONISHI, KOICHI OZAKI, PI AKIRA YAMADA
PC C12N15/09, C12Q1/68, C12N15/00
FH Description of Artificial Sequence: Primer
CC Key Location/Qualifiers
FT source 1..20
FT /organism="Artificial Sequence".
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1601 CAGCAGCAGCAACCAACATC 1620
|||||
Db 1 CAGCAGCAACCAACCGTC 20
RESULT 86
LOCUS CQ830190/c 20 bp DNA linear PAT 12-JUL-2004
DEFINITION Sequence 45 from Patent WO2004055049.
ACCESSION CQ830190
VERSION CQ830190.1 GI:50250683
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Morgan, R.G., Pettengell, R., Forraz, N.P. and Mcquckin, C.P.
TITLE Peptides impairing Pbx dependent gene regulation
JOURNAL Patent: WO 2004055049-A 45 01-JUL-2004;
ST. GEORGE'S ENTERPRISES LIMITED (GB)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 67 CAATCAGAGCAGCGGAGG 86
|||||
Db 20 CAATCAGAGGAGCGGAGG 1
RESULT 87
LOCUS A91543 21 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 70 from Patent WO9824928.
ACCESSION A91543
VERSION A91543.1 GI:6740498
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Pallisgaard, N. and Hokland, P.
TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES
JOURNAL Patent: WO 9824928-A 70 11-JUN-1998;
PALLISGAARD NIELS (DK); HOKLAND PETER (DK)
FEATURES Location/Qualifiers
source 1..21
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 815 TCTGCCCTCTCCACTTCGTC 834
|||||
Db 2 TCTGCCCTCTCCACTTTGTC 21
RESULT 88
LOCUS AX458851 21 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 91 from Patent WO0209295.
ACCESSION AX458851
VERSION AX458851.1 GI:21725463
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Shockey, J.M., Schnurr, J. and Browne, J.A.
TITLE Plant acyl-coa synthetases
JOURNAL Patent: WO 0209295-A 91 31-JAN-2002;
Shockey, Judy M. (US); Schnurr, Judy (US); Browne, John A. (US)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic"
Query Match 0.4%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0; Matches 18; Conservative 0; Mismatches 2;

QY 2902 CAGGGCTTTTCAAGGAAGT 2921
Db 2 CAGGGCTTCTCAGGAATG 21

RESULT 89
BD023325
LOCUS 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting abnormality in chromosome.
ACCESSION BD023325
VERSION BD023325.1 GI:22564548
KEYWORDS JP 2001505428-A/70.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 21)
AUTHORS Parigard, N. and Hukurando, P.
TITLE Method for detecting abnormality in chromosome
JOURNAL Patent: JP 2001505428-A 70 24-APR-2001;
NEILLS PARIGARD
COMMENT PN JP 2001505428-A/70
PD 24-APR-2001
PF 08-DEC-1997 JP 1998525090
PI NEILLS PARIGARD, PATER HOKURANDO
PC C12N15/09, C12Q1/68 G01N33/50, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'DNA (synthetic)'
FH Key Location/Qualifiers.
FEATURES
source 1..21
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.3e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 815 TCTGCCCTTCCACTTCGTC 834
Db 2 TCTGCCCTTCCACTTCGTC 21

RESULT 90
AR084526
LOCUS 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 15 from patent US 5981185.
ACCESSION AR084526
VERSION AR084526.1 GI:10011297
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 15 09-NOV-1999;
FEATURES
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1576 ACAACACACACACACA 1593
Db 1 ACAACACACACACACA 18

RESULT 91
AR084527
LOCUS 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 16 from patent US 5981185.
ACCESSION AR084527
VERSION AR084527.1 GI:10011298
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 16 09-NOV-1999;
FEATURES
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1574 CAACACACACACACAA 1591
Db 1 CAACACACACACACAA 18

RESULT 92
AR121115
LOCUS 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6159697.
ACCESSION AR121115
VERSION AR121115.1 GI:14104691
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Monia, B.P. and Cowser, L.M.
TITLE Antisense modulation of Smad7 expression
JOURNAL Patent: US 6159697-A 11 12-DEC-2000;
FEATURES
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1406 CAACACACACACACAG 1423
Db 1 CGACACACACACACAG 18

RESULT 93
BD266206
LOCUS 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Universal arrays.
ACCESSION BD266206
VERSION BD266206.1 GI:33075974
KEYWORDS JP 2002539849-A/206.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Fan, J.B., Hirschhorn, J.N., Huang, X., Kaplan, P., Lander, E.S., Lockhart, D.J., Ryder, T. and Sklar, P.
TITLE Universal arrays

JOURNAL	PATENT: JP 2002539849-A 206 26-NOV-2002;
COMMENT	WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
OS	Artificial Sequence
PN	JP 2002539849-A/206
PD	26-NOV-2002
PF	27-MAR-2000 JP 2000608794
PR	26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359 PI
PT	JIAN BING FAN, JOEL N HIRSCHORN, XIAOHUA HUANG, PAUL KAPLAN, ERIC S LANDER,
PI	DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
PC	C12Q1/68, C12M1/00, C12N15/09, C12N15/09, C12N15/09, G01N33/53, PC G01N33/566,
CC	G01N37/00, C12N15/00, C12N15/00, C12N15/00
PP	Primer
FH	Key Location/Qualifiers
FT	source 1..18 /organism='Artificial Sequence'.
FEATURES	Location/Qualifiers source 1..18 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"
Query Match	0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity	94.4%; Pred. No. 1.1e+02;
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	1395 AGCAACAGCAGCACGAC 1412
Db	1 AGCAACAGCAGCACGAC 18
RESULT 94	
BD230280	20 bp DNA linear PAT 17-JUL-2003
LOCUS	Total genome radiation hybrid map of canine genome and its use for identification of interesting genes.
DEFINITION	BD230280
ACCESSION	BD230280.1 GI:33040050
VERSION	JP 2002530091-A/149.
KEYWORDS	Canis familiaris (dog)
SOURCE	Canis familiaris
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE	Galibert,F. and Andre,C. Total genome radiation hybrid map of canine genome and its use for identification of interesting genes Patent: JP 2002530091-A 149 17-SEP-2002;
AUTHORS	CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
TITLE	Canis familiaris (dog)
JOURNAL	PN Canis familiaris (dog) PS JP 2002530091-A/149 PD 17-SEP-2002 PF 15-NOV-1999 JP 2000582596 PR 13-NOV-1998 US 60/108193 PI FRANCIS GALIBERT CATHERINE ANDRE PC C12N15/09, C12Q1/68, C12N15/00 CC A0102 Key Location/Qualifiers FT source 1..20 /organism='Canis familiaris (dog)'.
FEATURES	Location/Qualifiers source 1..20 /organism="Canis familiaris" /mol_type="genomic DNA" /db_xref="taxon:9615"
Query Match	0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity	94.4%; Pred. No. 1.3e+02;
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
JOURNAL	PAT 25-JUN-2003

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS      Holmberg, J. and Frisen, J.
TITLE        Method of proliferation in neurogenic regions
JOURNAL      Patent: WO 03040304-A 9 15-MAY-2003;
Neuronova AB (SE)
FEATURES
source       Location/Qualifiers
1..20
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer"

Query Match      0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1407 AACAGCAGCAGCAGCAGC 1424
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DB 19 AACAGCAGGAGCAGCAGC 2

RESULT 98
AX764066/c
LOCUS          AX764066          20 bp      DNA      linear      PAT 25-JUN-2003
DEFINITION     Sequence 11 from Patent WO03040304.
ACCESSION      AX764066
VERSION        AX764066.1 GI:32258390
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
1
REFERENCE
AUTHORS      Holmberg, J. and Frisen, J.
TITLE        Method of proliferation in neurogenic regions
JOURNAL      Patent: WO 03040304-A 11 15-MAY-2003;
Neuronova AB (SE)
FEATURES
source       Location/Qualifiers
1..20
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="PCR Primer"

Query Match      0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1407 AACAGCAGCAGCAGCAGC 1424
|||||
DB 19 AACAGCAGGAGCAGCAGC 2

RESULT 99
AX273039
LOCUS          AX273039          17 bp      RNA      linear      PAT 29-OCT-2001
DEFINITION     Sequence 608 from Patent WO0162911.
ACCESSION      AX273039
VERSION        AX273039.1 GI:16545776
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and
Ellis, J.H.
TITLE        Method and reagent for the inhibition of grid
JOURNAL      Patent: WO 0162911-A 608 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source       Location/Qualifiers
1..17
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 975 TGCAGCAGCAGCAGCA 990
|||||
DB 2 TGCAGCAGCAGCAGCA 17

RESULT 100
AX753819
LOCUS          AX753819          17 bp      DNA      linear      PAT 23-JUN-2003
DEFINITION     Sequence 166 from Patent WO03037931.
ACCESSION      AX753819
VERSION        AX753819.1 GI:32166516
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Shannon, M. and Phan, T.
TITLE        Human angiomotin-like protein 1
JOURNAL      Patent: WO 03037931-A 166 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source       Location/Qualifiers
1..17
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACAG 1444
|||||
DB 2 GCAGCAGCAGCAACAG 17

RESULT 101
AX753826
LOCUS          AX753826          17 bp      DNA      linear      PAT 23-JUN-2003
DEFINITION     Sequence 173 from Patent WO03037931.
ACCESSION      AX753826
VERSION        AX753826.1 GI:32166523
KEYWORDS       Homo sapiens (human)
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS      Shannon, M. and Phan, T.
TITLE        Human angiomotin-like protein 1
JOURNAL      Patent: WO 03037931-A 173 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source       Location/Qualifiers
1..17
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1402 GCAGCAACAGCAGCAG 1417
|||||
DB 1 GCAGCAACAGCAGCAG 16
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TITLE		Ribozyme therapy for the treatment of proliferative skin and eye diseases	
JOURNAL	Patent: WO 0130362-A 203 03-MAY-2001;		
IMMUSOL, INC. (US)			
FEATURES	Location/Qualifiers		
source	1..19		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
	/note="Cdk2 ribozyme binding site"		
Query Match		0.4%; Score 15.8; DB 1; Length 19;	
Best Local Similarity		89.5%; Pred. No. 1.4e+02;	
Matches	17; Conservative	0; Mismatches	2; Indels
		0; Gaps	0;
QY	930 AGCAGCTCAACAGATAGC 948		
Db	19 AGCAGCTGGACAGATAGC 1		
RESULT 105			
AR241963/c	LOCUS	33 bp DNA	linear
AR241963	DEFINITION	Sequence 251 from patent US 6472154.	
AR241963	ACCESSION		
AR241963.1	VERSION	GI:27287775	
AR241963.1	KEYWORDS	Unknown.	
AR241963.1	SOURCE	Unknown.	
AR241963.1	ORGANISM	Unknown.	
AR241963.1	REFERENCE	1 (bases 1 to 33)	
AR241963.1	AUTHORS	Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.	
AR241963.1	TITLE	Polymorphic repeats in human genes	
AR241963.1	JOURNAL	Patent: US 6472154-A 251 29-OCT-2002;	
AR241963.1	FEATURES	Location/Qualifiers	
AR241963.1	source	1..33	
AR241963.1		/organism="unknown"	
AR241963.1		/mol_type="genomic DNA"	
Query Match		0.4%; Score 15.6; DB 1; Length 33;	
Best Local Similarity		70.0%; Pred. No. 3e+02;	
Matches	21; Conservative	0; Mismatches	9; Indels
		0; Gaps	0;
QY	1925 CAGCACTTCTTCTCCAGCAGCAGATGCTG 1954		
Db	30 CTGCTACTGCTGCTGCTGCTGCTGCTG 1		
RESULT 106			
AR190113/c	LOCUS	17 bp DNA	linear
AR190113	DEFINITION	Sequence 5601 from patent US 6346398.	
AR190113	ACCESSION		
AR190113.1	VERSION	GI:20236078	
AR190113.1	KEYWORDS	Unknown.	
AR190113.1	SOURCE	Unknown.	
AR190113.1	ORGANISM	Unknown.	
AR190113.1	REFERENCE	1 (bases 1 to 17)	
AR190113.1	AUTHORS	Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.	
AR190113.1	TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor	
AR190113.1	JOURNAL	Patent: US 6346398-A 5601 12-FEB-2002;	
AR190113.1	FEATURES	Location/Qualifiers	
AR190113.1	source	1..17	
AR190113.1		/organism="unknown"	
AR190113.1		/mol_type="unassigned DNA"	
Query Match		0.4%; Score 15.4; DB 1; Length 17;	
Best Local Similarity		94.1%; Pred. No. 1.2e+02;	
Matches	16; Conservative	0; Mismatches	1; Indels
		0; Gaps	0;
QY	326 TTGCCTATGAGCCAAAGC 342		

RESULT 102		PAT 26-SEP-2002	
AR224718/c	LOCUS	20 bp DNA	linear
AR224718	DEFINITION	Sequence 23 from patent US 6440739.	
AR224718	ACCESSION		
AR224718.1	VERSION	GI:23333558	
AR224718.1	KEYWORDS	Unknown.	
AR224718.1	SOURCE	Unknown.	
AR224718.1	ORGANISM	Unknown.	
AR224718.1	REFERENCE	1 (bases 1 to 20)	
AR224718.1	AUTHORS	Bennett,C.F. and Freier,S.M.	
AR224718.1	TITLE	Antisense modulation of glioma-associated oncogene-2 expression	
AR224718.1	JOURNAL	Patent: US 6440739-A 23 27-AUG-2002;	
AR224718.1	FEATURES	Location/Qualifiers	
AR224718.1	source	1..20	
AR224718.1		/organism="unknown"	
AR224718.1		/mol_type="genomic DNA"	
Query Match		0.4%; Score 16; DB 1; Length 20;	
Best Local Similarity		100.0%; Pred. No. 1.4e+02;	
Matches	16; Conservative	0; Mismatches	0; Indels
		0; Gaps	0;
QY	1427 CAGCAGCAGCAGCAAC 1442		
Db	17 CAGCAGCAGCAGCAAC 2		
RESULT 103			
AX167902/c	LOCUS	20 bp DNA	linear
AX167902	DEFINITION	Sequence 86 from Patent WO0142307.	PAT 03-JUL-2001
AX167902	ACCESSION		
AX167902.1	VERSION	GI:14597222	
AX167902.1	KEYWORDS	synthetic construct	
AX167902.1	SOURCE	other sequences; artificial sequences.	
AX167902.1	ORGANISM	synthetic construct	
AX167902.1	REFERENCE	1	
AX167902.1	AUTHORS	Saito,K., Ohe,N. and Satoh,H.	
AX167902.1	TITLE	Mutant er_g(a) and test systems for transactivation	
AX167902.1	JOURNAL	Patent: WO 0142307-A 86 14-JUN-2001;	
AX167902.1	FEATURES	Sumitomo Chemical Company, Limited (JP)	
AX167902.1	source	Location/Qualifiers	
AX167902.1		1..20	
AX167902.1		/organism="synthetic construct"	
AX167902.1		/mol_type="unassigned DNA"	
AX167902.1		/db_xref="taxon:32630"	
AX167902.1		/note="Designed oligonucleotide primer for PCR"	
Query Match		0.4%; Score 16; DB 1; Length 20;	
Best Local Similarity		100.0%; Pred. No. 1.4e+02;	
Matches	16; Conservative	0; Mismatches	0; Indels
		0; Gaps	0;
QY	986 CAGCAGCAGCAGCAGC 1001		
Db	18 CAGCAGCAGCAGCAGC 3		
RESULT 104			
AX128985/c	LOCUS	19 bp DNA	linear
AX128985	DEFINITION	Sequence 203 from Patent WO0130362.	PAT 15-MAY-2001
AX128985	ACCESSION		
AX128985.1	VERSION	GI:14135290	
AX128985.1	KEYWORDS	Homo sapiens (human)	
AX128985.1	SOURCE	Homo sapiens	
AX128985.1	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AX128985.1	REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AX128985.1	AUTHORS	Robbins,J.M. and Tritz,R.	


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Db      17 TTGCCTGTGAGCCAAGC 1
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RESULT 107
AR325089/C
LOCUS   AR325089          17 bp    RNA          linear    PAT 17-AUG-2003
DEFINITION
Sequence 2491 from patent US 6566127.
ACCESSION AR325089
VERSION   AR325089.1 GI:33710897
KEYWORDS
SOURCE   Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE   Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 2491 20-MAY-2003;
Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 326 TTGCCTATGAGCCAAGC 342
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Db      17 TTGCCTGTGAGCCAAGC 1

RESULT 108
AR401835
LOCUS   AR401835          17 bp    DNA          linear    PAT 18-DEC-2003
DEFINITION
Sequence 175 from patent US 6623962.
ACCESSION AR401835
VERSION   AR401835.1 GI:40149285
KEYWORDS
SOURCE   Unknown.
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE   Enzymatic nucleic acid treatment of diseases of conditions related
JOURNAL to levels of epidermal growth factor receptors
Patent: US 6623962-A 175 23-SEP-2003;
Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3633 GAGAACCTAGAAATCAT 3649
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Db      1 GAGAACCTAGAAATCAT 17

RESULT 109
AX272791
LOCUS   AX272791          17 bp    RNA          linear    PAT 29-OCT-2001
DEFINITION
Sequence 360 from Patent WO0162911.
ACCESSION AX272791
VERSION   AX272791.1 GI:16545528
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE   Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 362 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
source 1..17
/organism="Homo sapiens"

REFERENCE 110
AX272792
LOCUS   AX272792          17 bp    RNA          linear    PAT 29-OCT-2001
DEFINITION
Sequence 361 from Patent WO0162911.
ACCESSION AX272792
VERSION   AX272792.1 GI:16545529
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE   Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 361 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 985 CCAGCAGCAGCAGCAGC 1001
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Db      1 CCTGCAGCAGCAGCAGC 17

RESULT 111
AX272793
LOCUS   AX272793          17 bp    RNA          linear    PAT 29-OCT-2001
DEFINITION
Sequence 362 from Patent WO0162911.
ACCESSION AX272793
VERSION   AX272793.1 GI:16545530
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE   Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 362 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
Location/Qualifiers
source 1..17
/organism="Homo sapiens"

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Df

/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 978 AGCAGCACCGACGACCAG 994
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Db 1 AGCAGCACCGACGACCAG 17

RESULT 112
AX272794 LOCUS linear PAT 29-OCT-2001
DEFINITION Sequence 363 from Patent WO0162911.
ACCESSION AX272794
VERSION AX272794.1 GI:16545531
KEYWORDS Homo sapiens (human)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES source

1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 979 GCAGCACCGACGACCAGC 995
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Db 1 GCAGCACCGACGACCAGC 17

RESULT 113
AX273040 LOCUS RNA linear PAT 29-OCT-2001
DEFINITION Sequence 609 from Patent WO0162911.
ACCESSION AX273040
VERSION AX273040.1 GI:16545777
KEYWORDS Homo sapiens (human)
SOURCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES source

1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 986 CAGCACGCCAGCCAGCC 1002
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Db 1 CAGCACGCCAGCCAGCC 17

ACCESSION AX753827
VERSION AX753827.1 GI:32166524
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Shannon,M. and Phan,T.
AUTHORS Human angiotensin-like protein 1
TITLE Patent: WO 03037931-A 174 08-MAY-2003;
JOURNAL Amersham Biosciences SV Corp. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1505 CAGCAACAGCAGCAGAG 1521
Db 1 CAGCAACAGCAGCAGGG 17
RESULT 117
AX757672/c
LOCUS 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 993 from Patent WO03040369.
ACCESSION AX757672
VERSION AX757672.1 GI:32252288
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 993 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1222 GCAAAAGCCTCAGGATC 1238
Db 17 GCCAAAGCCTCAGGATC 1
RESULT 118
AX761771
LOCUS 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5092 from Patent WO03040369.
ACCESSION AX761771
VERSION AX761771.1 GI:32256387
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Anson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 5092 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3633 GAGAACCTAGAAACAT 3649
Db 1 GAGAACCTAGAAATCAT 17
RESULT 120
AR028606/c
LOCUS 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5858728.
ACCESSION AR028606
VERSION AR028606.1 GI:5940579

TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 5092 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1909 GATCATGGAGCAGAAAC 1925
Db 1 GATCATGTAGCAGAAAC 17
RESULT 119
BD067335
LOCUS 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.
ACCESSION BD067335
VERSION BD067335.1 GI:22612938
KEYWORDS JP 2001511003-A/175.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 175 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT OS Unidentified
PN JP 2001511003-A/175
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1..17
/organism="Unidentified".
FEATURES Location/Qualifiers
source 1..17
/organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3633 GAGAACCTAGAAACAT 3649
Db 1 GAGAACCTAGAAATCAT 17
RESULT 120
AR028606/c
LOCUS 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5858728.
ACCESSION AR028606
VERSION AR028606.1 GI:5940579

KEYWORDS	Unknown.	Query Match	0.4%;	Score 15.4;	DB 1;	Length 18;	
SOURCE	Unknown.	Best Local Similarity	94.1%;	Pred. NO. 1.3e+02;			
ORGANISM	Unclassified.	Matches	16;	Conservative	0;	Mismatches	1;
REFERENCE	1 (bases 1 to 18)						
AUTHORS	Gram, H., Di Padova, F., Barclay, G. Robin. and Poxton, I. Raymond.						
TITLE	Monoclonal antibody against LPS core						
JOURNAL	Patent: US 5858728-A 10-12-JAN-1999;						
FEATURES	Location/Qualifiers						
source	1. .18						
	/organism="unknown"						
	/mol_type="unassigned DNA"						
Query Match	0.4%;	Score 15.4;	DB 1;	Length 18;			
Best Local Similarity	94.1%;	Pred. NO. 1.3e+02;					
Matches	16;	Conservative	0;	Mismatches	1;	Indels	0;
QY	593 AGTCACCTTGACCTGGA 609						
Db	17 AGTCACCTTGACCTGGA 1						
RESULT 121							
LOCUS	AR039671						
DEFINITION	Sequence 519 from patent US 5807743.						
ACCESSION	AR039671						
VERSION	AR039671.1 GI:5959034						
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 18)						
AUTHORS	Stinchcomb, D.T. and McSwiggen, J.A.						
TITLE	Interleukin-2 receptor gamma-chain ribozymes						
JOURNAL	Patent: US 5807743-A 519 15-SEP-1998;						
FEATURES	Location/Qualifiers						
source	1. .18						
	/organism="unknown"						
	/mol_type="unassigned DNA"						
Query Match	0.4%;	Score 15.4;	DB 1;	Length 18;			
Best Local Similarity	94.1%;	Pred. NO. 1.3e+02;					
Matches	16;	Conservative	0;	Mismatches	1;	Indels	0;
QY	993 AGCACCAGCCTACCAAC 1009						
Db	1 AGCCCCAGCCTACCAAC 17						
RESULT 122							
LOCUS	AX449138						
DEFINITION	Sequence 9 from Patent WO0229034.						
ACCESSION	AX449138						
VERSION	AX449138.1 GI:21697941						
KEYWORDS	synthetic construct						
SOURCE	synthetic construct						
ORGANISM	Other sequences; artificial sequences.						
REFERENCE	1						
AUTHORS	Ramos, J.L., Ben-Bassat, A., Godoy, P., Ramos-Gonzales, M.I. and Duque, E.						
TITLE	Methods for production of p-hydroxybenzoate in bacteria						
JOURNAL	Patent: WO 0229034-A 9 11-APR-2002;						
FEATURES	E.I. DUPONT DE NEMOURS AND COMPANY (US)						
source	Location/Qualifiers						
	1. .18						
	/organism="synthetic construct"						
	/mol_type="unassigned DNA"						
	/db_xref="taxon:32630"						
	/note="Primer"						
Query Match	0.4%;	Score 15.4;	DB 1;	Length 18;			
Best Local Similarity	94.1%;	Pred. NO. 1.3e+02;					
Matches	16;	Conservative	0;	Mismatches	1;	Indels	0;
QY	977 CAGCAGCACCAGCAGCA 993						
Db	1 CAGCAGCACCAGCAGCATCA 17						
RESULT 123							
LOCUS	AX453148						
DEFINITION	Sequence 27 from Patent WO0242444.						
ACCESSION	AX453148						
VERSION	AX453148.1 GI:21712655						
KEYWORDS	synthetic construct						
SOURCE	synthetic construct						
ORGANISM	Other sequences; artificial sequences.						
REFERENCE	1						
AUTHORS	Yoder, O., Turgeon, B.G. and Lu, S.W.						
TITLE	Fungal gene cluster associated with pathogenesis						
JOURNAL	Patent: WO 0242444-A 27 30-MAY-2002;						
FEATURES	Syngenta Participations AG (CH) ; CORNELL RESEARCH FOUNDATION, INC. (US) ; Yoder, Olen (US) ; Turgeon, Barbara G. (US) ; Lu, Shen-wen (US)						
source	Location/Qualifiers						
	1. .18						
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	/mol_type="unassigned DNA"						
	/db_xref="taxon:32630"						
	/note="Primer"						
Query Match	0.4%;	Score 15.4;	DB 1;	Length 18;			
Best Local Similarity	94.1%;	Pred. NO. 1.3e+02;					
Matches	16;	Conservative	0;	Mismatches	1;	Indels	0;
QY	978 AGCAGCACCAGCAGCAG 994						
Db	18 AGAAGCACCAGCAGCAG 2						
RESULT 124							
LOCUS	BD175148/c						
DEFINITION	Established periodontal cells.						
ACCESSION	BD175148						
VERSION	BD175148.1 GI:29120842						
KEYWORDS	JP 2002262862-A/16.						
SOURCE	synthetic construct						
ORGANISM	synthetic construct						
REFERENCE	1 (bases 1 to 19)						
AUTHORS	Miki, M., Kubota, M., Mitani, H., Obinata, M. and Ueda, M.						
TITLE	Established periodontal cells						
JOURNAL	Patent: JP 2002262862-A 16 17-SEP-2002;						
COMMENT	TOHOKU TECHNO ARCH CO LTD						
	OS Artificial Sequence						
	PN JP 2002262862-A/16						
	PD 17-SEP-2002						
	PF 12-MAR-2001 JP 2001069249						
	PI MIRI MIKI, MAMORU KUBOTA, HIDEO MITANI, MASUO OBINATA, MASATSUGU UEDA						
	PC C12N5/10, A01K67/027, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50// PC						
	C12N5/09, (C12R1:91), C12N5/00, C12N15/00, (C12N5:00, C12R1:91) CC						
	Description of Artificial Sequence: Oligonucleotide to act as a primer for						
	CC PCR						
	FH Key						
	FT source						
	FT						
FEATURES	Location/Qualifiers						
	1. .19						
	/organism='Artificial Sequence'.						
	/note="Primer"						

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1575 AACACAAACAGCAACAA 1591
DB 19 AACACAAACAGCAACAA 3

RESULT 125
AX129105
LOCUS      AX129105
DEFINITION Sequence 323 from Patent WO0130362.
ACCESSION AX129105
VERSION    AX129105.1 GI:14135410
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Robbins,J.M. and Tritz,R.
TITLE       Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL     Patent: WO 0130362-A 323 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES    source
            1. .19
            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="Cdk3 ribozyme binding site"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2942 TTGTGACTTCCTCAGCCA 2958
DB 3 TTGTGACTTCCTCAGCCA 19

RESULT 126
AX129106
LOCUS      AX129106
DEFINITION Sequence 324 from Patent WO0130362.
ACCESSION AX129106
VERSION    AX129106.1 GI:14135411
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Robbins,J.M. and Tritz,R.
TITLE       Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL     Patent: WO 0130362-A 324 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES    source
            1. .19
            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            /note="Cdk3 ribozyme binding site"

Query Match      0.4%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;

source      1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GGTTCCTTGAAAAGA 163
DB 17 GGTTCCTTGAAAAGA 3

RESULT 128
AX753818
LOCUS      AX753818
DEFINITION Sequence 165 from Patent WO03037931.
ACCESSION AX753818
VERSION    AX753818.1 GI:32166515
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Shannon,M. and Phan,T.
TITLE       Human angiotensin-like protein 1
JOURNAL     Patent: WO 03037931-A 165 08-MAY-2003;
            Amersham Biosciences SV Corp. (US)
FEATURES    source
            1. .17
            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACA 1443
DB 3 GCAGCAGCAGCAACA 17

RESULT 129
AR078304/c

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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2942 TTGTGACTTCCTCAGCCA 2958
DB 2 TTGTGACTTCCTCAGCCA 18

RESULT 127
AX737070/c
LOCUS      AX737070
DEFINITION Sequence 2660 from Patent WO03025177.
ACCESSION AX737070
VERSION    AX737070.1 GI:30516358
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijinder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL     Patent: WO 03025177-A 2660 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES    source
            1. .17
            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GGTTCCTTGAAAAGA 163
DB 17 GGTTCCTTGAAAAGA 3

RESULT 128
AX753818
LOCUS      AX753818
DEFINITION Sequence 165 from Patent WO03037931.
ACCESSION AX753818
VERSION    AX753818.1 GI:32166515
KEYWORDS   Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1
AUTHORS     Shannon,M. and Phan,T.
TITLE       Human angiotensin-like protein 1
JOURNAL     Patent: WO 03037931-A 165 08-MAY-2003;
            Amersham Biosciences SV Corp. (US)
FEATURES    source
            1. .17
            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1429 GCAGCAGCAGCAACA 1443
DB 3 GCAGCAGCAGCAACA 17

RESULT 129
AR078304/c

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LOCUS AR078304 31 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 14 from patent US 5962332.
ACCESSION AR078304
VERSION AR078304.1 GI:10005050
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS Singer,R.H. and Taneja,K.L.
TITLE Detection of trinucleotide repeats by in situ hybridization
JOURNAL Patent: US 5962332-A 14 05-OCT-1999;
FEATURES
Location/Qualifiers
1..31
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15; DB 1; Length 31;
Best Local Similarity 67.7%; Pred. No. 3.1e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1924 ACAGCACTTTCTTCAGCAGCAGATGCTG 1954
Db 31 ACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
RESULT 130
LOCUS AR084540 33 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 29 from patent US 5981185.
ACCESSION AR084540
VERSION AR084540.1 GI:10011311
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 33)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 29 09-NOV-1999;
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15; DB 1; Length 33;
Best Local Similarity 67.7%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1409 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1439
Db 1 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 31
RESULT 131
LOCUS AR096353 18 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 24 from patent US 6007995.
ACCESSION AR096353
VERSION AR096353.1 GI:10025087
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Baker,B.F. and Cowsert,L.M.
TITLE Antisense inhibition of TNFR1 expression
JOURNAL Patent: US 6007995-A 24 28-DEC-1999;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1406 CAACAGCAGCAGCAGCAGCAG 1423
Db 1 CACCAGCGCAGCAGCAGCAG 18
RESULT 132
LOCUS AR096354 18 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 25 from patent US 6007995.
ACCESSION AR096354
VERSION AR096354.1 GI:10025089
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Baker,B.F. and Cowsert,L.M.
TITLE Antisense inhibition of TNFR1 expression
JOURNAL Patent: US 6007995-A 25 28-DEC-1999;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 977 CAGCAGCAGCAGCAGCAGCAGCAG 994
Db 1 CAGGAGCAGCAGCAGCAGCAG 18
RESULT 133
LOCUS AR122214 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 60 from patent US 6165713.
ACCESSION AR122214
VERSION AR122214.1 GI:14106531
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Liskay,R.M., Bronner,C.Eric., Baker,S.M., Bollag,R.J. and Kolodner,R.D.
TITLE Composition and methods relating to DNA mismatch repair genes
JOURNAL Patent: US 6165713-A 60 26-DEC-2000;
FEATURES
Location/Qualifiers
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1223 CAAAAGCCTCAGGATCTC 1240
Db 1 CAAAAGCTTCAGATCTC 18
RESULT 134
LOCUS AR131188 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 60 from patent US 6191268.
ACCESSION AR131188
VERSION AR131188.1 GI:14119513
KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Liskay,R.M., Bronner,C.Eric., Baker,S.M., Bollag,R.J. and
              Kolodner,R.D.
TITLE        Compositions and methods relating to DNA mismatch repair genes
JOURNAL      Patent: US 6191268-A 60 20-FEB-2001;
FEATURES     Location/Qualifiers
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                1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1223 CAAAGCCTCAGGATCTC 1240
Db 1 CAAAGCCTCAGGATCTC 18

RESULT 135
LOCUS      AR142758          18 bp      DNA          linear      PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6204008.
ACCESSION  AR142758
VERSION     AR142758.1 GI:15104044
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Borneman,W.Scott., Goyal,A., Conder,M.J. and Vinci,V.A.
TITLE        Bioprocess for production of dipeptide based compounds
JOURNAL      Patent: US 6204008-A 3 20-MAR-2001;
FEATURES     Location/Qualifiers
              source
                1..18
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 983 CACCAGCAGCAGCACCAG 1000
Db 1 CACCAGCCTCAGCACCAG 18

RESULT 136
LOCUS      BD217401          18 bp      DNA          linear      PAT 17-JUL-2003
DEFINITION Antisense modulation of TNFR1 expression.
ACCESSION  BD217401
VERSION     BD217401.1 GI:33027171
KEYWORDS    JP 2002519015-A/24.
SOURCE      unidentified
ORGANISM     unidentified
REFERENCE    1 (bases 1 to 18)
AUTHORS      Baker,B.F. and Cowsewrt,L.M.
TITLE        Antisense modulation of TNFR1 expression
JOURNAL      Patent: JP 2002519015-A 24 02-JUL-2002;
COMMENT      ISIS PHARMACEUTICALS INC
              OS Unidentified
              PN JP 2002519015-A/24
              PD 02-JUL-2002
              PF 17-JUN-1999 JP 2000557265
              PR 26-JUN-1998 US 09/106038
              PI BRENDA F BAKER,LEX M COWSERT
              PC

QY 977 CAGCAGCAGCAGCAGCAG 994
Db 1 CAGGAGCAGCAGCGGCAG 18

RESULT 138
LOCUS      E39177/c          18 bp      DNA          linear      PAT 18-JUN-2001
DEFINITION DNA encoding novel fused protein and process for producing useful
```

protein mediating the expression thereof.		protein mediating the expression thereof.	
ACCESSION	E39177	ACCESSION	AR188983
VERSION	E39177.1	VERSION	AR188983.1
KEYWORDS	JP 1999341991-A/23	KEYWORDS	GI:20234948
SOURCE	synthetic construct	SOURCE	Unknown.
ORGANISM	synthetic construct	ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 18)	REFERENCE	1 (bases 1 to 18)
AUTHORS	Seiji, S., Masahiko, H., Toshiyuki, K. and Masaaki, K.	AUTHORS	Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE	DNA encoding novel fused protein and process for producing useful protein mediating the expression thereof	TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: JP 1999341991-A 23 14-DEC-1999;	JOURNAL	Patent: US 6346398-A 4471 12-FEB-2002;
COMMENT	ITO HAM KK JUZO UDAKA	FEATURES	Location/Qualifiers
	OS Artificial Sequence		1..18
	FN JP 1999341991-A/23		/organism="unknown"
	PD 14-DEC-1999		/mol_type="unassigned DNA"
	PF 30-MAR-1999		
	PR JP 1999089488		
	PI SEIJI SATO, MASAHIKO HITAGASHIKUJI, TOSHIYUKI KUDO, MASAOKI KONDO		
	PC C12N15/09, C12N1/21, C12P21/02, C12P21/02, C07K14/62,		
	PC C07K14/655, (C12N15/09, C12R1:08), (C12N1/21, C12R1:08), (C12P21/02,		
	PC C07K19/00, (C12N15/09, C12R1:08), (C12N1/21, C12R1:08),		
	PC C12R1:08),		
	PC C12N15/00, (C12N15/00, C12R1:08)		
	CC		
	FH Key		
	FT source		
	FT Location/Qualifiers		
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	/organism="Artificial Sequence".		
FEATURES	source	FEATURES	source
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	/organism="synthetic construct"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:32630"		
Query Match	0.4%; Score 14.8; DB 1; Length 18;	Query Match	0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity	88.9%; Pred. No. 1.6e+02;	Best Local Similarity	88.9%; Pred. No. 1.6e+02;
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1411 GCAGCAGCAGCAGCAGCA 1428	QY	1094 ACATTGACGCCACAGC 1111
	18 GCAGCAGCAGCAGCAGCA 1		1 ACATGCGCCCACTGAGC 18
RESULT 139		RESULT 141	
156663		AR242052	
LOCUS	Sequence 11 from patent US 5650277.	LOCUS	Sequence 340 from patent US 6472154.
DEFINITION	Sequence 11 from patent US 5650277.	DEFINITION	Sequence 340 from patent US 6472154.
ACCESSION	156663	ACCESSION	AR242052
VERSION	156663.1	VERSION	AR242052.1
KEYWORDS	GI:2477076	KEYWORDS	GI:27287864
SOURCE	Unknown.	SOURCE	Unknown.
ORGANISM	Unknown.	ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 18)	REFERENCE	1 (bases 1 to 18)
AUTHORS	Navot, N. and Eyal, N.	AUTHORS	Garner, H.R., Wren, J.D., Minna, J.D. and Pondon, J.W. III.
TITLE	Method of determining the presence and quantifying the number of di- and trinucleotide repeats	TITLE	Polymorphic repeats in human genes
JOURNAL	Patent: US 5650277-A 11 22-JUL-1997;	JOURNAL	Patent: US 6472154-A 340 29-OCT-2002;
FEATURES	Location/Qualifiers	FEATURES	Location/Qualifiers
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	/mol_type="unassigned DNA"		/mol_type="genomic DNA"
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Best Local Similarity	88.9%; Pred. No. 1.6e+02;	Best Local Similarity	88.9%; Pred. No. 1.6e+02;
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1448 CAGCAGCAGCAGCAGCA 1465	QY	1411 GCAGCAGCAGCAGCAGCA 1428
	1 CACCACGACGACGACGAA 18		1 GCAGCAGCAGCAGCAGCA 18
RESULT 140		RESULT 142	
156663		AR274644/c	
LOCUS	Sequence 11 from patent US 5650277.	LOCUS	Sequence 28 from patent US 6506595.
DEFINITION	Sequence 11 from patent US 5650277.	DEFINITION	Sequence 28 from patent US 6506595.
ACCESSION	156663	ACCESSION	AR274644
VERSION	156663.1	VERSION	AR274644.1
KEYWORDS	GI:2477076	KEYWORDS	GI:29707178
SOURCE	Unknown.	SOURCE	Unknown.
ORGANISM	Unknown.	ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 18)	REFERENCE	1 (bases 1 to 18)
AUTHORS	Navot, N. and Eyal, N.	AUTHORS	Sato, S., Higashikuni, N., Kudo, T. and Kondo, M.
TITLE	Method of determining the presence and quantifying the number of di- and trinucleotide repeats	TITLE	DNA encoding new fusion proteins and processes for preparing useful polypeptides through expression of the DNAs
JOURNAL	Patent: US 5650277-A 11 22-JUL-1997;	JOURNAL	Patent: US 6506595-A 28 14-JAN-2003;
FEATURES	Location/Qualifiers	FEATURES	Location/Qualifiers
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	/organism="unknown"		/organism="unknown"
	/mol_type="unassigned DNA"		/mol_type="genomic DNA"
Query Match	0.4%; Score 14.8; DB 1; Length 18;	Query Match	0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity	88.9%; Pred. No. 1.6e+02;	Best Local Similarity	88.9%; Pred. No. 1.6e+02;
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1448 CAGCAGCAGCAGCAGCA 1465	QY	1411 GCAGCAGCAGCAGCAGCA 1428
	1 CACCACGACGACGACGAA 18		1 GCAGCAGCAGCAGCAGCA 18
RESULT 140		RESULT 142	
156663		AR274644/c	
LOCUS	Sequence 11 from patent US 5650277.	LOCUS	Sequence 28 from patent US 6506595.
DEFINITION	Sequence 11 from patent US 5650277.	DEFINITION	Sequence 28 from patent US 6506595.

/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCACGACGACGACGACGA 1428
DB 18 GCACGACGACGACGACGA 1

RESULT 143
AX3101003
LOCUS AR301003 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 60 from patent US 6538108.
ACCESSION AR301003
VERSION AR301003.1 GI:31688693
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Liskay,R.M., Bronner,C.E., Baker,S.M., Bolleg,R.J. and Kolodner,R.D.
TITLE Compositions and methods relating to DNA mismatch repair genes
JOURNAL Patent: US 6538108-A 60 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1223 CAAAGCCTCAGATCTC 1240
DB 1 CAAAGCTTCAGATCTC 18

RESULT 144
AR324782
LOCUS AR324782 18 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 2184 from patent US 6566127.
ACCESSION AR324782
VERSION AR324782.1 GI:33710590
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2184 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1094 ACATGAGCCGACGAGC 1111
DB 1 ACATGAGCCGACGAGC 18

RESULT 145
AX317750
LOCUS AX317750 18 bp DNA linear PAT 14-DEC-2001

Sequence 11 from Patent WO0190313.
ACCESSION AX317750
VERSION AX317750.1 GI:17900635
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Feinberg,A.T., Strichman-Almashanu,L.T. and Jiang,S.C.
TITLE Methods for assaying gene imprinting and methylated cpg islands
JOURNAL Patent: WO 0190313-A 11 29-NOV-2001;
FEATURES The Johns Hopkins University (US)
Location/Qualifiers
source 1..18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1024 CTCCTCTGCTGCACCATC 1041
DB 1 CTCCTCTGCGGGCCATC 18

RESULT 146
AX796108
LOCUS AX796108 18 bp DNA linear PAT 04-OCT-2003
DEFINITION Sequence 451 from Patent WO03052135.
ACCESSION AX796108
VERSION AX796108.1 GI:37516774
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Burger,M., Field,J.K., Genc,B., Lilloglou,T., Lipscher,B., Maier,S. and Nimrich,I.
TITLE Method and nucleic acids for the analysis of a lung cell proliferative disorder
JOURNAL Patent: WO 03052135-A 451 26-JUN-2003;
FEATURES Epigenomics AG (DE)
Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for CACNA1G"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3583 TATAGTTTGTGGAGT 3600
DB 1 TTTAGTTTGTAGAGT 18

RESULT 147
A52143/c
LOCUS A52143 17 bp DNA linear PAT 11-MAR-1997
DEFINITION Sequence 9 from Patent WO9619579.
ACCESSION A52143
VERSION A52143.1 GI:2304748
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Hemmings,B.A. and Millward,T.A.

QY 3209 AAATGGAAAGCAGAAA 3224

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/db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1390 CCAACAGCAACAGCAG 1405
Db      |||||
17 CCAACAGCAACATCAG 2

RESULT 152
CQ622461
LOCUS      CQ622461      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 7201 from Patent WO0192524.
ACCESSION CQ622461
VERSION   CQ622461.1 GI:41672679
KEYWORDS  "Homo sapiens (human)"
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
           Shannon, M.E.
TITLE     Myosin-like gene expressed in human heart and muscle
JOURNAL   Patent: WO 0192524-A 7201 06-DEC-2001;
           Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 GACCTTGCCTATGAGC 337
Db      |||||
2 GACCTTGCCTATGAGC 17

RESULT 153
CQ622462
LOCUS      CQ622462      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 7202 from Patent WO0192524.
ACCESSION CQ622462
VERSION   CQ622462.1 GI:41672680
KEYWORDS  "Homo sapiens (human)"
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
           Shannon, M.E.
TITLE     Myosin-like gene expressed in human heart and muscle
JOURNAL   Patent: WO 0192524-A 7202 06-DEC-2001;
           Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 GACCTTGCCTATGAGC 337
Db      |||||
1 GACCTTGCCTATGAGC 16

RESULT 154
CQ623727
LOCUS      CQ623727      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 8467 from Patent WO0192524.
ACCESSION CQ623727
VERSION   CQ623727.1 GI:41673945
KEYWORDS  "Homo sapiens (human)"
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
           Shannon, M.E.
TITLE     Myosin-like gene expressed in human heart and muscle
JOURNAL   Patent: WO 0192524-A 8467 06-DEC-2001;
           Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 GAACCTGGAGACATGCA 617
Db      |||||
2 GAGCTGGAGACATGCA 17

RESULT 155
CQ623728
LOCUS      CQ623728      17 bp      DNA      linear      PAT 02-FEB-2004
DEFINITION Sequence 8468 from Patent WO0192524.
ACCESSION CQ623728
VERSION   CQ623728.1 GI:41673946
KEYWORDS  "Homo sapiens (human)"
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and
           Shannon, M.E.
TITLE     Myosin-like gene expressed in human heart and muscle
JOURNAL   Patent: WO 0192524-A 8468 06-DEC-2001;
           Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 GAACCTGGAGACATGCA 617
Db      |||||
1 GAGCTGGAGACATGCA 16

RESULT 156
CQ874816
LOCUS      CQ874816      17 bp      DNA      linear      PAT 27-SEP-2004
DEFINITION Sequence 13 from Patent WO2004076482.
ACCESSION CQ874816
VERSION   CQ874816.1 GI:52747968
KEYWORDS
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SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Soncin, F. and Mattot, V.
TITLE Soluble factor secreted by endothelial cells in blood vessels
JOURNAL Patent: WO 2004076482-A 13 10-SEP-2004;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description de la s quence artificielle:amorce"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1084 TGGTCAGCAGACATTC 1099
|||||
Db 1 TGGGAGCAGACATTC 16

RESULT 157
AR188500 17 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 3988 from patent US 6346398.
ACCESSION AR188500
VERSION AR188500.1 GI:20234465
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1988 12-FEB-2002;
FEATURES
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3494 AATTGCTCTAATAGA 3509
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Db 1 AATTGCTCTAATGA 16

RESULT 158
AR324353 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 1755 from patent US 6566127.
ACCESSION AR324353
VERSION AR324353.1 GI:33710161
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1755 20-MAY-2003;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3494 AATTGCTCTAATAGA 3509
|||||
Db 1 AATTGCTCTAATGA 16

RESULT 159
AR329005 17 bp RNA linear PAT 17-AUG-2003
LOCUS Sequence 6407 from patent US 6566127.
ACCESSION AR329005
VERSION AR329005.1 GI:33714813
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6407 20-MAY-2003;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3494 AATTGCTCTAATAGA 3509
|||||
Db 2 AATTGCTCTAATGA 17

RESULT 160
AR463524 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 7201 from patent US 6866188.
ACCESSION AR463524
VERSION AR463524.1 GI:42698581
KEYWORDS Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6866188-A 7201 03-FEB-2004;
FEATURES
source
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 GACCTTGCCTATGAGC 337
|||||
Db 2 GACCTTGCCTATGAGC 17

RESULT 161
AR463525 17 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 7202 from patent US 6866188.
ACCESSION AR463525

```
VERSION AR463525.1 GI:42698582
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 686188-A 7202 03-FEB-2004;
FEATURES
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        /organism="unknown"
        /mol_type="genomic DNA"
    Query Match 0.4%; Score 14.4; DB 1; Length 17;
    Best Local Similarity 93.8%; Pred. No. 1.5e+02;
    Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 GACCTTGCCCTATGAGC 337
Db 1 GACCTTGCCGATGAGC 16

RESULT 162
AR464790
LOCUS AR464790 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8467 from patent US 686188.
ACCESSION AR464790
VERSION AR464790.1 GI:42699847
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 686188-A 8467 03-FEB-2004;
FEATURES
    source
        1..17
        /organism="unknown"
        /mol_type="genomic DNA"
    Query Match 0.4%; Score 14.4; DB 1; Length 17;
    Best Local Similarity 93.8%; Pred. No. 1.5e+02;
    Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 GAACTGGAGAACATGA 617
Db 2 GAGCTGGAGAACATGA 17

RESULT 163
AR464791
LOCUS AR464791 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 8468 from patent US 686188.
ACCESSION AR464791
VERSION AR464791.1 GI:42699848
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 686188-A 8468 03-FEB-2004;
FEATURES
    source
        1..17
        /organism="unknown"
        /mol_type="genomic DNA"
    Query Match 0.4%; Score 14.4; DB 1; Length 17;
    Best Local Similarity 93.8%; Pred. No. 1.5e+02;
    Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 602 GAACTGGAGAACATGA 617
Db 1 GAGCTGGAGAACATGA 16

RESULT 164
AX088231/c
LOCUS AX088231 17 bp DNA linear PAT 17-MAR-2001
DEFINITION Sequence 15 from Patent WO0114520.
ACCESSION AX088231
VERSION AX088231.1 GI:13397142
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Wadskov-Hansen, S.L., Hammer, K. and Martinussen, J.
TITLE Phage resistant lactic acid bacterial mutants
JOURNAL Patent: WO 0114520-A 15 01-MAR-2001;
        Chr. Hansen A/S (DK)
FEATURES
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    Best Local Similarity 93.8%; Pred. No. 1.5e+02;
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QY 1570 GCAGCAACAAACACAG 1585
Db 17 GCAGCAACAAACACTG 2

RESULT 165
AX214792
LOCUS AX214792 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 234 from Patent WO0159103.
ACCESSION AX214792
VERSION AX214792.1 GI:15524835
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., Mcswiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 234 16-AUG-2001;
        RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
        Mcswiggen, James (US); Chowrira, Bharat M. (US)
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    Best Local Similarity 93.8%; Pred. No. 1.5e+02;
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QY 1689 TCCTACTTCAGCAAAAT 1704
Db 1 TCCTACTTCAGCAAAAT 1704
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RESULT 166			Homo sapiens		Homo sapiens	
AX214793			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
LOCUS	AX214793		17 bp		Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and	
DEFINITION	Sequence 235 from Patent WO0159103.		Ellis, J.H.		Method and reagent for the inhibition of grid	
ACCESSION	AX214793		Patent: WO 0162911-A 524 30-AUG-2001;		GLAXO GROUP LIMITED (GB)	
VERSION	AX214793.1 GI:15524836		RIBOZYME PHARMACEUTICALS, INC. (US)			
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AUTHORS	Blatt, L., Mcswiggen, J. and Chowrira, B.M.					
TITLE	Method and reagent for the modulation and diagnosis of cd20 and					
JOURNAL	nogo gene expression					
FEATURES	Patent: WO 0159103-A 235 16-AUG-2001;					
source	RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;					
	McSwiggen, James (US) ; Chowrira, Bharat M. (US)					
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DEFINITION	Sequence 383 from Patent WO0162911.					
ACCESSION	AX272814					
VERSION	AX272814.1 GI:16545551					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and					
TITLE	Ellis, J.H.					
JOURNAL	Method and reagent for the inhibition of grid					
FEATURES	Patent: WO 0162911-A 383 30-AUG-2001;					
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LOCUS	17 bp					
DEFINITION	Sequence 574 from Patent EP1239051.					
ACCESSION	AX531065					
VERSION	AX531065.1 GI:25253912					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Shannon, M.					
TITLE	Human posh-like protein 1					
JOURNAL	Patent: EP 1239051-A 574 11-SEP-2002;					
FEATURES	Aeomica, Inc. (US)					
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
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REFERENCE	1					
AUTHORS	Shannon, M.					
TITLE	Human posh-like protein 1					
JOURNAL	Patent: EP 1239051-A 575 11-SEP-2002;					
FEATURES	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Shannon, M.					
TITLE	Human posh-like protein 1					
JOURNAL	Patent: EP 1239051-A 575 11-SEP-2002;					
FEATURES	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
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ACCESSION	AX531066					
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REFERENCE	1					
AUTHORS	Shannon, M.					
TITLE	Human posh-like protein 1					
JOURNAL	Patent: EP 1239051-A 575 11-SEP-2002;					
FEATURES	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
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DEFINITION	Sequence 575 from Patent EP1239051.					
ACCESSION	AX531066					
VERSION	AX531066.1 GI:25253914					
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SOURCE	Homo sapiens					
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REFERENCE	1					
AUTHORS	Shannon, M.					
TITLE	Human posh-like protein 1					
JOURNAL	Patent: EP 1239051-A 575 11-SEP-2002;					
FEATURES	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
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Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
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DEFINITION	Sequence 575 from Patent EP1239051.					
ACCESSION	AX531066					
VERSION	AX531066.1 GI:25253914					
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SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
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REFERENCE	1					
AUTHORS	Shannon, M.					
TITLE	Human posh-like protein 1					
JOURNAL	Patent: EP 1239051-A 575 11-SEP-2002;					
FEATURES	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
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VERSION	AX531066.1 GI:25253914					
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
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REFERENCE	1					
AUTHORS	Shannon, M.					
TITLE	Human posh-like protein 1					
JOURNAL	Patent: EP 1239051-A 575 11-SEP-2002;					
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VERSION	AX531066.1 GI:25253914					
KEYWORDS	Homo sapiens (human)					
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
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AUTHORS	Shannon, M.					
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ACCESSION	AX531066					
VERSION	AX531066.1 GI:25253914					
KEYWORDS	Homo sapiens (human)					
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REFERENCE	1					
AUTHORS	Shannon, M.					
TITLE	Human posh-like protein 1					
JOURNAL	Patent: EP 1239051-A 575 11-SEP-2002;					
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VERSION	AX531066.1 GI:25253914					
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REFERENCE	1					
AUTHORS	Shannon, M.					
TITLE	Human posh-like protein 1					
JOURNAL	Patent: EP 1239051-A 575 11-SEP-2002;					
FEATURES	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
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Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
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ACCESSION	AX531066					
VERSION	AX531066.1 GI:25253914					
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SOURCE	Homo sapiens					
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Shannon, M.					
TITLE	Human posh-like protein 1					
JOURNAL	Patent: EP 1239051-A 575 11-SEP-2002;					
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RESULT 175
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LOCUS AX693264 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5996 from Patent EPI281758.
ACCESSION AX693264
VERSION AX693264.1 GI:29416228
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5996 05-FEB-2003;
Aesomica, Inc. (US)
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1368 AGCCTTCTCCTTACA 1383
Db 16 AGGCTTCTCCTTACA 1

RESULT 176
AX723745
LOCUS AX723745 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1432 from Patent WO03025176.
ACCESSION AX723745
VERSION AX723745.1 GI:30503088
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 1432 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 93.8%; Pred. No. 1.5e+02;
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Qy 3255 ATTCTTGTTTAAATC 3270
Db 2 ATCTTGTTTAAATC 17

RESULT 177
AX728782/c
LOCUS AX728782 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 416 from Patent WO03025175.
ACCESSION AX728782

VERSION AX728782.1 GI:30508125
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 416 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2778 AGCTAAGCACACAGAT 2793
Db 17 AGCTAAGCAACACAGAT 2

RESULT 178
AX736485
LOCUS AX736485 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2075 from Patent WO03025177.
ACCESSION AX736485
VERSION AX736485.1 GI:30515773
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL Patent: WO 03025177-A 2075 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 718 GATCAAAAGTGAATAC 733
Db 1 GATCAAAAGTGAACAC 16

RESULT 179
AX737300
LOCUS AX737300 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2890 from Patent WO03025177.
ACCESSION AX737300
VERSION AX737300.1 GI:30516588
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

AUTHORS	Telerman,A., Amson,R. and Tuijnder,M.									
TITLE	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments									
JOURNAL	Patent: WO 03025177-A 2890 27-MAR-2003; Molecular Engines Laboratories (FR)									
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Query Match	0.4%; Score 14.4; DB 1; Length 17;									
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Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	233 GATATCAAAAGAATTC 248									
Db	1 GATCTCAAAAGAATTC 16									
RESULT 180										
AX738735										
LOCUS	AX738735 17 bp DNA linear PAT 08-MAY-2003									
DEFINITION	Sequence 4325 from Patent WO03025177.									
ACCESSION	AX738735									
VERSION	AX738735.1 GI:30518025									
KEYWORDS										
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	1									
AUTHORS	Telerman,A., Amson,R. and Tuijnder,M.									
TITLE	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments									
JOURNAL	Patent: WO 03025177-A 4325 27-MAR-2003; Molecular Engines Laboratories (FR)									
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Query Match	0.4%; Score 14.4; DB 1; Length 17;									
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QY	3330 ATCCCAATTTATCCAAA 3345									
Db	2 ATCCCAATTTATCCAAA 17									
RESULT 181										
AX753828										
LOCUS	AX753828 17 bp DNA linear PAT 23-JUN-2003									
DEFINITION	Sequence 175 from Patent WO03037931.									
ACCESSION	AX753828									
VERSION	AX753828.1 GI:32166525									
KEYWORDS										
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	1									
AUTHORS	Shannon,M. and Phan,T.									
TITLE	Human angiomin-like protein 1									
JOURNAL	Patent: WO 03037931-A 175 08-MAY-2003; Amersham Biosciences SV Corp. (US)									
FEATURES	Location/Qualifiers									
source	1. .17									
Query Match	0.4%; Score 14.4; DB 1; Length 17;									
Best Local Similarity	93.8%; Pred. No. 1.5e+02;									
Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	3330 ATCCCAATTTATCCAAA 3345									
Db	2 ATCCCAATTTATCCAAA 17									
RESULT 182										
AX762770										
LOCUS	AX762770/c 17 bp DNA linear PAT 25-JUN-2003									
DEFINITION	Sequence 6091 from Patent WO03040369.									
ACCESSION	AX762770									
VERSION	AX762770.1 GI:32257386									
KEYWORDS										
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	1									
AUTHORS	Telerman,A., Amson,R. and Tuijnder,M.									
TITLE	Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines									
JOURNAL	Patent: WO 03040369-A 6091 15-MAY-2003; Molecular Engines Laboratories (FR)									
FEATURES	Location/Qualifiers									
source	1. .17									
Query Match	0.4%; Score 14.4; DB 1; Length 17;									
Best Local Similarity	93.8%; Pred. No. 1.5e+02;									
Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	3182 TGGACTACATGAGAT 3197									
Db	17 TGGACTACATGAGAT 2									
RESULT 183										
AX076398/c										
LOCUS	AR076398 18 bp DNA linear PAT 30-AUG-2000									
DEFINITION	Sequence 18 from patent US 5958773.									
ACCESSION	AR076398									
VERSION	AR076398.1 GI:10003144									
KEYWORDS										
SOURCE	Unknown.									
ORGANISM	Unknown.									
REFERENCE	1 (bases 1 to 18)									
AUTHORS	Monia,B.P. and Cowse,L.M.									
TITLE	Antisense modulation of AKT-1 expression									
JOURNAL	Patent: US 5958773-A 18 28-SEP-1999;									
FEATURES	Location/Qualifiers									
source	1. .18									
Query Match	0.4%; Score 14.4; DB 1; Length 18;									
Best Local Similarity	93.8%; Pred. No. 1.7e+02;									
Matches	15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	73 GAAGCAGCGGAGGAG 88									
Db	18 GAAGCAGCGGAGGAG 3									

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RESULT 184
LOCUS      ARI06771              18 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 19 from patent US 6107091.
ACCESSION  ARI06771
VERSION     ARI06771.1  GI:12821301
KEYWORDS
SOURCE      unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Cowsert,L.M.
TITLE       Antisense inhibition of G-alpha-16 expression
JOURNAL     Patent: US 6107091-A 19 22-AUG-2000;
FEATURES    Location/Qualifiers
             source
             1..18
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1532  GCCCAACAGCAGCAGC 1547
Db      3      GCCCAAAAGCAGCAGC 18
          ||||| ||||| |||||
          ||||| ||||| |||||

RESULT 185
LOCUS      BD250786/C              18 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Identification of genetic targets for modulation by
ACCESSION  BD250786.1  GI:33060556
VERSION     JP 2002511276-A/340.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Cowsert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M.,
            Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
TITLE       Identification of genetic targets for modulation by
            oligonucleotides and generation of oligonucleotides for gene
            modulation
JOURNAL     Patent: JP 2002511276-A 340 16-APR-2002;
COMMENT     ISIS PHARMACEUTICALS INC
            OS Artificial Sequence
            PN JP 2002511276-A/340
            PD 16-APR-2002
            PF 13-APR-1999 JP 2000543647
            PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
            LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
            M SASNOR,
            PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
            BORCHERS,
            PI TIMOTHY A VIKKARS
            PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
            C12N15/00
            CC Antisense Oligonucleotide
            FH Key
            FT source
            FT source
            FT Location/Qualifiers
             1..18
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      73      GAAGCAGCGGAGGAG 88
Db      18      GAAGCAGCGGAGGAG 3
          ||||| ||||| |||||
          ||||| ||||| |||||

RESULT 186
LOCUS      CQ808040              18 bp      DNA      linear      PAT 10-MAY-2004
DEFINITION Sequence 1490 from Patent WO2004035803.
ACCESSION  CQ808040
VERSION     CQ808040.1  GI:47113434
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F.,
            Nimrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
            Marx,A.
TITLE       Method and nucleic acids for the improved treatment of breast cell
            proliferative disorders
JOURNAL     Patent: WO 2004035803-A 1490 29-APR-2004;
FEATURES    Epigenomics AG (DE)
             Location/Qualifiers
             source
             1..18
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Detection oligonucleotide for CACNA1G"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3585  TAGGTTTGTGGAGT 3600
Db      1      TAGGTTTGTGGAGT 16
          ||||| ||||| |||||
          ||||| ||||| |||||

RESULT 187
LOCUS      AX111519              18 bp      DNA      linear      PAT 29-MAY-2002
DEFINITION Sequence 2252 from Patent WO0123604.
ACCESSION  AX111519
VERSION     AX111519.1  GI:13927811
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
TITLE       Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
JOURNAL     Patent: WO 0123604-A 2252 05-APR-2001;
FEATURES    Infectio Diagnostic (I.D.I.) INC. (CA)
             Location/Qualifiers
             source
             1..18
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Oligonucleotide"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2257  CACATACAGTGTCTCT 2272
Db      2      CACATACAGTGTCTCT 17
          ||||| ||||| |||||
          ||||| ||||| |||||

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RESULT 188
BD174259          26 bp  DNA  linear  PAT 18-FEB-2003
LOCUS             Novel physiological active peptide and its use.
DEFINITION        BD174259
ACCESSION         BD174259
VERSION           BD174259.1 GI:28415598
KEYWORDS          WO 02062944-A/6.
SOURCE            synthetic construct
ORGANISM          other sequences; artificial sequences.
REFERENCE         1 (bases 1 to 26)
AUTHORS           Otaki,T., Masuda,Y., Takatsu,Y., Watanabe,T., Terao,Y., Shintani,Y.
                  and Hinuma,S.
TITLE             Novel physiological active peptide and its use
JOURNAL           Patent: WO 02062944-A 6 15-AUG-2002;
                  TAKEDA CHEMICAL INDUSTRIES LTD,TETSUYA OTAKI,YASUSHI MASUDA,
                  YOSHITIRO TAKATSU,TAKUYA WATANABE,YASUKO TERAU,YASUSHI SHINTANI,
                  SHUJI HINUMA
COMMENT           OS Artificial Sequence
                  PN WO 02062944-A/6
                  PD 15-AUG-2002
                  PF 01-FEB-2002 WO 2002JP000852
                  PR 02-FEB-2001 JP 01P 026820
                  PI TETSUYA OTAKI,YASUSHI MASUDA,YOSHITIRO TAKATSU,TAKUYA
                  WATANABE,
                  PT YASUKO TERAU,YASUSHI SHINTANI,SHUJI HINUMA
                  PC C07K14/47,C07K14/705,C12N15/12,C12P21/02,C07K16/18,A61K67/027,
                  PC C12N5/10,
                  PC G01N33/15 G01N33/50,A61P1/00
                  CC DNA primer, hbv8-F1 primer
                  FH Key Location/Qualifiers
                  FT source 1..26
                  FT Location/Qualifiers
                  FT /organism='Artificial Sequence'.
FEATURES
source          1..26
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
Query Match     0.4%; Score 14.4; DB 1; Length 26;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1931 CTTCTTCTCCAGCAGCAGATGCTG 1954
Db 1 CTACTTCTGCTGCTGCGCTGCTG 24

RESULT 189
AX734811/c
LOCUS             Homo sapiens (human)
DEFINITION        Sequence 401 from Patent WO03025177.
ACCESSION         AX734811
VERSION           AX734811.1 GI:30514088
KEYWORDS          Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1
AUTHORS           Telerman,A., Amson,R. and Tuijnder,M.
TITLE             Sequences involved in phenomena of tumour suppression, tumour
                  reversion, apoptosis and/or resistance to viruses and the use
                  thereof as medicaments
JOURNAL           Patent: WO 03025177-A 401 27-MAR-2003;
                  Molecular Engines Laboratories (FR)
FEATURES
source          1..17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match     0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1931 CTTCTTCTCCAGCAGCAGATGCTG 1954
Db 1 CTACTTCTGCTGCTGCGCTGCTG 24

RESULT 190
AX737775
LOCUS             Homo sapiens (human)
DEFINITION        Sequence 3365 from Patent WO03025177.
ACCESSION         AX737775
VERSION           AX737775.1 GI:30517063
KEYWORDS          Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1
AUTHORS           Telerman,A., Amson,R. and Tuijnder,M.
TITLE             Sequences involved in phenomena of tumour suppression, tumour
                  reversion, apoptosis and/or resistance to viruses and the use
                  thereof as medicaments
JOURNAL           Patent: WO 03025177-A 3365 27-MAR-2003;
                  Molecular Engines Laboratories (FR)
FEATURES
source          1..17
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match     0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 536 GATCTCTGAGCTGCA 549
Db 1 GATCTCTGAGCTGCA 14

RESULT 191
AX744267/c
LOCUS             Homo sapiens (human)
DEFINITION        Sequence 232 from Patent WO03031621.
ACCESSION         AX744267
VERSION           AX744267.1 GI:30722934
KEYWORDS          Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE         1
AUTHORS           Zhang,J.
TITLE             A human G protein coupled receptor
JOURNAL           Patent: WO 03031621-A 232 17-APR-2003;
                  Amersham Biosciences (SV) Corp. (US)
FEATURES
source          1..17
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
Query Match     0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2660 GTGGCTCTCTCTAA 2673
Db 1 GTGGCTCTCTCTAA 4

RESULT 192
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AX744268/c
LOCUS AX744268 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 233 from Patent WO03031621.
ACCESSION AX744268
VERSION AX744268.1 GI:30722935
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 233 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 GTGGCTCCTCTCTAA 2673
Db 16 GTGGCTCCTCTCTAA 3
RESULT 193
AX744269/c
LOCUS AX744269 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 234 from Patent WO03031621.
ACCESSION AX744269
VERSION AX744269.1 GI:30722936
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 234 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 GTGGCTCCTCTCTAA 2673
Db 16 GTGGCTCCTCTCTAA 3
RESULT 194
AX744270/c
LOCUS AX744270 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 235 from Patent WO03031621.
ACCESSION AX744270
VERSION AX744270.1 GI:30722937
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 235 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 GTGGCTCCTCTCTAA 2673
Db 15 GTGGCTCCTCTCTAA 2
RESULT 195
AX753817
LOCUS AX753817 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 164 from Patent WO03037931.
ACCESSION AX753817
VERSION AX753817.1 GI:32166514
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon, M. and Phan, T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 164 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAAC 1442
Db 4 GCAGCAGCAGCAAC 17
RESULT 196
AR084541/c
LOCUS AR084541 30 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 30 from patent US 5981185.
ACCESSION AR084541
VERSION AR084541.1 GI:10011312
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C. Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 30 09-NOV-1999;
FEATURES
source
1. .30
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 235 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2660 GTGGCTCCTCTCTAA 2673
Db 14 GTGGCTCCTCTCTAA 1
RESULT 195
AX753817
LOCUS AX753817 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 164 from Patent WO03037931.
ACCESSION AX753817
VERSION AX753817.1 GI:32166514
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon, M. and Phan, T.
TITLE Human angiotensin-like protein 1
JOURNAL Patent: WO 03037931-A 164 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1429 GCAGCAGCAGCAAC 1442
Db 4 GCAGCAGCAGCAAC 17
RESULT 196
AR084541/c
LOCUS AR084541 30 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 30 from patent US 5981185.
ACCESSION AR084541
VERSION AR084541.1 GI:10011312
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C. Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 30 09-NOV-1999;
FEATURES
source
1. .30
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
|||||
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
|||||

RESULT 197
AR165925/c
LOCUS I84405 30 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 4 from patent US 6280938.
ACCESSION AR165925
VERSION AR165925.1 GI:16241014
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ranum,L.P.W., Koob,M.D., Moseley-Allredge,M.L. and Benzow,K.A.
TITLE SCA7 gene and method of use
JOURNAL Patent: US 6280938-A 4 28-AUG-2001;
FEATURES
source Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
|||||
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
|||||

RESULT 198
E34522/c
LOCUS E34522 30 bp DNA linear PAT 18-JUN-2001
DEFINITION SCA7 gene and utilization thereof.
ACCESSION E34522
VERSION E34522.1 GI:13018890
KEYWORDS JP 1999206393-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 30)
AUTHORS Laura,B.W.R. and Michael,D.K.
TITLE SCA7 gene and utilization thereof
JOURNAL Patent: JP 1999206393-A 4 03-AUG-1999;
COMMENT THE REGENTS OF THE UNIVERSITY OF MINNESOTA
OS Homo sapiens (human)
PN JP 1999206393-A/4
PD 03-AUG-1999
PF 19-AUG-1998 JP 1998294732
PR 19-AUG-1997 US 60/056170
PI LAURA B W RANUM,MICHAEL D KUBU
PC C12N15/09,C07K14/47,C07K16/18,C12Q1/68,G01N33/53, PC
G01N33/566//C12P21/02,
PC C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..30
FT /organism="Homo sapiens (human)".

FEATURES
source Location/Qualifiers
1..30
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954

Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
|||||

RESULT 199
I84405/c
LOCUS I84405 30 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 6 from patent US 5695933.
ACCESSION I84405
VERSION I84405.1 GI:3021925
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Schalling,M., Hudson,T.J. and Houseman,D.E.
TITLE Direct detection of expanded nucleotide repeats in the human genome
JOURNAL Patent: US 5695933-A 6 09-DEC-1997;
FEATURES
source Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
|||||
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
|||||

RESULT 200
I84410
LOCUS I84410 30 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 11 from patent US 5695933.
ACCESSION I84410
VERSION I84410.1 GI:3021930
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Schalling,M., Hudson,T.J. and Houseman,D.E.
TITLE Direct detection of expanded nucleotide repeats in the human genome
JOURNAL Patent: US 5695933-A 11 09-DEC-1997;
FEATURES
source Location/Qualifiers
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14; DB 1; Length 30;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1925 CAGCAACTTCTTCTCCAGCAGCAGATGCTG 1954
|||||
Db 30 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
|||||

RESULT 201
AR040055/c
LOCUS AR040055 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 903 from patent US 5807743.
ACCESSION AR040055
VERSION AR040055.1 GI:5959418
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes

Query Match 0.4%; Score 13.8; DB 1; Length 17;

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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 938 AAACAGATAGCTGCTAA 954
    ||||| ||||| |||||
Db 1 AAACAGATAGATGATAA 17

RESULT 206
BD202795/c
LOCUS          17 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION     Method and reagent for treating diseases or conditions concerning
                molecule participating in vasculogenic response.
ACCESSION      BD202795
VERSION        BD202795.1 GI:33012565
KEYWORDS       JP 2002509721-A/5821.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE         Method and reagent for treating diseases or conditions concerning
                molecule participating in vasculogenic response
JOURNAL        Patent: JP 2002509721-A 5821 02-APR-2002;
COMMENT        OS Homo sapiens (human)
                PN JP 2002509721-A/5821
                PD 02-APR-2002
                PF 24-MAR-1999 JP 2000541291
                PR 27-MAR-1998 US 60/079678
                PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
                PI JAMES A MCSWIGGEN
                PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'
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source
1..17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3090 AAAGAAGAAGGAAGA 3106
    ||||| ||||| |||||
Db 17 AAAGAAAAAAGGAAGA 1

RESULT 207
BD231281
LOCUS          17 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION     Genes for assessing cardiovascular status and compositions for use
                thereof.
ACCESSION      BD231281
VERSION        BD231281.1 GI:33041051
KEYWORDS       JP 2002527079-A/45.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Norberg,L.T., Andersson,M.K., Lindstrom,P.H.R. and Jonsson,L.
TITLE         Genes for assessing cardiovascular status and compositions for use
                thereof.
JOURNAL        Patent: JP 2002527079-A 45 27-AUG-2002;
                PAIROSEAKENSINGU AB
COMMENT        OS Artificial Sequence
                PN JP 2002527079-A/51
                PD 27-AUG-2002
                PF 13-OCT-1999 JP 2000576056
                PR 14-OCT-1998 US 60/104286,14-OCT-1998 US 60/104302 PI
                LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
                RUTGER LINDSTROM,
                PI LENA JONSSON
                PC C12Q1/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC Genes
                for assessing cardiovascular status
                and compositions for
                use thereof
                CC Key Location/Qualifiers
                FT source 1..17
                FT /organism='Artificial Sequence'.
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source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
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thereof
Patent: JP 2002527079-A 45 27-AUG-2002;
                PAIROSEAKENSINGU AB
COMMENT        OS Artificial Sequence
                PN JP 2002527079-A/45
                PD 27-AUG-2002
                PF 13-OCT-1999 JP 2000576056
                PR 14-OCT-1998 US 60/104286,14-OCT-1998 US 60/104302 PI
                LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
                RUTGER LINDSTROM,
                PI LENA JONSSON
                PC C12Q1/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC Genes
                for assessing cardiovascular status
                and compositions for
                use thereof
                CC Key Location/Qualifiers
                FT source 1..17
                FT /organism='Artificial Sequence'.
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source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 CAGCAGCAGCAGCAACA 1443
    ||||| ||||| |||||
Db 1 CGCGCGCAGCAGCAACA 17

RESULT 208
BD231287
LOCUS          17 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION     Genes for assessing cardiovascular status and compositions for use
                thereof.
ACCESSION      BD231287
VERSION        BD231287.1 GI:33041057
KEYWORDS       JP 2002527079-A/51.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Norberg,L.T., Andersson,M.K., Lindstrom,P.H.R. and Jonsson,L.
TITLE         Genes for assessing cardiovascular status and compositions for use
                thereof.
JOURNAL        Patent: JP 2002527079-A 51 27-AUG-2002;
                PAIROSEAKENSINGU AB
COMMENT        OS Artificial Sequence
                PN JP 2002527079-A/51
                PD 27-AUG-2002
                PF 13-OCT-1999 JP 2000576056
                PR 14-OCT-1998 US 60/104286,14-OCT-1998 US 60/104302 PI
                LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
                RUTGER LINDSTROM,
                PI LENA JONSSON
                PC C12Q1/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC Genes
                for assessing cardiovascular status
                and compositions for
                use thereof
                CC Key Location/Qualifiers
                FT source 1..17
                FT /organism='Artificial Sequence'.
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
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QY 3369 ATTAATGTCTAAATA 3385
Db 1 ATTCATTTCTAAATA 17

RESULT 212
BD259675/c
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD259675
VERSION BD259675.1 GI:33069445
KEYWORDS JP 2002541795-A/7468.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 7468 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/7468
PD 10-DEC-2002
PE 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN
PC C12N15/09, A61K38/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02/A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules PH
KEY source Location/Qualifiers
FT 1..17
FT /organism='Eukaryote'.

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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3351 CTGTGTGTCAATGTGT 3367
Db 17 CTGTGGAGTAAATGTGT 1

RESULT 213
BD266197
LOCUS
DEFINITION Universal arrays.
ACCESSION BD266197
VERSION BD266197.1 GI:33075965
KEYWORDS JP 2002539849-A/197.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pan,J.B., Hirschhorn,J.N., Huang,X., Kaplan,P., Lander,E.S.,
Lockhart,D.J., Ryder,T. and Sklar,P.
TITLE Universal arrays
JOURNAL Patent: JP 2002539849-A 197 26-NOV-2002;
COMMENT WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
OS Artificial Sequence
PN JP 2002539849-A/197
PD 26-NOV-2002
PF 27-MAR-2000 JP 2000608794

PR 26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359 PI
JIAN BING FAN, JOEL N HIRSCHHORN, XIAOHUA
HUANG, PAUL KAPLAN, ERIC
PI S LANDER,
PI DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
PC C12Q1/68, C12M1/00, C12N15/09, C12N15/09, C12N15/09, G01N33/53, PC
G01N33/566,
PC G01N37/00, C12N15/00, C12N15/00, C12N15/00
CC Primer
PH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.

FEATURES
source
1..17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 815 TCTGCCCTCTCCACTTC 831
Db 1 TCTGCCCTCTGCACCTC 17

RESULT 214
CQ615924
LOCUS
DEFINITION Sequence 664 from Patent WO0192524.
ACCESSION CQ615924
VERSION CQ615924.1 GI:41666142
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 664 06-DEC-2001;
Aeomica, Inc. (US)

FEATURES
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/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 664 TCAGCAAGCCAGAGGA 680
Db 1 TCAGCAAGCCAGAGAA 17

RESULT 215
CQ615925
LOCUS
DEFINITION Sequence 665 from Patent WO0192524.
ACCESSION CQ615925
VERSION CQ615925.1 GI:41666143
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.

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TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 665 06-DEC-2001;
 FEATURES
 source Location/Qualifiers
 1. .17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 665 CAGCAAGCCAGAGAG 681
 Db 1 CAGCAAGCCAGAGAG 17

RESULT 216
 CQ617132
 LOCUS 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 1872 from Patent WO0192524.
 ACCESSION CQ617132
 VERSION CQ617132.1 GI:41667350
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 1872 06-DEC-2001;
 Aecomica, Inc. (US)

FEATURES
 source Location/Qualifiers
 1. .17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1022 CCCTCCTCTGCTGGACC 1038
 Db 1 CCCTCCTGAGCTGGACC 17

RESULT 217
 CQ617133
 LOCUS 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 1873 from Patent WO0192524.
 ACCESSION CQ617133
 VERSION CQ617133.1 GI:41667351
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 1873 06-DEC-2001;
 Aecomica, Inc. (US)

FEATURES
 source Location/Qualifiers
 1. .17
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1023 CCTCCTCTGCTGGACCA 1039
 Db 1 CCTCCTGAGCTGGACCA 17

RESULT 218
 CQ617993
 LOCUS 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 2733 from Patent WO0192524.
 ACCESSION CQ617993
 VERSION CQ617993.1 GI:41668211
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 2733 06-DEC-2001;
 Aecomica, Inc. (US)

FEATURES
 source Location/Qualifiers
 1. .17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 765 CTCCTCAGCTGAGGCC 781
 Db 1 CTCAGCAGCTGAGGCC 17

RESULT 219
 CQ623062
 LOCUS 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 7802 from Patent WO0192524.
 ACCESSION CQ623062
 VERSION CQ623062.1 GI:41673280
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 7802 06-DEC-2001;
 Aecomica, Inc. (US)

FEATURES
 source Location/Qualifiers
 1. .17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1425
 Db 1 CAGCAGCAGCTGAAGCA 17

RESULT 220
LOCUS CQ623063 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 7803 from Patent WO0192524.
ACCESSION CQ623063
VERSION CQ623063.1 GI:41673281
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7803 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1425 AGCAGCAGCAGCAGCAA 1441
Db |||||||
1 AGCAGCAGCAGCAGCAA 17
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
LOCUS CQ625507 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 10247 from Patent WO0192524.
ACCESSION CQ625507
VERSION CQ625507.1 GI:41675725
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10247 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
LOCUS CQ626007 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 10747 from Patent WO0192524.
ACCESSION CQ626007
VERSION CQ626007.1 GI:41676225
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10247 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
LOCUS CQ626607 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 10747 from Patent WO0192524.
ACCESSION CQ626607
VERSION CQ626607.1 GI:41676225
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10747 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10747 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1771 TGTGTAGCCGAGCA 1787
Db |||||||
1 TGTGTGTGGCTGAACA 17
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
LOCUS I37425 17 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 438 from patent US 5612215.
ACCESSION I37425
VERSION I37425.1 GI:2085385
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T.
TITLE Stromelysin targeted ribozymes
JOURNAL Patent: US 5612215-A 438 18-MAR-1997;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 560 AATGAAGTGCACCAACAT 576
Db |||||||
17 ACTGAAGTGACCAACAT 1
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
LOCUS I37439 17 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 452 from patent US 5612215.
ACCESSION I37439
VERSION I37439.1 GI:2085399
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T.
TITLE Stromelysin targeted ribozymes
JOURNAL Patent: US 5612215-A 452 18-MAR-1997;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 88.2%; Pred. No. 1.8e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Unclassified. 1 (bases 1 to 17) Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T. Method of reducing stromelysin RNA via ribozymes Patent: US 5731295-A 438 24-MAR-1998; Location/Qualifiers 1. .17 /organism="unknown" /mol_type="unassigned DNA"	
QY	1432 GCAGCAGCAACAGCAGC 1448 	LOCUS	17 bp DNA PAT 07-OCT-1997
Db	17 GCAGCATCAACAGCATC 1	DEFINITION	Sequence 1513 from patent US 5646042.
RESULT 225		ACCESSION	I53772
LOCUS	I53772	VERSION	I53772.1 GI:2474975
DEFINITION	Sequence 1513 from patent US 5646042.	KEYWORDS	Unknown.
ACCESSION	I53772	SOURCE	Unknown.
VERSION	I53772.1 GI:2474975	ORGANISM	Unknown.
KEYWORDS	Unknown.	REFERENCE	1 (bases 1 to 17)
SOURCE	Unknown.	AUTHORS	Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
ORGANISM	Unknown.	TITLE	C-myb targeted ribozymes
REFERENCE	1 (bases 1 to 17)	JOURNAL	Patent: US 5646042-A 1513 08-JUL-1997;
AUTHORS	Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.	FEATURES	Location/Qualifiers
TITLE	C-myb targeted ribozymes	1. .17	source
JOURNAL	Patent: US 5646042-A 1513 08-JUL-1997;	/organism="unknown"	
FEATURES	Location/Qualifiers	/mol_type="unassigned DNA"	
1. .17	source		
Query Match 0.4%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.8e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Unclassified. 1 (bases 1 to 17) Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T. Method of reducing stromelysin RNA via ribozymes Patent: US 5731295-A 452 24-MAR-1998; Location/Qualifiers 1. .17 /organism="unknown" /mol_type="unassigned DNA"	
QY	3008 GATCTTTATTGACAC 3024 	LOCUS	17 bp DNA PAT 10-JUN-1998
Db	1 GATCTTTCTTGAACAC 17	DEFINITION	Sequence 2 from patent US 5700922.
RESULT 226		ACCESSION	I86370
LOCUS	I86370	VERSION	I86370.1 GI:3206088
DEFINITION	Sequence 2 from patent US 5700922.	KEYWORDS	Unknown.
ACCESSION	I86370	SOURCE	Unknown.
VERSION	I86370.1 GI:3206088	ORGANISM	Unknown.
KEYWORDS	Unknown.	REFERENCE	1 (bases 1 to 17)
SOURCE	Unknown.	AUTHORS	Cook,P.Dan.
ORGANISM	Unknown.	TITLE	PNA-DNA-PNA chimeric macromolecules
REFERENCE	1 (bases 1 to 17)	JOURNAL	Patent: US 5700922-A 2 23-DEC-1997;
AUTHORS	Cook,P.Dan.	FEATURES	Location/Qualifiers
TITLE	PNA-DNA-PNA chimeric macromolecules	1. .17	source
JOURNAL	Patent: US 5700922-A 2 23-DEC-1997;	/organism="unknown"	
FEATURES	Location/Qualifiers	/mol_type="unassigned DNA"	
1. .17	source		
Query Match 0.4%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.8e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Unclassified. 1 (bases 1 to 17) Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 1480 12-FEB-2002; Location/Qualifiers 1. .17 /organism="unknown" /mol_type="unassigned DNA"	
QY	38 CGGAATTCAGCGAGAA 54 	LOCUS	17 bp DNA PAT 01-DEC-1998
Db	17 CTGAATTCAGCGAGAA 1	DEFINITION	Sequence 438 from patent US 5731295.
RESULT 227		ACCESSION	I94275
LOCUS	I94275	VERSION	I94275.1 GI:3938745
DEFINITION	Sequence 438 from patent US 5731295.	KEYWORDS	Unknown.
ACCESSION	I94275	SOURCE	Unknown.
VERSION	I94275.1 GI:3938745	ORGANISM	Unknown.
KEYWORDS	Unknown.	REFERENCE	1 (bases 1 to 17)
SOURCE	Unknown.	AUTHORS	Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
ORGANISM	Unknown.	TITLE	Method and reagent for the treatment of diseases or conditions
REFERENCE	1 (bases 1 to 17)	JOURNAL	related to levels of vascular endothelial growth factor receptor
AUTHORS	Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.	FEATURES	Location/Qualifiers
TITLE	Method and reagent for the treatment of diseases or conditions	1. .17	source
JOURNAL	related to levels of vascular endothelial growth factor receptor	/organism="unknown"	
FEATURES	Location/Qualifiers	/mol_type="unassigned DNA"	
1. .17	source		
Query Match 0.4%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.8e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Unclassified. 1 (bases 1 to 17) Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T. Method of reducing stromelysin RNA via ribozymes Patent: US 5731295-A 438 24-MAR-1998; Location/Qualifiers 1. .17 /organism="unknown" /mol_type="unassigned DNA"	
QY	560 AATGACTGACCAACAT 576 	LOCUS	17 bp DNA PAT 01-DEC-1998
Db	17 ACTGAAGTGACCAACAT 1	DEFINITION	Sequence 452 from patent US 5731295.
RESULT 228		ACCESSION	I94289
LOCUS	I94289	VERSION	I94289.1 GI:3938759
DEFINITION	Sequence 452 from patent US 5731295.	KEYWORDS	Unknown.
ACCESSION	I94289	SOURCE	Unknown.
VERSION	I94289.1 GI:3938759	ORGANISM	Unknown.
KEYWORDS	Unknown.	REFERENCE	1 (bases 1 to 17)
SOURCE	Unknown.	AUTHORS	Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
ORGANISM	Unknown.	TITLE	Stinchcomb,D.T.
REFERENCE	1 (bases 1 to 17)	JOURNAL	Method of reducing stromelysin RNA via ribozymes
AUTHORS	Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and	FEATURES	Location/Qualifiers
TITLE	Stinchcomb,D.T.	1. .17	source
JOURNAL	Method of reducing stromelysin RNA via ribozymes	/organism="unknown"	
FEATURES	Location/Qualifiers	/mol_type="unassigned DNA"	
1. .17	source		
Query Match 0.4%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.8e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Unclassified. 1 (bases 1 to 17) Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6346398-A 1480 12-FEB-2002; Location/Qualifiers 1. .17 /organism="unknown" /mol_type="unassigned DNA"	
QY	1432 GCAGCAGCAACAGCAGC 1448 	LOCUS	17 bp DNA PAT 20-APR-2002
Db	17 GCAGCATCAACAGCATC 1	DEFINITION	Sequence 1480 from patent US 6346398.
RESULT 229		ACCESSION	AR185992
LOCUS	AR185992	VERSION	AR185992.1 GI:20231957
DEFINITION	Sequence 1480 from patent US 6346398.	KEYWORDS	Unknown.
ACCESSION	AR185992	SOURCE	Unknown.
VERSION	AR185992.1 GI:20231957	ORGANISM	Unknown.
KEYWORDS	Unknown.	REFERENCE	1 (bases 1 to 17)
SOURCE	Unknown.	AUTHORS	Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
ORGANISM	Unknown.	TITLE	Method and reagent for the treatment of diseases or conditions
REFERENCE	1 (bases 1 to 17)	JOURNAL	related to levels of vascular endothelial growth factor receptor
AUTHORS	Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.	FEATURES	Location/Qualifiers
TITLE	Method and reagent for the treatment of diseases or conditions	1. .17	source
JOURNAL	related to levels of vascular endothelial growth factor receptor	/organism="unknown"	
FEATURES	Location/Qualifiers	/mol_type="unassigned DNA"	
1. .17	source		
Query Match 0.4%; Score 13.8; DB 1; Length 17; Best Local Similarity 88.2%; Pred. No. 1.8e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Unclassified. 1 (bases 1 to 17) Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and Stinchcomb,D.T. Method of reducing stromelysin RNA via ribozymes Patent: US 5731295-A 438 24-MAR-1998; Location/Qualifiers 1. .17 /organism="unknown" /mol_type="unassigned DNA"	
QY	560 AATGACTGACCAACAT 576 	LOCUS	17 bp DNA PAT 01-DEC-1998
Db	17 ACTGAAGTGACCAACAT 1	DEFINITION	Sequence 452 from patent US 5731295.
RESULT 228		ACCESSION	I94289
LOCUS	I94289	VERSION	I94289.1 GI:3938759
DEFINITION	Sequence 452 from patent US 5731295.	KEYWORDS	Unknown.
ACCESSION	I94289	SOURCE	Unknown.
VERSION	I94289.1 GI:3938759	ORGANISM	Unknown.
KEYWORDS	Unknown.	REFERENCE	1 (bases 1 to 17)
SOURCE	Unknown.	AUTHORS	Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and
ORGANISM	Unknown.	TITLE	Stinchcomb,D.T.
REFERENCE	1 (bases 1 to 17)	JOURNAL	Method of reducing stromelysin RNA via ribozymes
AUTHORS	Draper,K.G., Pavco,P., McSwiggen,J., Gustofson,J. and	FEATURES	Location/Qualifiers
TITLE	Stinchcomb,D.T.	1. .17	source
JOURNAL	Method of reducing stromelysin RNA via ribozymes	/organism="unknown"	
FEATURES	Location/Qualifiers	/mol_type="unassigned DNA"	
1. .17	source		

QY 2166 TGCTACTTCTCAGGG 2182
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Db 1 TGCTGCTTCTCAGG 17

RESULT 230
LOCUS AR185993 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1481 from patent US 6346398.
ACCESSION AR185993
VERSION AR185993.1 GI:20231958
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1481 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2167 GTCTACTTCTCAGGGA 2183
||||| ||||| ||||| |||||
Db 1 GTCTGCTTCTCAGGA 17

RESULT 231
LOCUS AR186381 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1869 from patent US 6346398.
ACCESSION AR186381
VERSION AR186381.1 GI:20232346
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1869 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2167 GTCTACTTCTCAGGGA 2183
||||| ||||| ||||| |||||
Db 1 GTCTGCTTCTCAGGA 17

RESULT 231
LOCUS AR186381 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1869 from patent US 6346398.
ACCESSION AR186381
VERSION AR186381.1 GI:20232346
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1869 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 GGAGCCAGGAGACTC 446
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Db 17 GGAGCCAGAGAGAGTC 1

RESULT 232
LOCUS AR186382 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1870 from patent US 6346398.
ACCESSION AR186382
VERSION AR186382.1 GI:20232347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1870 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 GGAGCCAGGAGACTC 446
||||| ||||| ||||| |||||
Db 17 GGAGCCAGAGAGAGTC 1

RESULT 232
LOCUS AR186382 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1870 from patent US 6346398.
ACCESSION AR186382
VERSION AR186382.1 GI:20232347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1870 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 430 GGAGCCAGGAGACTC 446
||||| ||||| ||||| |||||
Db 17 GGAGCCAGAGAGAGTC 1

REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 1870 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 429 AGGAGCCAGGAGACT 445
||||| ||||| ||||| |||||
Db 17 AGGAGCCAGAGAGACT 1

RESULT 233
LOCUS AR187083 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2571 from patent US 6346398.
ACCESSION AR187083
VERSION AR187083.1 GI:20233048
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2571 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 224 TCATTTCCTTGATATCAA 240
||||| ||||| ||||| |||||
Db 1 TCATGCTTGTGATTTCAA 17

RESULT 234
LOCUS AR188877 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4365 from patent US 6346398.
ACCESSION AR188877
VERSION AR188877.1 GI:20234842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 4365 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 224 TCATTTCCTTGATATCAA 240
||||| ||||| ||||| |||||
Db 1 TCATGCTTGTGATTTCAA 17

RESULT 234
LOCUS AR188877/c 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4365 from patent US 6346398.
ACCESSION AR188877
VERSION AR188877.1 GI:20234842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 4365 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1509 AACAGCAGCAGAGCTCA 1525

AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 7450 12-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2757 GTCTGAATCTCAGACC 2773
 Db 1 GGCTGACTCTCAGACC 17
 RESULT 238
 LOCUS AR283934/c 17 bp DNA linear PAT 10-APR-2003
 DEFINITION Sequence 13 from patent US 6528257.
 ACCESSION AR283934
 VERSION AR283934.1 GI:29720834
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sharma,V.M. and Ganesan,K.
 TITLE Method for the simultaneous monitoring of individual mutants in mixed populations
 JOURNAL Patent: US 6528257-A 13 04-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2753 AGGGTCTGAATCTCAG 2769
 Db 17 AGGGTCTGACGCTCAG 1
 RESULT 239
 LOCUS AR322623 17 bp RNA linear PAT 17-AUG-2003
 DEFINITION Sequence 25 from patent US 6566127.
 ACCESSION AR322623
 VERSION AR322623.1 GI:33708431
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6566127-A 25 20-MAY-2003;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned RNA"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2166 TGCTTACTTCTCAGGG 2182
 Db 1 TGCTGCTTCTCAGGG 17

Db 17 AACAGGAGGAGAGCTCA 1
 RESULT 235
 LOCUS AR191745 17 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 7233 from patent US 6346398.
 ACCESSION AR191745
 VERSION AR191745.1 GI:20237710
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 7233 12-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2166 TGCTTACTTCTCAGGG 2182
 Db 1 TGCTGCTTCTCAGGG 17
 RESULT 236
 LOCUS AR191746 17 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 7234 from patent US 6346398.
 ACCESSION AR191746
 VERSION AR191746.1 GI:20237711
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 7234 12-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2167 GTCTACTTCTCAGGGA 2183
 Db 1 GTCTGCTTCTCAGGGA 17
 RESULT 237
 LOCUS AR191962 17 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 7450 from patent US 6346398.
 ACCESSION AR191962
 VERSION AR191962.1 GI:20237927
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)

TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6566127-A 415 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..17
	/organism="unknown"
	/mol_type="unassigned RNA"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.8e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	429 AGGAGCCAGGAGACT 445
Db	17 AGGAGCCAGGAGAGT 1
RESULT 243	
AR323693	
LOCUS	AR323693 17 bp RNA linear PAT 17-AUG-2003
DEFINITION	Sequence 1095 from patent US 6566127.
ACCESSION	AR323693
VERSION	AR323693.1 GI:33709501
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6566127-A 1095 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..17
	/organism="unknown"
	/mol_type="unassigned RNA"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.8e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	224 TCATTTCTTGATTCAA 240
Db	1 TCATGTCTTGATTCAA 17
RESULT 244	
AR324730/C	
LOCUS	AR324730 17 bp RNA linear PAT 17-AUG-2003
DEFINITION	Sequence 2132 from patent US 6566127.
ACCESSION	AR324730
VERSION	AR324730.1 GI:33710538
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL	Patent: US 6566127-A 2132 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..17
	/organism="unknown"
	/mol_type="unassigned RNA"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.8e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1509 AACAGCAGCAGACTCA 1525
Db	17 AACAGGAGGAGACTCA 1

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related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 6437 20-MAY-2003;
JOURNAL
FEATURES
    source
    1..17
    /organism="unknown"
    /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1095 CATTGAGCCACAGACC 1111
Db 1 CATGAGCCCACTGAGC 17

RESULT 248
AR434101
LOCUS AR434101 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 524 from patent US 6656700.
ACCESSION AR434101
VERSION AR434101.1 GI:40196944
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y. and Shannon, M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 524 02-DEC-2003;
FEATURES
    source
    1..17
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    /mol_type="genomic DNA"

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Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 473 CAAATGACCCACAGAGAA 489
Db 1 CAAAGGAACCAAGAGAA 17

RESULT 249
AR456987
LOCUS AR456987 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 664 from patent US 6686188.
ACCESSION AR456987
VERSION AR456987.1 GI:42692044
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 664 03-FEB-2004;
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    /mol_type="genomic DNA"

Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 664 TCAGCAAGCCACAGAGAA 680
Db 1 TCAGCAAGCCACAGAGAA 17

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AR325854
LOCUS AR325854 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3256 from patent US 6566127.
ACCESSION AR325854
VERSION AR325854.1 GI:33711662
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3256 20-MAY-2003;
FEATURES
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    /organism="unknown"
    /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2757 GTCTGATCTCAGACCC 2773
Db 1 GGCTGACTCTCAGACCC 17

RESULT 246
AR326810
LOCUS AR326810 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 4212 from patent US 6566127.
ACCESSION AR326810
VERSION AR326810.1 GI:33712618
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4212 20-MAY-2003;
FEATURES
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    /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2165 CTGTCTACTTCTCACGG 2181
Db 1 CTGTCTGCTTCTCACAG 17

RESULT 247
AR329035
LOCUS AR329035 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6437 from patent US 6566127.
ACCESSION AR329035
VERSION AR329035.1 GI:33714843
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions

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RESULT 250
AR456988
LOCUS AR456988 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 665 from patent US 6686188.
ACCESSION AR456988
VERSION AR456988.1 GI:42692045
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 665 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
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QY 665 CAGCAAGCCAGAGGAG 681
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Db 1 CAGCAAGCCAGAGAG 17
RESULT 251
AR458195
LOCUS AR458195 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1872 from patent US 6686188.
ACCESSION AR458195
VERSION AR458195.1 GI:42693252
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 1872 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1022 CCTCTCTGCTGGACC 1038
|||||
Db 1 CCTCTCTGCTGGACC 17
RESULT 252
AR458196
LOCUS AR458196 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1873 from patent US 6686188.
ACCESSION AR458196
VERSION AR458196.1 GI:42693253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 1873 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"
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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
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QY 765 CTCTCAGCTGAGGCC 781
|||||
Db 1 CTACCGAGCTGAGGCC 17
RESULT 254
AR464125
LOCUS AR464125 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7802 from patent US 6686188.
ACCESSION AR464125
VERSION AR464125.1 GI:42699182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7802 03-FEB-2004;
FEATURES Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1023 CCTCTCTGCTGGACCA 1039
|||||
Db 1 CCTCTCTGCTGGACCA 17
RESULT 253
AR459056
LOCUS AR459056 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2733 from patent US 6686188.
ACCESSION AR459056
VERSION AR459056.1 GI:42694113
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2733 03-FEB-2004;
FEATURES Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 765 CTCTCAGCTGAGGCC 781
|||||
Db 1 CTACCGAGCTGAGGCC 17
RESULT 254
AR464125
LOCUS AR464125 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7802 from patent US 6686188.
ACCESSION AR464125
VERSION AR464125.1 GI:42699182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7802 03-FEB-2004;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1022 CCTCTCTGCTGGACC 1038
|||||
Db 1 CCTCTCTGCTGGACC 17
RESULT 252
AR458196
LOCUS AR458196 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1873 from patent US 6686188.
ACCESSION AR458196
VERSION AR458196.1 GI:42693253
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 1873 03-FEB-2004;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 765 CTCTCAGCTGAGGCC 781
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RESULT 254
AR464125
LOCUS AR464125 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7802 from patent US 6686188.
ACCESSION AR464125
VERSION AR464125.1 GI:42699182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7802 03-FEB-2004;
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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1023 CCTCTCTGCTGGACCA 1039
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Db 1 CCTCTCTGCTGGACCA 17
RESULT 253
AR459056
LOCUS AR459056 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2733 from patent US 6686188.
ACCESSION AR459056
VERSION AR459056.1 GI:42694113
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2733 03-FEB-2004;
FEATURES Location/Qualifiers
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RESULT 255			
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DEFINITION	Sequence 7803 from patent US 6686188.	17 bp	DNA
ACCESSION	AR464126		
VERSION	AR464126.1	GI:42699183	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unklassified.		
REFERENCE	1 (bases 1 to 17)		
AUTHORS	Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.		
TITLE	Polyucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle		
JOURNAL	Patent: US 6686188-A 7803 03-FEB-2004;		
FEATURES	Location/Qualifiers		
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QY	1425	AGCAGCAGCAGCAGCAA	1441
Dd			
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RESULT 256			
LOCUS	AR466570		
DEFINITION	Sequence 10247 from patent US 6686188.	17 bp	DNA
ACCESSION	AR466570		
VERSION	AR466570.1	GI:42701627	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unklassified.		
REFERENCE	1 (bases 1 to 17)		
AUTHORS	Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.		
TITLE	Polyucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle		
JOURNAL	Patent: US 6686188-A 10247 03-FEB-2004;		
FEATURES	Location/Qualifiers		
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QY	1187	TCAGCCCGGTGGGCA	1203
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	1	TCAGCCAAAGTGGGCA	17
RESULT 257			
LOCUS	AR467070		
DEFINITION	Sequence 10747 from patent US 6686188.	17 bp	DNA
ACCESSION	AR467070		
VERSION	AR467070.1	GI:42702127	
KEYWORDS	Unknown.		
SOURCE	Unknown.		

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 10747 03-FEB-2004;
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QY 1771 TGTGGTAGGCCAGAACCA 1787
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DB 1 TGTGGTTGGCTGAACA 17
RESULT 258
AX037420
LOCUS AX037420 linear PAT 16-NOV-2000
DEFINITION Sequence 45 from Patent WO0056922.
ACCESSION AX037420
VERSION AX037420.1 GI:11226845
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Norberg, L.T., Olaisson, E., Jonsson, L., Lindstrom, P.H. and Sanders, R.
TITLE Genetic polymorphism and polymorphic pattern for assessing disease status, and compositions for use thereof
JOURNAL Patent: WO 0056922-A 45 28-SEP-2000;
NORBERG LEIF TORBJORN (SE) ; OLAISSON ERIK (SE) ; JONSSON LENA (SE) ; GEMINI GENOMICS AB (SE) ; LINDSTROM PER HARRY RUTGER (SE) ; SANDERS RHIANNON (SE)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1427 CAGCAGCAGCAGCAACA 1443
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DB 1 CGCGCGCAGCAGCAACA 17
RESULT 259
AX037426
LOCUS AX037426 linear PAT 16-NOV-2000
DEFINITION Sequence 51 from Patent WO0056922.
ACCESSION AX037426
VERSION AX037426.1 GI:11226851
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Norberg, L.T., Olaisson, E., Jonsson, L., Lindstrom, P.H. and Sanders, R.
TITLE Genetic polymorphism and polymorphic pattern for assessing disease status, and compositions for use thereof
JOURNAL Patent: WO 0056922-A 51 28-SEP-2000;

NORBERG LEIF TORBJORN (SE) ; OLAISSON ERIK (SE) ; JONSSON LENA (SE)
; GEMINI GENOMICS AB (SE) ; LINDSTROM PER HARRY RUTGER (SE) ;
SANDERS RHIANNON (SE)

FEATURES
source
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Location/Qualifiers

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1427 GCAGCAGCAGCAACA 1443

Db 1 CGCGGCAGCAGCAACA 17

RESULT 260

AX215324

LOCUS AX215324 17 bp RNA linear PAT 07-SEP-2001

DEFINITION Sequence 766 from Patent WO0159103.

ACCESSION AX215324

VERSION AX215324.1 GI:15525367

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression

JOURNAL Patent: WO 0159103-A 766 16-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

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/organism="synthetic construct"

/mol_type="unassigned RNA"

/db_xref="taxon:32630"

/note="Nucleic Acid"

Query Match

Best Local Similarity 88.2%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGC 1427

Db 1 CGCGGCAGCAGCAGC 17

RESULT 261

AX215325

LOCUS AX215325 17 bp RNA linear PAT 07-SEP-2001

DEFINITION Sequence 767 from Patent WO0159103.

ACCESSION AX215325

VERSION AX215325.1 GI:15525368

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression

JOURNAL Patent: WO 0159103-A 767 16-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

source

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/organism="synthetic construct"

/mol_type="unassigned RNA"

/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGC 1427

Db 1 GCAGCAGCTGCAGCATC 17

RESULT 262

AX215661

LOCUS AX215661 17 bp RNA linear PAT 07-SEP-2001

DEFINITION Sequence 1103 from Patent WO0159103.

ACCESSION AX215661

VERSION AX215661.1 GI:15525704

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression

JOURNAL Patent: WO 0159103-A 1103 16-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

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/organism="synthetic construct"

/mol_type="unassigned RNA"

/db_xref="taxon:32630"

/note="Nucleic Acid"

Query Match

Best Local Similarity 88.2%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1687 GCTCCTACTTCAGCAA 1703

Db 1 GATCCTACTTCAGAAA 17

RESULT 263

AX216107

LOCUS AX216107 17 bp RNA linear PAT 07-SEP-2001

DEFINITION Sequence 1549 from Patent WO0159103.

ACCESSION AX216107

VERSION AX216107.1 GI:15526150

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and

nogo gene expression

JOURNAL Patent: WO 0159103-A 1549 16-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES

source

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/organism="synthetic construct"

/mol_type="unassigned RNA"

/db_xref="taxon:32630"

/note="Nucleic Acid"

Query Match

Best Local Similarity 88.2%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1409 CAGCAGCAGCAGCAGCA 1425
Db 1 CAGCAGTCGAGCATCA 17

RESULT 264
AX216350
LOCUS AX216350 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1792 from Patent WO0159103.
ACCESSION AX216350
VERSION AX216350.1 GI:15526411
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1409 CAGCAGCAGCAGCAGCA 1425
Db 1 CGGCAGCAGCTGCAGCA 17

RESULT 265
AX217014
LOCUS AX217014 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2456 from Patent WO0159103.
ACCESSION AX217014
VERSION AX217014.1 GI:15527075
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
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/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1700 CAATGCAGATCAGCC 1716
Db 1 CAATGCAGATCTGCC 17

RESULT 266
AX217450/c
LOCUS AX217450 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2892 from Patent WO0159103.
ACCESSION AX217450
VERSION AX217450.1 GI:15527511
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3416 TAAAAAAGGTAATAGAA 3432
Db 17 TAAAAAAGGAACAGAA 1

RESULT 267
AX217453/c
LOCUS AX217453 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2895 from Patent WO0159103.
ACCESSION AX217453
VERSION AX217453.1 GI:15527514
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3201 ATGCTTAAAAATGAAA 3217
Db 17 ATGTTAAAAAAGGAAA 1

RESULT 268
AX226753/c
LOCUS AX226753 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 125 from Patent WO0157206.
ACCESSION AX226753
VERSION AX226753.1 GI:15555894
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

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other sequences; artificial sequences.
1
REFERENCE
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Boher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 125 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 666 AGCAAGCCAGGAGC 682
Db 17 AGCAGAGCTAGAGGAGC 1

RESULT 269
AX227106/c
LOCUS AX227106 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 478 from Patent WO0157206.
ACCESSION AX227106
VERSION AX227106.1 GI:15556247
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0157206-A 478 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 667 GCAAGCCAGGAGCA 683
Db 17 GCAGAGCTAGAGGAGCA 1

RESULT 270
AX227461/c
LOCUS AX227461 17 bp RNA linear PAT 10-SEP-2001
DEFINITION Sequence 833 from Patent WO0157206.
ACCESSION AX227461
VERSION AX227461.1 GI:15556602
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Boher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 833 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

other sequences; artificial sequences.
1
REFERENCE
AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Boher,R.N. and Holman,P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL Patent: WO 0157206-A 125 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 665 CAGCAAGCCAGGAGC 681
Db 17 CAGCAGAGCTAGAGGAG 1

RESULT 271
AX272889
LOCUS AX272889 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 458 from Patent WO0162911.
ACCESSION AX272889
VERSION AX272889.1 GI:16545626
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 458 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2508 CACCAAACTGGGCTCT 2524
Db 1 CAACAAGCTGGGCTCT 17

RESULT 272
AX273038
LOCUS AX273038 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 607 from Patent WO0162911.
ACCESSION AX273038
VERSION AX273038.1 GI:16545775
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 607 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 983 CACCAGCAGCAGCACCA 999
Db 1 CCCTGCAGCAGCACCA 17

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RESULT 273	AX325009/c	17 bp	DNA	linear	PAT 02-SEP-2002
LOCUS	Sequence 1147 from Patent WO0192512.				
DEFINITION	AX325009				
ACCESSION	AX325009.1	GI:18095764			
VERSION					
KEYWORDS	Cucumis sativus (cucumber)				
SOURCE	Cucumis sativus				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.				
REFERENCE	1				
AUTHORS	Knier, E.B., Gamper, H.B., Rice, M.C. and Kim, J.				
TITLE	Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides				
JOURNAL	Patent: WO 0192512-A 1147 06-DEC-2001; UNIVERSITY OF DELAWARE (US)				
FEATURES	Location/Qualifiers				
source	1..17				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:3659"				
Query Match	0.4%;	Score 13.8;	DB 1;	Length 17;	
Best Local Similarity	88.2%;	Pred. No. 1.8e+02;			
Matches	15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	928 CCAGCAGCTCAAAACAGA 944				
DB	17 CCAGCTGCTCAAAACCGA 1				
RESULT 274	AX325010	17 bp	DNA	linear	PAT 02-SEP-2002
LOCUS	Sequence 1148 from Patent WO0192512.				
DEFINITION	AX325010				
ACCESSION	AX325010.1	GI:18095765			
VERSION					
KEYWORDS	Cucumis sativus (cucumber)				
ORGANISM	Cucumis sativus				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.				
REFERENCE	1				
AUTHORS	Knier, E.B., Gamper, H.B., Rice, M.C. and Kim, J.				
TITLE	Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides				
JOURNAL	Patent: WO 0192512-A 1148 06-DEC-2001; UNIVERSITY OF DELAWARE (US)				
FEATURES	Location/Qualifiers				
source	1..17				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:3659"				
Query Match	0.4%;	Score 13.8;	DB 1;	Length 17;	
Best Local Similarity	88.2%;	Pred. No. 1.8e+02;			
Matches	15;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	928 CCAGCAGCTCAAAACAGA 944				
DB	1 CCAGCTGCTCAAAACCGA 17				
RESULT 275	AX325029/c	17 bp	DNA	linear	PAT 19-JUN-2002
LOCUS	Sequence 1167 from Patent WO0192512.				
DEFINITION	AX325029				

REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
Patent: WO 0192512-A 2559 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1. .17
/organism="Brassica napus"
/mol_type="unassigned DNA"
/db_xref="taxon:3708"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAACAGATA 946
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Db 17 AGCAGCTCAACAGCTA 1

RESULT 278
AX326422 17 bp DNA linear PAT 02-SEP-2002
LOCUS
DEFINITION Sequence 2560 from Patent WO0192512.
ACCESSION AX326422
VERSION AX326422.1 GI:18097186
KEYWORDS
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1
AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
JOURNAL single stranded oligonucleotides
Patent: WO 0192512-A 2560 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1. .17
/organism="Brassica napus"
/mol_type="unassigned DNA"
/db_xref="taxon:3708"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 930 AGCAGCTCAACAGATA 946
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Db 1 AGCAGCTCAACAGCTA 17

RESULT 279
AX328593 17 bp DNA linear PAT 08-JAN-2002
LOCUS
DEFINITION Sequence 90 from Patent EP1164203.
ACCESSION AX328593
VERSION AX328593.1 GI:18101792
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1
AUTHORS Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
Xiang,G., Lough,D.M., Ruppert,A. and Hallenkamp,F.
TITLE Dna diagnostics based on mass spectrometry
JOURNAL Patent: EP 1164203-A 90 19-DEC-2001;
SEQUENOM, INC. (US)
FEATURES
source
1. .17
/organism="unidentified"

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1399 ACAGCAGCAACAGCAGC 1415
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Db 1 ACAGCAGCAACAGCATC 17

RESULT 280
AX429297/c 17 bp DNA linear PAT 21-JUN-2002
LOCUS
DEFINITION Sequence 2 from Patent EP1201676.
ACCESSION AX429297
VERSION AX429297.1 GI:21540603
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Cook,P.D.
TITLE Pna-dna-pna chimeric macromolecules
JOURNAL Patent: EP 1201676-A 2 02-MAY-2002;
ISIS PHARMACEUTICALS, INC. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="PNA analogue"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 38 CGGAAATTCAGCGAGAA 54
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Db 17 CTGAAATGCAGCGAGAA 1

RESULT 281
AX467582 17 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 18 from Patent WO224889.
ACCESSION AX467582
VERSION AX467582.1 GI:21900774
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Epstein,N.D., Hassanzadeh,S., Winitzky,S. and Davis,J.S.
TITLE Optimized cardiac contraction through differential phosphorylation
JOURNAL Patent: WO 0224889-A 18 28-MAR-2002;
The Secretary of the Department of Health and Human Services (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 845 TCAGTCCCTCAGAGCCA 861
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Db 1 TCAGACCCCGCAGAGCCA 17

RESULT 282	AX527213	17 bp	DNA	linear	PAT 21-NOV-2002
LOCUS	Sequence 243 from Patent WO0226818.				
DEFINITION	AX527213				
ACCESSION	AX527213				
VERSION	AX527213.1	GI:25171828			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Gu, Y. and Corrigan, A.				
TITLE	Human nedd-1				
JOURNAL	Patent: WO 0226818-A 243 04-APR-2002;				
FEATURES	source				
	1. .17				
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	/db_xref="taxon:9606"				
Query Match	0.4%; Score 13.8; DB 1; Length 17;				
Best Local Similarity	88.2%; Pred. No. 1.8e+02;				
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	2673	ACCAGTTAACACGACGCA 2689			
DB	1	ACCAAGTTAGACCATCA 17			
LOCUS	AX527214	17 bp	DNA	linear	PAT 21-NOV-2002
DEFINITION	Sequence 244 from Patent WO0226818.				
ACCESSION	AX527214				
VERSION	AX527214.1	GI:25171829			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Gu, Y. and Corrigan, A.				
TITLE	Human nedd-1				
JOURNAL	Patent: WO 0226818-A 244 04-APR-2002;				
FEATURES	source				
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Query Match	0.4%; Score 13.8; DB 1; Length 17;				
Best Local Similarity	88.2%; Pred. No. 1.8e+02;				
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	2674	CCAGTTAACACGACGAG 2690			
DB	1	CCAGTTAGACCATCAG 17			
LOCUS	AX527215	17 bp	DNA	linear	PAT 21-NOV-2002
DEFINITION	Sequence 245 from Patent WO0226818.				
ACCESSION	AX527215				
VERSION	AX527215.1	GI:25171830			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Gu, Y. and Corrigan, A.				
TITLE	Human nedd-1				
JOURNAL	Patent: WO 0226818-A 245 04-APR-2002;				
FEATURES	source				
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Query Match	0.4%; Score 13.8; DB 1; Length 17;				
Best Local Similarity	88.2%; Pred. No. 1.8e+02;				
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	2675	CAGTTAACACGACGAGT 2691			
DB	1	CAGTTAGACCATCAGT 17			
LOCUS	AX527216	17 bp	DNA	linear	PAT 21-NOV-2002
DEFINITION	Sequence 246 from Patent WO0226818.				
ACCESSION	AX527216				
VERSION	AX527216.1	GI:25171831			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Gu, Y. and Corrigan, A.				
TITLE	Human nedd-1				
JOURNAL	Patent: WO 0226818-A 246 04-APR-2002;				
FEATURES	source				
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Query Match	0.4%; Score 13.8; DB 1; Length 17;				
Best Local Similarity	88.2%; Pred. No. 1.8e+02;				
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	2676	AGTTAACACGACGAGTG 2692			
DB	1	AGTTAGACCATCAGTG 17			
LOCUS	AX527217	17 bp	DNA	linear	PAT 21-NOV-2002
DEFINITION	Sequence 247 from Patent WO0226818.				
ACCESSION	AX527217			</	


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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2677 GTTAACACCGACGCTGC 2693
Db 1 GTTAAGACCATCAGTGC 17

RESULT 287
AX531063
LOCUS AX531063 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 572 from Patent EP1239051.
ACCESSION AX531063
VERSION AX531063.1 GI:25253908
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 572 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2550 AAGCCCTGACGCTCTGCA 2566
Db 1 AACCCAGACGCTCTGCA 17

RESULT 288
AX531064
LOCUS AX531064 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 573 from Patent EP1239051.
ACCESSION AX531064
VERSION AX531064.1 GI:25253910
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 573 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2551 AGCCCTGACGCTCTGCA 2567
Db 1 ACCCCAGACGCTCTGCA 17

RESULT 289
AX531472/c
LOCUS AX531472 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 981 from Patent EP1239051.
ACCESSION AX531472
VERSION AX531472.1 GI:25254721
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 981 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3090 AAAGAAGAAAGGGAAGA 3106
Db 17 AACAGAGTAGGGAAGA 1

RESULT 290
AX532058/c
LOCUS AX532058 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1567 from Patent EP1239051.
ACCESSION AX532058
VERSION AX532058.1 GI:25255879
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1567 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2211 TTCAGAAATATGGGGATG 2227
Db 17 TTCTGAAATGGGGATG 1

RESULT 291
AX578494
LOCUS AX578494 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 332 from Patent WO0211674.
ACCESSION AX578494
VERSION AX578494.1 GI:27647696
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 332 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1648 CCAGCCTTTGCTAAGGT 1664
Db 1 CCAGGCAATTGCTAAGGT 17
RESULT 292
AX578973/c 17 bp RNA linear PAT 10-JAN-2003
LOCUS
DEFINITION Sequence 811 from Patent WO0211674.
ACCESSION AX578973
VERSION AX578973.1 GI:27648175
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 811 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 269 GCAGGACAGGTGGCCT 285
Db 17 GCAGGAAAAGCTGGCCT 1
RESULT 293
AX615899 17 bp DNA linear PAT 20-FEB-2003
LOCUS
DEFINITION Sequence 706 from Patent EPI262488.
ACCESSION AX615899
VERSION AX615899.1 GI:28446945
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y. and Nguyen,C.T.
TITLE Human lcl-domain containing protein
JOURNAL Patent: EP 1262488-A 706 04-DEC-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 765 CTCCTCAGCTGAGGCC 781
Db 1 CTCCTCAGCCAGGCC 17
RESULT 295
AX672024 17 bp DNA linear PAT 27-MAR-2003
LOCUS
DEFINITION Sequence 469 from Patent WO03004526.
ACCESSION AX672024
VERSION AX672024.1 GI:29330372
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 469 16-JAN-2003;
Molecular Engines Laboratories (FR)
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/db_xref="taxon:9606"
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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1180 CGGCCCTCAGCCAGG 1196
Db 1 CTGCTCTCAGCCAGG 17
RESULT 294
AX615902 17 bp DNA linear PAT 20-FEB-2003
LOCUS
DEFINITION Sequence 709 from Patent EPI262488.
ACCESSION AX615902
VERSION AX615902.1 GI:28446948
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y. and Nguyen,C.T.
TITLE Human lcl-domain containing protein
JOURNAL Patent: EP 1262488-A 709 04-DEC-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 765 CTCCTCAGCTGAGGCC 781
Db 1 CTCCTCAGCCAGGCC 17
RESULT 295
AX672024 17 bp DNA linear PAT 27-MAR-2003
LOCUS
DEFINITION Sequence 469 from Patent WO03004526.
ACCESSION AX672024
VERSION AX672024.1 GI:29330372
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 469 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1982 GATCAGATAAACCGACA 1998
Db 1 GATCAGAAACAGACA 17

RESULT 296
AX674529
LOCUS AX674529 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2974 from Patent WO03004526.
ACCESSION AX674529
VERSION AX674529.1 GI:29332877
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 2974 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3348 GAACGTGGTGTCATG 3364
Db 1 GATCTGGTGGCAATG 17

RESULT 297
AX687647/c
LOCUS AX687647 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 379 from Patent EPI281758.
ACCESSION AX687647
VERSION AX687647.1 GI:29410343
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 379 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
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/mol_type="unassigned DNA"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 980 CAGCACCAGCAGCAGCA 996
Db 17 CAGCACCAGCAGCTCCA 1

RESULT 298
AX687651/c
LOCUS AX687651 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 383 from Patent EPI281758.
ACCESSION AX687651
VERSION AX687651.1 GI:29410347
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 383 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 976 GCACGACGACCCAGCAGC 992
Db 17 GCTCCAGCACCAGCAGC 1

RESULT 299
AX687652/c
LOCUS AX687652 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 384 from Patent EPI281758.
ACCESSION AX687652
VERSION AX687652.1 GI:29410348
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 384 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 975 TGCAGCAGCAGCAGCAGCAG 991
Db 17 TGCTCCAGCACCAGCAGC 1

RESULT 300
AX688238
LOCUS AX688238 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 970 from Patent EPI281758.
ACCESSION AX688238
VERSION AX688238.1 GI:29410938
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 970 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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1. .17
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2578 CCCACAGGTACACCTG 2594
Db 1 CCCACAGGAGACCTG 17

RESULT 301
LOCUS AX688403 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1135 from Patent EP1281758.
ACCESSION AX688403
VERSION AX688403.1 GI:29411105
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1135 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/db_xref="taxon:9606"

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Best Local Similarity 88.2%; Pred. No. 1.8e+02;
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QY 2941 TTTTGACTTCTCAGCC 2957
Db 17 TTTTGACTTCGTGAGC 1

RESULT 303
LOCUS AX688406 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1138 from Patent EP1281758.
ACCESSION AX688406
VERSION AX688406.1 GI:29411108
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1138 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2939 GCTTTTGACTTCTCTCAG 2955
Db 17 GGTTTTGACTTCGTGAG 1

RESULT 304
LOCUS AX690658 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 3390 from Patent EP1281758.
ACCESSION AX690658
VERSION AX690658.1 GI:29413539
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 3390 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
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QY 976 GCAGCAGCAGCAGCAGC 992
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Db 17 GCTCCAGCACCAGCAGC 1

RESULT 305
AX690659/c
LOCUS AX690659 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 3391 from Patent EP1281758.
ACCESSION AX690659
VERSION AX690659.1 GI:29413540
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon, M., Gu, Y., and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 3391 05-FEB-2003;
Aecomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 975 TGCAGCAGCACCAGCAGC 991
Db 17 TGCTCCAGCACCAGCAGC 1

RESULT 306
AX694226
LOCUS AX694226 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 6958 from Patent EP1281758.
ACCESSION AX694226
VERSION AX694226.1 GI:29417356
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon, M., Gu, Y., and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 6958 05-FEB-2003;
Aecomica, Inc. (US)
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1664 TCACCTTTGCCACTTCA 1680
Db 1 TCACCTTGCACCTTAA 17

RESULT 307
AX724636
LOCUS AX724636 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2323 from Patent WO03025176.
ACCESSION AX724636
VERSION AX724636.1 GI:30503979

KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Teleman, A., Anson, R., and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 2323 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/organism="Mus musculus"
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/db_xref="taxon:10090"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2756 GGTCGTAATCTCAGACC 2772
Db 1 GATCTGAATCTCAGAAC 17

RESULT 308
AX724729
LOCUS AX724729 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2416 from Patent WO03025176.
ACCESSION AX724729
VERSION AX724729.1 GI:30504072
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Teleman, A., Anson, R., and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 2416 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/mol_type="unassigned DNA"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1982 GATCAGATAAACCCACA 1998
Db 1 GATCAGATAAACCCATCA 17

RESULT 309
AX725477/c
LOCUS AX725477 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3164 from Patent WO03025176.
ACCESSION AX725477
VERSION AX725477.1 GI:30504820
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Teleman, A., Anson, R., and Tuijnder, M.

Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines		Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines	
Patent: WO 03025176-A 3164 27-MAR-2003; Molecular Engines Laboratories (FR)		Patent: WO 03025176-A 3164 27-MAR-2003; Molecular Engines Laboratories (FR)	
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Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;		Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;	
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 3013 TTTATTGAAGCAGAGC 3029		QY 3013 TTTATTGAAGCAGAGC 3029	
DB 17 TTTATTGAAGTCAGATC 1		DB 17 TTTATTGAAGTCAGATC 1	
RESULT 312		RESULT 312	
LOCUS AX727570		LOCUS AX727570	
DEFINITION Sequence 5257 from Patent WO03025176.		DEFINITION Sequence 5257 from Patent WO03025176.	
ACCESSION AX727570		ACCESSION AX727570	
VERSION AX727570.1 GI:30506913		VERSION AX727570.1 GI:30506913	
KEYWORDS		KEYWORDS	
SOURCE Mus musculus (house mouse)		SOURCE Mus musculus (house mouse)	
ORGANISM Mus musculus		ORGANISM Mus musculus	
REFERENCE 1		REFERENCE 1	
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.		AUTHORS Telerman,A., Amson,R. and Tuijnder,M.	
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines		TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines	
JOURNAL Patent: WO 03025176-A 5257 27-MAR-2003;		JOURNAL Patent: WO 03025176-A 5257 27-MAR-2003;	
FEATURES Molecular Engines Laboratories (FR)		FEATURES Molecular Engines Laboratories (FR)	
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/db_xref="taxon:10090"		/db_xref="taxon:10090"	
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 1909 GATCATGCAGCAGAAC 1925		QY 1909 GATCATGCAGCAGAAC 1925	
DB 1 GATCATGCAGCAGAGC 17		DB 1 GATCATGCAGCAGAGC 17	
RESULT 313		RESULT 313	
LOCUS AX729275/c		LOCUS AX729275/c	
DEFINITION Sequence 909 from Patent WO03025175.		DEFINITION Sequence 909 from Patent WO03025175.	
ACCESSION AX729275		ACCESSION AX729275	
VERSION AX729275.1 GI:30508618		VERSION AX729275.1 GI:30508618	
KEYWORDS		KEYWORDS	
SOURCE Homo sapiens (human)		SOURCE Homo sapiens (human)	
ORGANISM Homo sapiens		ORGANISM Homo sapiens	
REFERENCE 1		REFERENCE 1	
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.		AUTHORS Telerman,A., Amson,R. and Tuijnder,M.	
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines		TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines	
JOURNAL Patent: WO 03025175-A 909 27-MAR-2003;		JOURNAL Patent: WO 03025175-A 909 27-MAR-2003;	
FEATURES Molecular Engines Laboratories (FR)		FEATURES Molecular Engines Laboratories (FR)	
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	

Qy 1747 ACAACAGACAGCAGATC 1763
Db 17 ACAACAGACATAGGATC 1

RESULT 314
AX731043
LOCUS AX731043 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2677 from Patent WO03025175.
ACCESSION AX731043
VERSION AX731043.1 GI:30510386
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 2677 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 536 GATCCTGAGCTGCAGGA 552
Db 1 GATCCTGAGCTGCCGAA 17

RESULT 315
AX731511
LOCUS AX731511 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3145 from Patent WO03025175.
ACCESSION AX731511
VERSION AX731511.1 GI:30510854
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 3145 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1909 GATCATGACAGCAAAAC 1925
Db 1 GATCCTGGAACAGAAAC 17

RESULT 316

AX731550/c
LOCUS AX731550 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3184 from Patent WO03025175.
ACCESSION AX731550
VERSION AX731550.1 GI:30510893
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 3184 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3417 AAAAAGGTAATAGAAC 3433
Db 17 AAAAAGGTAAGAGATC 1

RESULT 317
AX731740/c
LOCUS AX731740 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3374 from Patent WO03025175.
ACCESSION AX731740
VERSION AX731740.1 GI:30511083
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 3374 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2186 AGAATGCCATCATATC 2202
Db 17 AGAAGGCCATCATGATC 1

RESULT 318
AX734784/c
LOCUS AX734784 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 374 from Patent WO03025177.
ACCESSION AX734784
VERSION AX734784.1 GI:30514061
KEYWORDS
SOURCE Homo sapiens (human)

JOURNAL	thereof as medicaments Patent: WO 03025177-A 1121 27-MAR-2003; Molecular Engines Laboratories (FR)
FEATURES	Location/Qualifiers
source	1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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Best Local Similarity	88.2%; Pred. No. 1.8e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1909 GATCATGGAGCAGAAAC 1925
Dd	1 GATCATGCAGCAGACC 17
RESULT 321	
AX736303	
LOCUS	AX736303 17 bp DNA linear PAT 08-MAY-2003
DEFINITION	Sequence 1893 from Patent WO03025177.
ACCESSION	AX736303
VERSION	AX736303.1 GI:30515580
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1
AUTHORS	Telerman,A., Anson,R. and Tuijnder,M.
TITLE	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL	Patent: WO 03025177-A 1893 27-MAR-2003; Molecular Engines Laboratories (FR)
FEATURES	Location/Qualifiers
source	1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 1.8e+02;
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1108 GAGCTCCCCCATGCGCTG 1124
Dd	1 GATCTCTCCCATGCGCTG 17
RESULT 322	
AX736455	
LOCUS	AX736455 17 bp DNA linear PAT 08-MAY-2003
DEFINITION	Sequence 2045 from Patent WO03025177.
ACCESSION	AX736455
VERSION	AX736455.1 GI:30515743
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1
AUTHORS	Telerman,A., Anson,R. and Tuijnder,M.
TITLE	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL	Patent: WO 03025177-A 2045 27-MAR-2003; Molecular Engines Laboratories (FR)
FEATURES	Location/Qualifiers
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/db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1339 GATCCCTTCGTGTTTGC 1355
| | | | | | | | | | | | | | | |
Db 1 GATCCTTCTGTTGTTGC 17

RESULT 323
LOCUS AX736569 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2159 from Patent WO03025177.
ACCESSION AX736569
VERSION AX736569.1 GI:30515857
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2159 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3066 ATGAATCTTGGGGAAC 3082
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Db 17 ATGATACTTGGGGATC 1

RESULT 324
LOCUS AX736585 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2175 from Patent WO03025177.
ACCESSION AX736585
VERSION AX736585.1 GI:30515873
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2175 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2898 GTTCCAGGCTTTTCAA 2914
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Db 1 GATCCAGGCTTTTCAA 17

RESULT 325
LOCUS AX736642 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2232 from Patent WO03025177.
ACCESSION AX736642
VERSION AX736642.1 GI:30515930
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2232 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1662 GGTCACTTGGCCACTT 1678
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Db 1 GATCACCTTGGCCACTT 17

RESULT 326
LOCUS AX738717 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4307 from Patent WO03025177.
ACCESSION AX738717
VERSION AX738717.1 GI:30518007
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 4307 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1687 GCTCTACTTCAGCAAA 1703
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Db 1 GATCCTACTTCAGAAAA 17

RESULT 327
LOCUS AX739573 17 bp DNA linear PAT 08-MAY-2003
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DEFINITION Sequence 5163 from Patent WO03025177.
ACCESSION AX739573
VERSION AX739573.1 GI:30518870
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 5163 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1918 GCAGAACAGCACTTC 1934
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Db 17 GCAGAACAGCAAGATC 1

RESULT 328
AX745081/c
LOCUS AX745081 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 1046 from Patent WO03031621.
ACCESSION AX745081
VERSION AX745081.1 GI:30723748
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhang,J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 1046 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2367 CAAGTAATAATCAAT 2383
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Db 17 CAATCATATATCAAT 1

RESULT 329
AX754462
LOCUS AX754462 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 809 from Patent WO03037931.
ACCESSION AX754462
VERSION AX754462.1 GI:32167159
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 531 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2756 GGTCTGAATCTCAGACC 2772
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Db 17 GTTCTGAATCTCAGATC 1

RESULT 331
AX758667/c
LOCUS AX758667 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 1988 from Patent WO03040369.
ACCESSION AX758667
VERSION AX758667.1 GI:32253283
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 531 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2756 GGTCTGAATCTCAGACC 2772
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Db 17 GTTCTGAATCTCAGATC 1

AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 809 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 150 GTTCCTTGAAGAGAAA 166
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Db 1 GTTCTTTGAAAGGAAA 17

RESULT 330
AX757210/c
LOCUS AX757210 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 531 from Patent WO03040369.
ACCESSION AX757210
VERSION AX757210.1 GI:32251826
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 531 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2756 GGTCTGAATCTCAGACC 2772
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Db 17 GTTCTGAATCTCAGATC 1
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1896 CTCTACAGAGGAGATC 1912
Db 17 CTCTGAGAGGAGATC 1

RESULT 332
AX758768
LOCUS AX758768 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 2089 from Patent WO03040369.
ACCESSION AX758768
VERSION AX758768.1 GI:32253384
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 2089 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1909 GATCATGGAGCAGAAC 1925
Db 1 GATCATGGAGATGAAC 17

RESULT 333
AX759017
LOCUS AX759017 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 2338 from Patent WO03040369.
ACCESSION AX759017
VERSION AX759017.1 GI:32253633
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 2338 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 536 GATCCTGAGCTGCAGGA 552
Db 1 GATCCTGAGCTGCAGGA 17

RESULT 334
AX760215
LOCUS AX760215 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3536 from Patent WO03040369.
ACCESSION AX760215
VERSION AX760215.1 GI:32254831
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 3536 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2966 GATAACATGGGCCCTGC 2982
Db 1 GATCACTTGGGCCCTGC 17

RESULT 335
AX760680/c
LOCUS AX760680 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 4001 from Patent WO03040369.
ACCESSION AX760680
VERSION AX760680.1 GI:32255296
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 4001 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3486 AACTCCTTAATTGCTC 3502
Db 17 AACTCCTTAATATGATC 1

RESULT 336
AX761769
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LOCUS AX761769 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5090 from Patent WO03040369.
ACCESSION AX761769
VERSION AX761769.1 GI:32256385
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5090 15-MAY-2003;
Molecular Engines Laboratories (FR)
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Qy 55 GATCGCGCTGCACAAATC 71
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LOCUS AX762326 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5647 from Patent WO03040369.
ACCESSION AX762326
VERSION AX762326.1 GI:32256942
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5647 15-MAY-2003;
Molecular Engines Laboratories (FR)
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RESULT 338
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LOCUS AX762501 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5822 from Patent WO03040369.
ACCESSION AX762501
VERSION AX762501.1 GI:32257117
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5822 15-MAY-2003;
Molecular Engines Laboratories (FR)
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RESULT 339
AX762673
LOCUS AX762673 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5994 from Patent WO03040369.
ACCESSION AX762673
VERSION AX762673.1 GI:32257289
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Telerman,A., Amson,R. and Tuijnder,M.
AUTHORS Sequences involved in tumoral suppression, tumoral reversion,
TITLE apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5994 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
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LOCUS AX773291 17 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 265 from Patent WO03045426.
ACCESSION AX773291
VERSION AX773291.1 GI:32485234
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
REFERENCE Ellendoorn,K., Baker,M., Williams,S. and Carr,F.J.
AUTHORS T-cell epitopes in carboxypeptidase g2
TITLE Patent: WO 03045426-A 265 05-JUN-2003;
JOURNAL MERCK PATENT GmbH (DE)
FEATURES Location/Qualifiers

Query Match 0.4%; Score 13.8; DB 1; Length 17;
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Db 1 CGGCGGCAGCAGCAACA 17

RESULT 345
BD075178 17 bp DNA linear PAT 27-AUG-2002
LOCUS Methods for assessing cardiovascular status and compositions for
DEFINITION use thereof.
ACCESSION BD075178
VERSION BD075178.1 GI:22620781
KEYWORDS JP 2001519660-A/51.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 17)
Norberg,L.T., Andersson,M.K. and Lindstrom,P.H.R.
TITLE Methods for assessing cardiovascular status and compositions for
use thereof
JOURNAL Patent: JP 2001519660-A 51 23-OCT-2001;
EURONA MEDICAL AB
COMMENT OS Artificial Sequence
PN JP 2001519660-A/51
PD 23-OCT-2001
PF 01-APR-1998 JP 1998542530
PR 04-APR-1997 US 60/042930
PI LEIF TOREBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
RUTGER LINDSTROM
PC C12Q1/68,C07K14/72,C07K14/575,C12N9/48
CC Description of Artificial Sequence: PCR PRIMER FH Key
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Job time : 15 secs

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RESULT 346
BD132158 17 bp DNA linear PAT 18-SEP-2002
LOCUS DNA diagnosis method based on mass spectrometry.
DEFINITION
ACCESSION BD132158
VERSION BD132158.1 GI:23227103
KEYWORDS JP 2002507883-A/90.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
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Koster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Boom,D.V.D., Jurinke,C. and Rupert,A.
TITLE DNA diagnosis method based on mass spectrometry
JOURNAL Patent: JP 2002507883-A 90 12-MAR-2002;
SEQUENOM INC
COMMENT PN JP 2002507883-A/90
PD 12-MAR-2002
PF 06-NOV-1997 JP 1998521832
PR 06-NOV-1996 US 08/744481,06-NOV-1996 US 08/746036 PR

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RESULT 346
BD132158 17 bp DNA linear PAT 18-SEP-2002
LOCUS DNA diagnosis method based on mass spectrometry.
DEFINITION
ACCESSION BD132158
VERSION BD132158.1 GI:23227103
KEYWORDS JP 2002507883-A/90.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 17)
Koster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Boom,D.V.D., Jurinke,C. and Rupert,A.
TITLE DNA diagnosis method based on mass spectrometry
JOURNAL Patent: JP 2002507883-A 90 12-MAR-2002;
SEQUENOM INC
COMMENT PN JP 2002507883-A/90
PD 12-MAR-2002
PF 06-NOV-1997 JP 1998521832
PR 06-NOV-1996 US 08/744481,06-NOV-1996 US 08/746036 PR

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Search completed: August 16, 2005, 12:48:45
Job time : 15 secs

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 346
BD132158 17 bp DNA linear PAT 18-SEP-2002
LOCUS DNA diagnosis method based on mass spectrometry.
DEFINITION
ACCESSION BD132158
VERSION BD132158.1 GI:23227103
KEYWORDS JP 2002507883-A/90.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 17)
Koster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Boom,D.V.D., Jurinke,C. and Rupert,A.
TITLE DNA diagnosis method based on mass spectrometry
JOURNAL Patent: JP 2002507883-A 90 12-MAR-2002;
SEQUENOM INC
COMMENT PN JP 2002507883-A/90
PD 12-MAR-2002
PF 06-NOV-1997 JP 1998521832
PR 06-NOV-1996 US 08/744481,06-NOV-1996 US 08/746036 PR

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
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 Seq primer: CGTGTAAACGACGCCAGT
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 High quality sequence stop: 27.

FEATURES

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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli Xl10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
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FEATURES

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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli Xl10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

Query Match 0.7%; Score 27; DB 1; Length 27;
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 ACCESSION AZ779573
 VERSION AZ779573.1 GI:12910362
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606

Query Match

Best Local Similarity 100.0%; Pred. No. 1.4; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1411 GCAGCAGCAGCAGCAGCAGCAGCA 1434
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 ACCESSION AZ831993
 VERSION AZ831993.1 GI:13001901
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: M column: 01
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES

source

Location/Qualifiers

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 0.001 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
918.832 Million cell updates/sec

Title: US-10-698-070-2

Perfect score: 73

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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SUMMARIES

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8	25.6	35.1	256171	4	US-09-949-016-12822
9	25.6	35.1	256176	4	US-09-949-016-15524
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15	25.2	34.5	601	4	US-09-949-016-153205
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24.4	33.4	95621	4	US-09-949-016-13237	Sequence 13237, A
24.4	33.4	161124	4	US-09-949-016-11760	Sequence 11760, A
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23.4	32.1	601	4	US-09-949-016-151882	Sequence 151882, A
23.4	32.1	10365	4	US-08-892-695-9	Sequence 9, Appl
23.4	32.1	20022	4	US-09-949-016-12604	Sequence 12604, A
23.4	32.1	20023	4	US-09-949-016-16004	Sequence 16004, A
23.4	32.1	24508	4	US-09-949-016-16005	Sequence 16005, A
23.4	32.1	24519	4	US-09-949-016-11864	Sequence 11864, A
23.4	32.1	28355	4	US-09-949-016-16975	Sequence 16975, A
23.4	32.1	162841	4	US-09-949-016-13733	Sequence 13733, A
23.4	32.1	177669	4	US-09-949-016-13713	Sequence 13713, A
23.2	31.8	1551	4	US-09-107-532A-3502	Sequence 3502, Ap
23.2	31.8	2830	2	US-09-010-928B-1	Sequence 1, Appl
23	31.5	411	2	US-08-449-287-7	Sequence 7, Appl
23	31.5	732	2	US-08-860-882A-29	Sequence 29, Appl
23	31.5	732	3	US-09-011-769A-26	Sequence 26, Appl
23	31.5	2426	4	US-09-949-016-5365	Sequence 5365, Ap
23	31.5	2910	3	US-09-206-942-31	Sequence 31, Appl
23	31.5	2928	3	US-09-206-942-29	Sequence 29, Appl
23	31.5	41454	4	US-09-949-016-17107	Sequence 17107, A
23	31.5	110243	4	US-09-949-016-13698	Sequence 13698, A
23	31.5	124211	4	US-09-949-016-13877	Sequence 13877, A
23	31.5	312474	4	US-09-949-016-17434	Sequence 17434, A
22.8	31.2	601	4	US-09-949-016-129219	Sequence 129219, A
22.8	31.2	601	4	US-09-949-016-147718	Sequence 147718, A
22.8	31.2	1084	4	US-09-293-826-1	Sequence 1, Appl
22.8	31.2	1519	4	US-09-270-767-12348	Sequence 12348, A
22.8	31.2	1759	4	US-08-600-991-22	Sequence 22, Appl
22.8	31.2	2199	4	US-08-605-221-3	Sequence 3, Appl
22.8	31.2	2214	4	US-08-605-221-1	Sequence 1, Appl
22.8	31.2	33536	4	US-09-949-016-17034	Sequence 17034, A
22.8	31.2	33536	4	US-09-949-016-17035	Sequence 17035, A
22.8	31.2	144922	4	US-09-949-016-15890	Sequence 15890, A
22.6	31.0	601	4	US-09-949-016-64710	Sequence 64710, A
22.6	31.0	601	4	US-09-949-016-135512	Sequence 135512, A
22.6	31.0	601	4	US-09-949-016-135532	Sequence 135532, A
22.6	31.0	1506	4	US-09-949-016-2284	Sequence 2284, Ap
22.6	31.0	1893	1	US-08-271-667B-5	Sequence 5, Appl
22.6	31.0	1893	3	US-08-765-889C-18	Sequence 18, Appl
22.6	31.0	1893	5	PCT-US95-07855-18	Sequence 18, Appl
22.6	31.0	2101	3	US-08-765-889C-5	Sequence 5, Appl
22.6	31.0	2101	5	PCT-US95-07855-5	Sequence 5, Appl
22.6	31.0	2200	1	US-09-949-016-3863	Sequence 3863, Ap
22.6	31.0	2304	1	US-08-271-667B-6	Sequence 6, Appl
22.6	31.0	2304	3	US-08-765-889C-19	Sequence 19, Appl
22.6	31.0	2304	5	PCT-US95-07855-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-17375
; Sequence 17375, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17375
; LENGTH: 84296
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(84296)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17375

Query Match 37.3%; Score 27.2; DB 4; Length 84296;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 32; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 13 AGGTTAACTACTGTTGAGCTTGACGAGGTGGTTAACT 52
Db 11530 AAGTTAATTAAGTATTAATCTTGACGAGGTGGTGAAGCT 11569

RESULT 2
US-08-311-731A-130
; Sequence 130, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616

; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36941 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-130

Query Match 36.2%; Score 26.4; DB 4; Length 36941;
Best Local Similarity 65.0%; Pred. No. 16;
Matches 39; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 2 TGCAGGAGATAGGTTAACTTACCTGTTGAAGCTTGACGAGGTGGTTAACTATCTCTCTGC 61
Db 25498 TGGATGGAGATTGGTAAACCAACCAAGCTCAACCATGACGAGGTGGTGTCTCCAGC 25557

RESULT 3

US-09-949-016-82614
; Sequence 82614, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82614
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82614

Query Match 35.3%; Score 25.8; DB 4; Length 601;
Best Local Similarity 67.9%; Pred. No. 8.5;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 18 AACTACCTGTTGAAGCTTGACGAGGTGGTTAACTATCTCTCTACAGTTT 70
Db 123 AATCAGCTGTTGAAGCTTGTGCATGTGTACGTAGTTCTCGTGCCATGATTTT 175

RESULT 4

US-09-949-016-82615
; Sequence 82615, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82615
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82615

Query Match 35.3%; Score 25.8; DB 4; Length 601;
Best Local Similarity 67.9%; Pred. No. 8.5;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 18 AACTACCTGTTGAAGCTTGAGCGGTGGTTAACTATCTCTCTGCTACAGTTT 70
Db 184 AATCAGCTGTGAAGCTTGGCATGTGTACGTAGTTCTCGTGCCATGATTTT 236

RESULT 5

US-09-949-016-82616
; Sequence 82616, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82616
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82616

Query Match 35.3%; Score 25.8; DB 4; Length 601;
Best Local Similarity 67.9%; Pred. No. 8.5;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 18 AACTACCTGTTGAAGCTTGAGCGGTGGTTAACTATCTCTCTGCTACAGTTT 70
Db 456 AATCAGCTGTGAAGCTTGGCATGTGTACGTAGTTCTCGTGCCATGATTTT 508

RESULT 6

US-09-949-016-14138/c
; Sequence 14138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14138
; LENGTH: 121068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14138

Query Match 35.3%; Score 25.8; DB 4; Length 121068;
Best Local Similarity 67.9%; Pred. No. 38;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 18 AACTACCTGTTGAAGCTTGAGCGGTGGTTAACTATCTCTCTGCTACAGTTT 70
Db 94693 AATCAGCTGTGAAGCTTGGCATGTGTACGTAGTTCTCGTGCCATGATTTT 94641

RESULT 7

US-09-949-016-135083
; Sequence 135083, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135083
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-135083

Query Match 35.1%; Score 25.6; DB 4; Length 601;
Best Local Similarity 77.5%; Pred. No. 10;
Matches 31; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 14 GGTTAACTACCTGTTGAAGCTTGAGCGGTGGTTAACTCTA 53
Db 167 GGTAGGACCTGTTGTAGCTAAAGCAGGTGGTTAAATGTA 206

RESULT 8

US-09-949-016-12822/c
; Sequence 12822, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12822
; LENGTH: 256171
; TYPE: DNA
; ORGANISM: Human

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(256171)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12822

Query Match      35.1%; Score 25.6; DB 4; Length 256171;
Best Local Similarity 77.5%; Pred. No. 56;
Matches 31; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 14 GGTAACTACCTGTTGAAGCTTGACGAGTGTTAACTCTA 53
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230491 GGGTAGGAACCTGTTGTAGCTAAAGCAGGTGGTAAATGTA 230452

RESULT 9
US-09-949-016-15524/c
; Sequence 15524, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15524
; LENGTH: 256176
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(256176)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15524

Query Match      35.1%; Score 25.6; DB 4; Length 256176;
Best Local Similarity 77.5%; Pred. No. 56;
Matches 31; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 14 GGTAACTACCTGTTGAAGCTTGACGAGTGTTAACTCTA 53
    ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230491 GGGTAGGAACCTGTTGTAGCTAAAGCAGGTGGTAAATGTA 230452

RESULT 10
US-09-949-016-58/c
; Sequence 58, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David, et al.
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; FILE REFERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/09/809,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/545,199
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 5798
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (698)..(1468)
; OTHER INFORMATION: unknown D2
US-09-809-665A-60/c

Query Match      34.8%; Score 25.4; DB 4; Length 5798;
Best Local Similarity 64.4%; Pred. No. 23;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 TTGCAGGAGATAGGTTAACTCTGTTGAAGCTTGACGAGTGTTAACTCTCTCT 59
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3177 TTCACAAACAATAGGTTTACGACGTGCATCTCATTAGCTGTAGGTAATCTAACTCTCT 3119

RESULT 11
US-09-809-665A-60/c
; Sequence 60, Application US/09809665A
; Patent No. 6790950
; GENERAL INFORMATION:
; APPLICANT: Lowery E., David, et al.
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
; FILE REFERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/09/809,665A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/153,453
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 09/545,199
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 5798
; TYPE: DNA
; ORGANISM: Pasteurella multocida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (698)..(1468)
; OTHER INFORMATION: unknown D2
US-09-809-665A-60

Query Match      34.8%; Score 25.4; DB 4; Length 5798;
Best Local Similarity 64.4%; Pred. No. 23;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 TTGCAGGAGATAGGTTAACTCTGTTGAAGCTTGACGAGTGTTAACTCTCTCT 59
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3177 TTCACAAACAATAGGTTTACGACGTGCATCTCATTAGCTGTAGGTAATCTAACTCTCT 3119

RESULT 12
US-09-949-016-58673
; Sequence 58673, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 5798
```

; SEQ ID NO 58673
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58673

Query Match 34.5%; Score 25.2; DB 4; Length 601;
Best Local Similarity 62.9%; Pred. No. 14;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 9 AGATAGTTAACTACCTGTTGAAGCTTGACGAGTGTAACTATCTCTGCTAACAGT 68
Db 524 AGCTAGATGATGAGCCTGTTGAAGCGGAGGCTGTTGCTAATATTTCTCTTTTTCACAGT 583
Qy 69 TT 70
Db 584 CT 585

RESULT 13

US-09-949-016-58674
; Sequence 58674, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58674
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58674

Query Match 34.5%; Score 25.2; DB 4; Length 601;
Best Local Similarity 62.9%; Pred. No. 14;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 9 AGATAGTTAACTACCTGTTGAAGCTTGACGAGTGTAACTATCTCTGCTAACAGT 68
Db 218 AGCTAGATGATGAGCCTGTTGAAGCGGAGGCTGTTGCTAATATTTCTCTTTTTCACAGT 277
Qy 69 TT 70
Db 278 CT 279

RESULT 14

US-09-949-016-58675
; Sequence 58675, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58675
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58675

Query Match 34.5%; Score 25.2; DB 4; Length 601;
Best Local Similarity 62.9%; Pred. No. 14;
Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 9 AGATAGTTAACTACCTGTTGAAGCTTGACGAGTGTAACTATCTCTGCTAACAGT 68
Db 46 AGCTAGATGATGAGCCTGTTGAAGCGGAGGCTGTTGCTAATATTTCTCTTTTTCACAGT 105
Qy 69 TT 70
Db 106 CT 107

RESULT 15

US-09-949-016-153205
; Sequence 153205, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153205
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-153205

Query Match 34.5%; Score 25.2; DB 4; Length 601;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 42; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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Db 160 TTTCAGGATGATTGTAATAACTCACTGAAGTGGCTGGTGGTCTCATCCCTGTAATC 219
Qy 61 CTAACAGTTT 70
Db 220 CCAACACTTT 229

Search completed: August 14, 2005, 21:50:17
Job time : 135 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 20:21:10 ; Search time 636 Seconds
(without alignments)
744.708 Million cell updates/sec

Title: US-10-698-070-2

Perfect score: 73

Sequence: 1 ttggcaggagataggtaaac.....tctctgctaacagttttt 73

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7305758 seqs, 3244068913 residues

Total number of hits satisfying chosen parameters: 14611516

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	48	65.8	73	21	Sequence 2, Appli
C 3	29	39.7	101507	20	US-10-698-070-2
C 4	28.2	38.6	600	22	US-10-719-993-6772
5	28	38.4	28	21	Sequence 41910, A
C 6	28	38.4	3763	21	US-10-698-070-5
C 7	28	38.4	5419	19	US-10-698-070-1
					Sequence 3, Appli

Sequence 4710, Ap	5458	38.4	28	21	US-10-956-157-4710
Sequence 5783, Ap	1240	36.7	26.8	18	US-10-425-114-5783
Sequence 3768, A	1984	36.7	26.8	18	US-10-425-114-3768
Sequence 2243, A	2381	36.7	26.8	20	US-10-425-115-2243
Sequence 1, Appli	3763	36.4	26.6	21	US-10-698-070-1
Sequence 3, Appli	5419	36.4	26.6	19	US-10-479-546-3
Sequence 4710, Ap	5458	36.4	26.6	21	US-10-956-157-4710
Sequence 655, App	71678	36.4	26.6	13	US-10-087-192-655
Sequence 146, App	138837	36.4	26.6	19	US-10-322-281-146
Sequence 163609,	462	36.2	26.4	20	US-10-425-115-163609
Sequence 392, App	805	35.3	25.8	9	US-09-764-864-392
Sequence 1915, Ap	2874	35.3	25.8	17	US-10-104-047-1915
Sequence 1416, Ap	3818	35.3	25.8	17	US-10-108-260A-1416
Sequence 739, App	564	34.8	25.4	20	US-10-723-860-739
Sequence 58, App	5798	34.8	25.4	11	US-09-809-665A-58
Sequence 60, Appl	5798	34.8	25.4	11	US-09-809-665A-60
Sequence 58, Appl	5798	34.8	25.4	11	US-10-854-299-58
Sequence 60, Appl	5798	34.8	25.4	21	US-10-854-299-60
Sequence 32, Appl	8705	34.8	25.4	17	US-10-336-093-32
Sequence 27658, A	476	34.5	25.2	17	US-10-242-535A-27658
Sequence 16484, A	1062	34.5	25.2	18	US-10-085-783A-16484
Sequence 5727, Ap	216929	34.5	25.2	19	US-10-741-601-5727
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Sequence 201893,	637	34.2	25	13	US-10-027-632-201893
Sequence 201894,	637	34.2	25	13	US-10-027-632-201894
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Sequence 201893,	637	34.2	25	13	US-10-027-632-201893
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Sequence 9, Appli	1201	33.7	24.6	19	US-10-813-805-9
Sequence 5, Appli	2393	33.7	24.6	21	US-10-432-985-5
Sequence 5231, Ap	5893	33.7	24.6	18	US-10-956-157-5231
Sequence 3708, Ap	5898	33.7	24.6	9	US-09-880-107-3708
Sequence 586, App	5898	33.7	24.6	21	US-10-505-680-586
Sequence 5264, Ap	5941	33.7	24.6	20	US-10-723-860-5264
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Sequence 70, Appl	133300	33.7	24.6	19	US-10-331-053-70
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Sequence 139896,	380	33.4	24.4	20	US-10-425-115-139896
Sequence 14160, A	466	33.4	24.4	9	US-09-864-761-14160
Sequence 226524,	591	33.4	24.4	13	US-10-027-632-226524
Sequence 13761, A	591	33.4	24.4	13	US-10-027-632-226524
Sequence 4741, Ap	985	33.4	24.4	19	US-10-767-701-13761
Sequence 96175, A	1981	33.4	24.4	20	US-10-425-115-4741
Sequence 11, Appl	4344	33.4	24.4	19	US-10-437-963-96175
Sequence 11, Appl	5402	33.4	24.4	16	US-10-072-977-11
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Sequence 15735, A	728	33.2	24.2	13	US-10-027-632-15735
Sequence 3183, Ap	862	33.2	24.2	17	US-10-260-238-3183
Sequence 57350, A	971	33.2	24.2	19	US-10-437-963-57350
Sequence 29562, A	1118	33.2	24.2	17	US-10-369-493-29562
Sequence 129082,	1188	33.2	24.2	18	US-10-424-599-129082
Sequence 91601, A	2169	33.2	24.2	18	US-10-424-599-91601
Sequence 459, App	2934	33.2	24.2	19	US-10-437-963-459
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Sequence 59, Appl	3357	33.2	24.2	13	US-10-154-419-59
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Sequence 39, Appl	3408	33.2	24.2	10	US-09-921-159-3
Sequence 7, Appli	3760	33.2	24.2	19	US-10-467-685-39
Sequence 57, Appl	4632	33.2	24.2	13	US-10-024-623-7
Sequence 23, Appl	4632	33.2	24.2	13	US-10-154-419-57
Sequence 52, Appl	4632	33.2	24.2	16	US-10-146-733-52
Sequence 34, Appl	4632	33.2	24.2	17	US-10-352-684A-23
Sequence 7351, Ap	9144	33.2	24.2	17	US-10-336-091-34
Sequence 78, Appl	22073	33.2	24.2	10	US-09-764-891-7351
Sequence 78, Appl	64275	33.2	24.2	22	US-10-737-082-78
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c 90      24 32.9 663 17 US-10-027-632-211619 Sequence 211619,
c 91      24 32.9 763 13 US-10-027-632-151369 Sequence 151369,
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c 95      24 32.9 1431 17 US-10-282-122A-16477 Sequence 16477, A
c 96      24 32.9 2046 15 US-10-102-524-1783 Sequence 1783, AP
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c 98      24 32.9 2550 18 US-10-424-599-52068 Sequence 52068, A
c 99      24 32.9 2622 17 US-10-282-122A-38751 Sequence 38751, A
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ALIGNMENTS

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RESULT 1
US-10-698-070-2
; Sequence 2, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiyu, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: RNAi clone
US-10-698-070-2
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Best Local Similarity 100.0%; Pred. No. 6.5e-17;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCAGGAGATAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCTG 60
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Qy 61 CTAACAGTTTTTT 73
Db 61 CTAACAGTTTTTT 73
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RESULT 2
US-10-698-070-2/c
; Sequence 2, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiyu, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: RNAi clone
US-10-698-070-2
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Best Local Similarity 84.4%; Pred. No. 1.1e-07;
Matches 54; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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Qy 1 TTGGCAGGAGATAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCTG 60
Db 64 TTAGCAGGAGATAGATTACCACTGCTCAAGCTTCAACAGGTAGTTAACTATCTCTCTG 5

Qy 61 CTA 64
Db 4 CCA 1
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RESULT 3
US-10-719-993-6772/c
; Sequence 6772, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6772
; LENGTH: 101507
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-6772
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Best Local Similarity 67.2%; Pred. No. 13;
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Qy 70 T 70
Db 92144 T 92144
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RESULT 4
US-10-972-079-41910/c
; Sequence 41910, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; CURRENT FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41910
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894278239_1
US-10-972-079-41910

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Best Local Similarity 61.6%; Pred. No. 4.7;
Matches 45; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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DB 267 TTGGCTGCAGCTGTATGGAGCTTTGTGGAAATCCAGCAGATGGTTATTTTCGTGCTG 208

QY 61 CTAAACAGTTTTTT 73
DB 207 CAAACGTTGTTTT 195

RESULT 5
US-10-698-070-5
; Sequence 5, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiya, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: fragment of Mect1-MAML2 sequence
US-10-698-070-5

Query Match 38.4%; Score 28; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCAGGAGATAGGTTAACTACTCTGT 28
DB 1 TTGGCAGGAGATAGGTTAACTACTCTGT 28

RESULT 6
US-10-698-070-1/c
; Sequence 1, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiya, Takefumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 3763
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-698-070-1

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Best Local Similarity 100.0%; Pred. No. 10;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGGCAGGAGATAGGTTAACTACTCTGT 28
DB 192 TTGGCAGGAGATAGGTTAACTACTCTGT 165

RESULT 7
US-10-479-546-3/c
; Sequence 3, Application US/10479546
; Publication No. US20040180349A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Tonon, Giovanni
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER INVOLVING THE NOTCH PATHWAY
; FILE REFERENCE: 225402
; CURRENT APPLICATION NUMBER: US/10/479,546
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/US02/21344
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,788
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 5419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-546-3

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Best Local Similarity 100.0%; Pred. No. 12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCAGGAGATAGGTTAACTACTCTGT 28
DB 1848 TTGGCAGGAGATAGGTTAACTACTCTGT 1821

RESULT 8
US-10-956-157-4710/c
; Sequence 4710, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4710
; LENGTH: 5458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4710

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Best Local Similarity 100.0%; Pred. No. 12;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCAGGAGATAGGTTAACTACTCTGT 28
DB 1878 TTGGCAGGAGATAGGTTAACTACTCTGT 1851

RESULT 9
US-10-425-114-5783/c
; Sequence 5783, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

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; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5783
; LENGTH: 1240
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700472565_FLI
US-10-425-114-5783

Query Match          36.7%; Score 26.8; DB 18; Length 1240;
Best Local Similarity 68.5%; Pred. No. 20;
Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Db 1142 TAATTCAACGACATCTTCAAACTTGAGCAGGTGGTTCCTCTTAACGCCTCTTTAC 1089

RESULT 10
US-10-425-114-33768/c
; Sequence 33768, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
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; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17168H09_FLI
US-10-425-114-33768

Query Match          36.7%; Score 26.8; DB 18; Length 1984;
Best Local Similarity 68.5%; Pred. No. 23;
Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 12 TAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCGCTAAC 65
   |||||
Db 1854 TAATTCAACGACATCTTCAAACTTGAGCAGGTGGTTCCTCTTAACGCCTCTTTAC 1801

RESULT 11
US-10-425-115-22243/c
; Sequence 22243, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

```
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 22243
; LENGTH: 2381
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_120288C.1
US-10-425-115-22243

Query Match          36.7%; Score 26.8; DB 20; Length 2381;
Best Local Similarity 68.5%; Pred. No. 25;
Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 12 TAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCGCTAAC 65
   |||||
Db 1994 TAATTCAACGACATCTTCAAACTTGAGCAGGTGGTTCCTCTTAAGGCCTCTTTAC 1941

RESULT 12
US-10-698-070-1
; Sequence 1, Application US/10698070
; Publication No. US20050095709A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Komiyama, Taketumi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING TRANSLATION OF A CHIMERIC
; FILE REFERENCE: 221749
; CURRENT APPLICATION NUMBER: US/10/698,070
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 3763
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-698-070-1

Query Match          36.4%; Score 26.6; DB 21; Length 3763;
Best Local Similarity 78.0%; Pred. No. 34;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 27 TTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCTCGCTAACAG 67
   |||||
Db 155 TTGAAAAGAAACAGAGTAGTTAACTATCTCTCTGCAACAG 195

RESULT 13
US-10-479-546-3
; Sequence 3, Application US/10479546
; Publication No. US20040180349A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Frederic J.
; APPLICANT: Tonon, Giovanni
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CANCER INVOLVING THE NOTCH PATHWAY
; FILE REFERENCE: 225402
; CURRENT APPLICATION NUMBER: US/10/479,546
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: PCT/US02/21344
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/302,788
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 5419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-479-546-3
```

Query Match 36.4%; Score 26.6; DB 19; Length 5419;
Best Local Similarity 78.0%; Pred. No. 38;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 27 TTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCTGCTAACAG 67
|||||
DB 1811 TTGAAGAAGAAACAGGTAGTTACCTATCTCTGCCAACAG 1851

RESULT 14

US-10-956-157-4710
; Sequence 4710, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4710
; LENGTH: 5458
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4710

Query Match 36.4%; Score 26.6; DB 21; Length 5458;
Best Local Similarity 78.0%; Pred. No. 38;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 27 TTGAAGCTTGAGCAGGTGGTTAATCTATCTCTGCTAACAG 67
|||||
DB 1841 TTGAAGAAGAAACAGGTAGTTACCTATCTCTGCCAACAG 1881

RESULT 15

US-10-087-192-655
; Sequence 655, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 655
; LENGTH: 71678
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(71678)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-655

Query Match 36.4%; Score 26.6; DB 13; Length 71678;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 15 GTTAACCTACCTGTGAAGCTTGAGCAGGTGGTTAATCTATCTCTGCTAACAGTTTT 71
|||||

Db 44626 GTGAACCTTTGTGTGTAGCTGGATCAGCTGGTAGATCTATTTCTAGCACATTGATTT 44682

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Listing first 100 summaries

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12: Geneseqn2004as:.*
13: Geneseqn2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	28	38.4	3459	10	Adc59309 DNA encod
C 2	28	38.4	5419	8	Abao00947 MAML2 cod
C 3	26.6	36.4	633	4	Aah32177 Human olf
C 4	26.6	36.4	3459	10	Adc59309 DNA encod
C 5	26.6	36.4	5419	8	Abao00947 MAML2 cod
C 6	26.6	36.4	60747	4	Abli16128 Drosophil
C 7	26.6	36.4	71678	11	Acn44284 Mouse gen
C 8	26.6	36.4	13837	13	Abd33163 Human can
C 9	26.4	36.2	36941	10	Adb74381 Mycobacte
C 10	25.8	35.3	805	4	Aas26213 Human cdn
C 11	25.8	35.3	805	8	Abx73554 Human nov
C 12	25.8	35.3	2874	10	Adb63761 Human cdn
C 13	25.8	35.3	3352	13	Adc509779 Human the
C 14	25.8	35.3	3363	10	Adc29954 Human nov
C 15	25.8	35.3	3597	13	Adc08359 Full leng
C 16	25.8	35.3	3818	11	Adm02731 Human cdn
C 17	25.8	35.3	3828	10	Adc31891 Human nov
C 18	25.8	35.3	3828	13	Adsi11143 Human the
C 19	25.8	35.3	4078	13	Adr06863 Full leng
C 20	25.6	35.1	110000	6	Abn71527_07 Continuation (8 of

C 94 24.2 33.2 3519 10 ADC10059 Human NOV
 C 95 24.2 33.2 3583 10 ADC10053 Human NOV
 C 96 24.2 33.2 3760 8 RAD47366 Human tra
 C 97 24.2 33.2 4632 6 ABQ74264 Human 544
 C 98 24.2 33.2 4632 10 ADD37480 Human tra
 C 99 24.2 33.2 4632 10 ADK52565 Hematolog
 C 100 24.2 33.2 4632 12 ADI27959 Human 544

ALIGNMENTS

RESULT 1
 ADC59309/c
 ID ADC59309 standard; DNA; 3459 BP.
 XX
 AC ADC59309;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE DNA encoding human polypeptide #1.
 XX
 KW Human; ds; polyglutamine disease; Gene;
 KW Genealogical polyglutamine disease; nontropic; anticonvulsant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3459
 FT /*tag= a
 FT /product= "Polypeptide #1"
 XX
 PN JP2002360268-A.
 XX
 PD 17-DEC-2002.
 XX
 PF 03-AUG-2001; 2001JP-00236788.
 XX
 PR 04-AUG-2000; 2000JP-00236839.
 PR 06-APR-2001; 2001JP-00108723.
 XX
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
 PA (DAUC) DAIICHI PHARM CO LTD.
 XX
 DR WPI; 2003-516153/49.
 DR P-PSDB; ADC59310.
 XX
 PT A genealogical line diagnostic marker for polyglutamine disease, useful
 PT in the diagnosis, prevention and/or treatment, comprises a polyglutamine
 PT related gene and its encoded polypeptide.
 XX
 PS Claim 1; SEQ ID NO 1; 72pp; Japanese.
 XX
 CC The invention discloses polyglutamine disease related genes and their
 CC encoded polypeptides. Also claimed is a recombinant vector,
 CC transformants, preparation of the polynucleotides and resultant
 CC polypeptides, diagnostic methods and a kit. The genes and encoded
 CC polypeptides are useful in the diagnosis, prevention and treatment of
 CC genealogical polyglutamine disease. The sequence presented is a DNA
 CC encoding one of the polypeptides of the invention.
 XX
 SQ Sequence 3459 BP; 1023 A; 1031 C; 767 G; 638 T; 0 U; 0 Other;

Query Match 38.4%; Score 28; DB 10; Length 3459;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCAGGAGATAGGTTAACTACCTGTT 28
 |||||
 Db 563 TTGGCAGGAGATAGGTTAACTACCTGTT 536
 |||||

RESULT 2

ABA00947/c
 ID ABA00947 standard; cDNA; 5419 BP.
 XX
 AC ABA00947;
 XX
 DT 28-APR-2003 (first entry)
 XX
 DE MAML2 coding sequence.
 XX
 KW Consensus sequence; NOTCH; Mastermind-like; gene family; screening; t(11;
 KW 19)(q14-21; p12-13); translocation; MECT1-MAML2 chimera; MECT1; MAML2;
 KW cancer; mucoepidermoid carcinoma; malignant; salivary gland; tumour;
 KW chromosome 11q21; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1286..4747
 FT /*tag= a
 FT /product= "MAML2"
 XX
 PN WC2003004645-A1.
 XX
 PD 16-JAN-2003.
 XX
 PF 03-JUL-2002; 2002WO-US021344.
 XX
 PR 03-JUL-2001; 2001US-0302788P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Kaye FJ, Tonon G;
 XX
 DR WPI; 2003-210364/20.
 DR P-PSDB; AAG79910.
 XX
 PT Screening a tissue sample from a subject for a t(11;19)(q14-21;p12-13)
 PT translocation, useful for treating mucoepidermoid carcinoma comprises
 PT detecting the presence of MECT1-MAML2 chimeric nucleic acid or protein in
 PT a tissue sample.
 XX
 PS Disclosure; Page 57-58; 65pp; English.
 XX
 CC This sequence encodes human MAML2. The MAML2 gene contains 5 exons and
 CC spans 340 kb at human 11q21. MAML2 exon 1 is contained within the BAC
 CC RP11-16K5, while exon 2 was separated by a 270 kb intron 1, confirming
 CC the MAML2 was disrupted by a chromosomal breakpoint near the 3' end of
 CC the large MAML2 intron 1. The method of the invention allows for
 CC screening of a tissue sample from a subject for a t(11;19)(q14-21;p12-13)
 CC translocation and comprises detecting the presence of MECT1-MAML2
 CC chimeric nucleic acid or protein in a tissue sample. Direct sequencing
 CC demonstrated a chimeric RNA species representing exon 1 of MECT1 fused in
 CC frame to MAML2 exons 2-5. The method of the invention is useful for
 CC diagnosing and treating cancer, including cancer that involves the NOTCH
 CC pathway, particularly cancer of mucoepidermoid carcinoma, the most common
 CC malignant salivary gland tumour
 XX
 SQ Sequence 5419 BP; 1627 A; 1438 C; 1163 G; 1191 T; 0 U; 0 Other;

Query Match 38.4%; Score 28; DB 8; Length 5419;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCAGGAGATAGGTTAACTACCTGTT 28
 |||||
 Db 1848 TTGGCAGGAGATAGGTTAACTACCTGTT 1821
 |||||

RESULT 3
 AAH32177/c
 ID AAH32177 standard; DNA; 633 BP.
 XX
 AC AAH32177;


```

XX DT 30-JUL-2001 (first entry)
XX DE Human olfactory receptor polynucleotide, SEQ ID NO: 750.
XX KW Human; olfactory receptor; OR; primary scent determination;
XX KW secondary scent determination; polypeptide library; odour receptor;
XX KW scent profile; scent fingerprint; scent representation; ds.
XX OS Homo sapiens.
XX PN WO200127158-A2.
XX PD 19-APR-2001.
XX PF 06-OCT-2000; 2000WO-US027582.
XX PR 08-OCT-1999; 99US-0158615P.
XX PR 24-FEB-2000; 2000US-0184809P.
XX PA (DIGI-) DIGISCENTS.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WIPI; 2001-290713/30.
XX New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.
XX Claim 8; Page 481-482; 1857pp; English.
XX The present sequence is one of a number of isolated polynucleotides which
CC encode polypeptides involved in olfactory sensation. The polynucleotides
CC can be used in screening for olfactory agonists and antagonists. The
CC methods allow for the determination of primary scents and the
CC identification of the odour receptors used to detect these primary
CC scents. The methods also enable determination of secondary scents and the
CC identification of combinations of odour receptors that are involved in
CC detecting such secondary scents. This enables the construction of a scent
CC representation (also called a scent fingerprint or scent profile), which
CC may be used to re-create and edit scents. Libraries of olfactory
CC receptors are useful for determining the interaction pattern of a
CC composition with the receptors, and can be used for determining
CC differences in the olfactory faculties of different individuals
XX SQ Sequence 633 BP; 138 A; 157 C; 135 G; 203 T; 0 U; 0 Other;

Query Match 36.4%; Score 26.6; DB 4; Length 633;
Best Local Similarity 63.1%; Pred. No. 11;
Matches 41; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 8 GAGATAGTTAACTACCTGTTGAAGCTTGAGCTTGAGCAGGTGGTTAATCTATCTCTCTTAACAG 67
DB 111 GACAAGATACGTGATGCTGATCTCTGTAAGAGAGATAGTTCTATCTTCCGCAACCAA 52

QY 68 TTTT 72
DB 51 GTTCT 47

RESULT 4
ADCS9309
ID ADCS9309 standard; DNA; 3459 BP.
XX AC ADCS9309;
XX DT 18-DEC-2003 (first entry)
XX DE DNA encoding human polypeptide #1.
XX KW Human; ds; polyglutamine disease; gene;
XX KW genealogical polyglutamine disease; nootropic; anticonvulsant.

XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX CDS 1286..4747
/*tag= a
/product= "MAML2"

WO2003004645-A1.
16-JAN-2003.

XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX CDS 1..3459
/*tag= a
/product= "Polypeptide #1"

JP2002360268-A.
17-DEC-2002.
XX 03-AUG-2001; 2001JP-00236788.
XX 04-AUG-2000; 2000JP-00236839.
XX 06-APR-2001; 2001JP-00108723.
XX (KAZU-) ZH KAZUSA DNA KENKYUSHO.
XX PA (DAUC ) DAICHI PHARM CO LTD.
XX WIPI; 2003-516153/49.
XX DR P-PSDB; ADCS9310.
XX A genealogical line diagnostic marker for polyglutamine disease, useful
PT in the diagnosis, prevention and/or treatment, comprises a polyglutamine
PT related gene and its encoded polypeptide.
XX Claim 1; SEQ ID NO 1; 72pp; Japanese.
XX The invention discloses polyglutamine disease related genes and their
CC encoded polypeptides. Also claimed is a recombinant vector,
CC transformants, preparation of the polynucleotides and resultant
CC polypeptides, diagnostic methods and a kit. The genes and encoded
CC polypeptides are useful in the diagnosis, prevention and treatment of
CC genealogical polyglutamine disease. The sequence presented is a DNA
CC encoding one of the polypeptides of the invention.
XX SQ Sequence 3459 BP; 1023 A; 1031 C; 767 G; 638 T; 0 U; 0 Other;

Query Match 36.4%; Score 26.6; DB 10; Length 3459;
Best Local Similarity 78.0%; Pred. No. 17;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 27 TTGAAGCTTGACAGCTGGTTAATCTATCTCTCTGTAACAG 67
DB 526 TTGAAAGAAACAGGTAGTTAACTATCTCTCTGCAACAG 566

RESULT 5
ABA00947
ID ABA00947 standard; cDNA; 5419 BP.
XX AC ABA00947;
XX DT 28-APR-2003 (first entry)
XX DE NAML2 coding sequence.
XX KW Consensus sequence; NOTCH; Mastermind-like; gene family; screening; t(11;
XX KW 19)(q14-21; p12-13); translocation; MECT1-MAML2 chimera; MECT1; MAML2;
XX KW cancer; mucoepidermoid carcinoma; malignant; salivary gland; tumour;
XX KW chromosome 11q21; ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX CDS 1286..4747
/*tag= a
/product= "MAML2"

WO2003004645-A1.
16-JAN-2003.

```


CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US200218586A1, for which no sequence data was published
XX
SQ Sequence 71678 BP; 20309 A; 14954 C; 15127 G; 20103 T; 0 U; 1185 Other;
Query Match 36.4%; Score 26.6; DB 11; Length 71678;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 15 GTTAACCTACCTGTTGAAGCTTGAGCAGGTGGTAACTATCTCTCTAAACAGTTT 71
DB 44626 GTGACCTTGTGGTGTAGCTGATCAGTGTAGTACTATTTCTAGCACATTGATTT 44692
RESULT 8
ABD33163
ID ABD33163 standard; DNA; 138837 BP.
XX
AC ABD33163;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated (CA) gene HD07-022.
XX
KW Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW db; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004058146-A2.
XX
PD 15-JUL-2004.
XX
PF 15-DEC-2003; 2003WO-US040081.
XX
PR 17-DEC-2002; 2002US-00322281.
XX
PS (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Malandro MS;
XX
DR WPI; 2004-499109/47.
XX
PT Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
XX
PS Claim 16; SEQ ID NO 146; 182pp; English.
XX
CC The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a human CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at fp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 138837 BP; 34853 A; 26094 C; 29642 G; 41293 T; 0 U; 6955 Other;

Query Match 36.4%; Score 26.6; DB 13; Length 138837;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 17 TAACTACCTGTTGAAGCTTGAGCAGGTGGTAACTATCTCTCTAAACAGTTT 73
DB 58591 TTAGTACTATTCACGCTTGTCTAGCTGGTAACTGTAAGCTGTTAAAAATTTT 58647
RESULT 9
ADB74381
ID ADB74381 standard; DNA; 36941 BP.
XX
AC ADB74381;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mycobacterium leprae DNA #15.
XX
KW Non-naturally occurring peptide; anion pump protein; tuberculosis;
KW hypersensitivity reaction; tuberculostatic; gene; db.
XX
OS Mycobacterium leprae.
XX
PN US6583266-B1.
XX
PD 24-JUN-2003.
XX
PF 16-SEP-1994; 94US-00311731.
XX
PR 19-AUG-1993; 93US-00109181.
PR 22-OCT-1993; 93US-00142558.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Smith DR, Mao J;
XX
DR WPI; 2003-656441/62.
XX
PT New Mycobacterium tuberculosis anion pump peptide useful for as
PT tuberculosis vaccine and diagnosis of tuberculosis infection.
XX
PS Disclosure; SEQ ID NO 130; 26pp; English.
XX
CC The invention relates to a non-naturally occurring peptide of
CC Mycobacterium tuberculosis comprising an amino acid sequence
CC corresponding to an anion pump protein. The invention also relates to a
CC non-naturally occurring nucleic acid corresponding to a DNA sequence of
CC Mycobacterium tuberculosis or Mycobacterium leprae. The new peptide is
CC useful as a vaccine against Mycobacterium tuberculosis or Mycobacterium
CC leprae or for screening for new tuberculosis drugs. Purified proteins
CC derived from the sequences of the invention may elicit a specific immune
CC response. The peptide may also be used to detect hypersensitivity
CC reactions of individuals exposed to Mycobacterium tuberculosis or
CC Mycobacterium leprae. The proteins and peptides may be affixed to solid
CC supports to detect antibodies typical of hypersensitivity reactions, from
CC a patient's sera. This sequence represents Mycobacterium leprae DNA of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification but was obtained in electronic format
CC directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 36941 BP; 8242 A; 11465 C; 10255 G; 6979 T; 0 U; 0 Other;
Query Match 36.2%; Score 26.4; DB 10; Length 36941;
Best Local Similarity 65.0%; Pred. No. 40;
Matches 39; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 2 TGCGAGGAGATAGGTTAACTACCTGTTGAAGTTTGAGCGAGGTGTTAATCTATCTCTGCG 61
DB 25498 TGGATGGATGTTGGTAAACCAACCACTCAACCATGAGCGAGTGGCTGCTCCAGC 25557
RESULT 10

AA526213	07-SEP-2000;	2000US-02312444P
ID	AA526213 standard; cDNA; 805 BP.	PR 08-SEP-2000;
XX	AA526213;	PR 08-SEP-2000;
AC		PR 08-SEP-2000;
XX		PR 08-SEP-2000;
DT		PR 08-SEP-2000;
XX	07-NOV-2001 (first entry)	PR 12-SEP-2000;
XX		PR 14-SEP-2000;
DE	Human cDNA encoding a novel secreted protein, Seq ID 392.	PR 14-SEP-2000;
XX		PR 14-SEP-2000;
KW	Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic;	PR 14-SEP-2000;
KW	cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;	PR 14-SEP-2000;
KW	antibacterial; virucide; fungicide; opthalmological; vulnerary;	PR 14-SEP-2000;
KW	secreted protein; rheumatoid arthritis; hyperproliferative disorder;	PR 14-SEP-2000;
KW	cardiovascular disorder; cardiac arrest; cerebrovascular disorder;	PR 14-SEP-2000;
KW	cerebral ischaemia; angiogenesis; nervous system disorder;	PR 21-SEP-2000;
KW	Alzheimer's disease; infection; ocular disorder; corneal infection;	PR 21-SEP-2000;
KW	wound healing; epithelial cell proliferation; skin ageing; food additive;	PR 25-SEP-2000;
KW	preservative; antiproliferative.	PR 26-SEP-2000;
XX		PR 27-SEP-2000;
OS	Homo sapiens.	PR 27-SEP-2000;
XX		PR 29-SEP-2000;
XX	WO200155322-A2.	PR 29-SEP-2000;
PD	02-AUG-2001.	PR 29-SEP-2000;
XX		PR 29-SEP-2000;
XX	17-JAN-2001; 2001WO-US001341.	PR 29-SEP-2000;
XX		PR 02-OCT-2000;
XX		PR 02-OCT-2000;
PR	31-JAN-2000; 2000US-0179065P.	PR 02-OCT-2000;
PR	04-FEB-2000; 2000US-0180628P.	PR 02-OCT-2000;
PR	24-FEB-2000; 2000US-0184664P.	PR 02-OCT-2000;
PR	02-MAR-2000; 2000US-0186350P.	PR 02-OCT-2000;
PR	16-MAR-2000; 2000US-0189874P.	PR 13-OCT-2000;
PR	17-MAR-2000; 2000US-0190076P.	PR 13-OCT-2000;
PR	18-APR-2000; 2000US-01981123P.	PR 20-OCT-2000;
PR	19-MAY-2000; 2000US-0205515P.	PR 20-OCT-2000;
PR	07-JUN-2000; 2000US-0209467P.	PR 20-OCT-2000;
PR	28-JUN-2000; 2000US-0214886P.	PR 20-OCT-2000;
PR	30-JUN-2000; 2000US-0215135P.	PR 20-OCT-2000;
PR	07-JUL-2000; 2000US-0216647P.	PR 20-OCT-2000;
PR	07-JUL-2000; 2000US-0216880P.	PR 20-OCT-2000;
PR	11-JUL-2000; 2000US-0217487P.	PR 20-OCT-2000;
PR	14-JUL-2000; 2000US-0217486P.	PR 20-OCT-2000;
PR	14-JUL-2000; 2000US-0218290P.	PR 20-OCT-2000;
PR	26-JUL-2000; 2000US-0220963P.	PR 20-OCT-2000;
PR	26-JUL-2000; 2000US-0220964P.	PR 20-OCT-2000;
PR	14-AUG-2000; 2000US-0224518P.	PR 20-OCT-2000;
PR	14-AUG-2000; 2000US-0224519P.	PR 01-NOV-2000;
PR	14-AUG-2000; 2000US-0225213P.	PR 08-NOV-2000;
PR	14-AUG-2000; 2000US-0225214P.	PR 08-NOV-2000;
PR	14-AUG-2000; 2000US-0225266P.	PR 08-NOV-2000;
PR	14-AUG-2000; 2000US-0225267P.	PR 08-NOV-2000;
PR	14-AUG-2000; 2000US-0225268P.	PR 08-NOV-2000;
PR	14-AUG-2000; 2000US-0225270P.	PR 08-NOV-2000;
PR	14-AUG-2000; 2000US-0225447P.	PR 08-NOV-2000;
PR	14-AUG-2000; 2000US-0225757P.	PR 08-NOV-2000;
PR	14-AUG-2000; 2000US-0225758P.	PR 08-NOV-2000;
PR	14-AUG-2000; 2000US-0225759P.	PR 08-NOV-2000;
PR	18-AUG-2000; 2000US-0226279P.	PR 08-NOV-2000;
PR	22-AUG-2000; 2000US-0226681P.	PR 08-NOV-2000;
PR	22-AUG-2000; 2000US-0226868P.	PR 08-NOV-2000;
PR	22-AUG-2000; 2000US-0226869P.	PR 08-NOV-2000;
PR	22-AUG-2000; 2000US-0227182P.	PR 08-NOV-2000;
PR	23-AUG-2000; 2000US-0227009P.	PR 08-NOV-2000;
PR	30-AUG-2000; 2000US-0228924P.	PR 08-NOV-2000;
PR	01-SEP-2000; 2000US-0229287P.	PR 08-NOV-2000;
PR	01-SEP-2000; 2000US-0229343P.	PR 17-NOV-2000;
PR	01-SEP-2000; 2000US-0229344P.	PR 17-NOV-2000;
PR	01-SEP-2000; 2000US-0229345P.	PR 17-NOV-2000;
PR	05-SEP-2000; 2000US-0229509P.	PR 17-NOV-2000;
PR	05-SEP-2000; 2000US-0229513P.	PR 17-NOV-2000;
PR	06-SEP-2000; 2000US-0230437P.	PR 17-NOV-2000;
PR	06-SEP-2000; 2000US-0230438P.	PR 17-NOV-2000;
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PR	08-SEP-2000; 2000US-0231243P.	PR 17-NOV-2000;


```

PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI ROSEN CA, Ruben SM, Barash SC;
XX
DR WPI; 2003-147444/14.
DR P-PSDB; ABU55294.
XX
XX New polypeptides and nucleic acids, useful in gene therapy for treating,
XX inhibiting or preventing e.g. neural, immune system, muscular,
XX respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
XX renal disorders.
XX
XX Claim 1; SEQ ID NO 392; 402pp; English.
XX
XX The invention relates to human novel polypeptides and their associated
XX polynucleotides. The polypeptides and polynucleotides are useful in gene
XX therapy for treating, inhibiting or preventing neural disorders, immune
XX system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis
XX and multiple sclerosis), muscular disorders, respiratory diseases (e.g.
XX nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders,
XX gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
XX (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left
XX heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
XX renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and
XX leukaemia), inflammatory diseases (e.g. septic shock, bursitis and
XX appendicitis), allergic reactions and conditions (e.g. asthma), blood
XX related disorders (e.g. thrombosis, atherosclerosis and myocardial
XX infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
XX human novel polynucleotides of the invention
XX
SQ Sequence 805 BP; 196 A; 196 C; 187 G; 221 T; 0 U; 5 Other;

Query Match 35.3%; Score 25.8; DB 8; Length 805;
Best Local Similarity 63.9%; Pred. No. 23;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 13 AGGTTAACTACTGTTGAGCTTGAGCAGGTTGTTATCTATCTCTCCGCTAACAGTTT 72
DB 407 ACGGTACCTTCTCTGAACTTGAGGAAGTCTTTTGTCTCCAGCTGCTCAGGGTCTC 466
QY 73 T 73
DB 467 T 467

RESULT 12
ADB63761
ID ADB63761 standard; cDNA; 2874 BP.
XX
XX ADB63761;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human cDNA encoding clone UTERU20016580.
XX
XX Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
XX tissue regeneration; cell regeneration; membrane protein;
XX signal transduction-related protein; transcription-related protein;
XX osteoporosis; neurological disease; cancer; tumour.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 25..1287
FT /tag= a
FT /product= "Clone UTERU20016580 protein"
XX
XX EP1308459-A2.
XX
XX 07-MAY-2003.
XX

```

```

PF 28-MAR-2002; 2002EP-00007401.
XX
PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-450961/43.
XX P-PSDB; ADB65731.
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
XX marker or medicines for regulation of their expression and activity, or
XX as targets of gene therapy.
XX
XX Claim 1; Page; 222pp; English.
XX
XX The invention discloses a polynucleotide comprising a sequence selected
XX from 1970 fully defined nucleotide sequences which encode novel
XX polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
XX or its partial peptide, an antibody binding to the polypeptide or peptide
XX of the polynucleotide, immunologically assaying the polypeptide or
XX peptide of the polynucleotide by contacting the polypeptide or peptide
XX with the antibody of the encoded protein, and observing the binding
XX between the two, a transformant carrying the polynucleotide in an
XX expressible manner and an antisense polynucleotide. The oligonucleotide
XX is useful as a primer for synthesising the polynucleotide, or as a probe
XX for detecting the polynucleotide. The polynucleotides and encoded
XX proteins are useful as pharmaceutical agents and many disease-related
XX genes may be included in them, for developing a diagnostic marker or
XX medicines for regulation of their expression and activity, or as targets
XX of gene therapy. The genes are involved in tissue and/or cell
XX regeneration. Membrane proteins, signal transduction-related proteins,
XX transcription-related proteins, disease-related proteins and genes
XX encoding them can be used as indicators for diseases (e.g. osteoporosis,
XX neurological diseases, cancer, tumours. The cDNA may be used to regulate
XX the activity or expression of the encoded protein to treat diseases. The
XX sequence presented is a cDNA of the invention. Note: Some of the sequence
XX data for this patent is not represented in the printed specification, but
XX is based on sequence information supplied by the European Patent Office.
XX
XX Sequence 2874 BP; 669 A; 766 C; 808 G; 631 T; 0 U; 0 Other;

Query Match 35.3%; Score 25.8; DB 10; Length 2874;
Best Local Similarity 63.9%; Pred. No. 32;
Matches 39; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 13 AGGTTAACTACTGTTGAACTTGAGCAGGTTGTTATCTATCTCTCGCTAACAGTTT 72
DB 2527 ACGGTACCTTCTCTGAACTTGAGGAAGTCTTTTGTCTCCAGCTGCTCAGGGTCTC 2586
QY 73 T 73
DB 2587 T 2587

RESULT 13
ADS09779
ID ADS09779 standard; DNA; 3352 BP.
XX
XX ADS09779;
XX
XX 16-DEC-2004 (first entry)
XX
XX Human therapeutic DNA - SEQ ID 16.
XX
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

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Search completed: August 14, 2005, 20:21:40
Job time : 449 secs

AD R08359 standard; cDNA; 3597 BP.
AD R08359;
04-NOV-2004 (first entry)
Full length human cDNA useful for treating neurological disease Seq 1865.
gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
osteoporosis; neurological disease; Alzheimer's disease;
Parkinson's disease; dementia; short memory; cancer;
sense or motor function; emotional reaction; fear response; panic;
osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
tranquilliser.
XX Homo sapiens.
XX
XX EP1447413-A2.
XX
XX 18-AUG-2004.
XX
XX 12-FEB-2004; 2004EP-00003145.
XX
XX 14-FEB-2003; 2003JP-00102207.
PR 09-MAY-2003; 2003JP-00131452.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX
XX WPI; 2004-583265/57.
DR P-PSDB; ADR10315.
XX
XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
XX Claim 1; SEQ ID NO 1865; 2686pp; English.
XX
XX This invention relates to novel, isolated full length human cDNA
molecules and the encoded proteins thereof. Specifically, it refers to
cDNA clones obtained by an oligo-capping method, where none of these
clones are identical to any known human mRNAs. The present invention
describes an immunoassay to identify agonists and antagonists, as well as
antibodies, antisense molecules and siRNAs that can all be used to bind
to and modulate expression of the cDNA molecules. As such, these
molecules are useful for diagnostic markers or therapeutic targets for
the various diseases or morbid states. In particular, they are useful in
the gene therapy for treating osteoporosis, neurological disease, Alzheimer's
disease, Parkinson's disease, dementia, short memory and various cancers,
as well as for maintaining equilibrium of sense or motor function, and
for treating emotional reaction, fear response and panic. Accordingly,
they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
cytostatic and tranquilliser activities. This polynucleotide is a full
length human cDNA sequence of the invention. NOTE: This sequence is not
given in the sequence listing of the specification but can be obtained on
CD-ROM from the European Patent Office, Vienna Sub-office.
XX
XX Sequence 3597 BP; 793 A; 943 C; 920 G; 941 T; 0 U; 0 Other;
SQ
Query Match 35.3%; Score 25.8; DB 13; Length 3597;
Best Local Similarity 60.9%; Pred. No. 35;
Matches 42; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 1 TTGGCAGGAGATAGTTTAACTACCTGTTGACGCTTGACGAGTGTATATCTCTG 60
DB 803 TTGGAATAGTTCCTTTAAATCTGTTGAAATGGAACAGTTCCTCTCTC 862
QY 61 CTACAGTT 69
DB 863 CCATGTGT 871

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 14:09:25 ; Search time 1916 Seconds
(without alignments)
1846.154 Million cell updates/sec

Title: US-10-698-070-2

Perfect score: 73

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_ots.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	31.8	43.6	178468	10	AL845354
c 2	31.8	43.6	233378	8	AL122277 Mus muscu
c 3	30.2	41.4	178468	10	AL845354
c 4	30.2	41.4	233378	2	AL122277 Mus muscu
c 5	29.6	40.5	107660	2	AL151668
c 6	29.6	40.5	116983	8	AL139709
c 7	29.6	40.5	120033	2	AL141364
c 8	29.6	40.5	123355	2	AL137835
c 9	29.6	40.5	124033	8	AC093544
c 10	29.6	40.5	124158	2	AL142142
c 11	29.6	40.5	124977	2	AL126018
c 12	29.6	40.5	320731	2	AL149573
c 13	29.4	40.3	147552	2	AC019298
c 14	29.4	40.3	151329	9	AC025623
c 15	29.4	40.3	154866	2	AC079965
c 16	29.4	40.3	211445	9	AC103794
c 17	29.2	40.0	152884	9	AC138625
c 18	29.2	40.0	158420	9	AC137788
c 19	29	39.7	157610	9	AC087235

39.7	252925	2	AC021048	Homo sapi
39.2	104229	9	AC097458	Homo sapi
38.4	1791	6	CQ739826	Sequence
38.4	3302	9	AY186997	Homo sapi
38.4	3459	6	BD183247	Marker fo
38.4	3763	9	AY040324	Homo sapi
38.4	5419	9	AB058722	Homo sapi
38.4	5419	9	AY040322	Homo sapi
38.4	125557	2	AC145820	Cicer ari
38.4	139665	2	AP000865	Homo sapi
38.4	196606	9	AP000779	Homo sapi
38.4	156279	2	AC136205	Sus scrofa
38.1	162335	2	AC115535	Sus scrofa
38.1	184256	10	AL929163	Mouse DNA
38.1	191580	8	AP003847	Oryza sat
38.1	228572	5	EX248236	Zebrafish
37.8	154729	2	AC138879	Homo sapi
37.8	157462	9	AC130459	Homo sapi
37.8	157838	9	AC004626	Homo sapi
37.8	175099	9	AC109135	Homo sapi
37.8	176981	9	AC136634	Homo sapi
37.8	204490	2	CR847537	Danio rer
37.5	85671	9	AL160008	Human DNA
37.5	198761	5	EX511027	Zebrafish
37.3	792	1	BGNPAPBR	B.garini b
37.3	35417	3	AF067936	Caenorhab
37.3	145167	9	HSJ308B17	Human DNA
37.3	170074	9	AC011726	Homo sapi
37.3	176063	9	AC022911	Homo sapi
37.3	215611	2	AL359768	Homo sapi
37.3	221068	2	AC102378	Homo sapi
37.0	363	11	BV094778	Mus muscu
37.0	154456	2	AL126320	Mus muscu
37.0	207295	9	AL353572	Human DNA
37.0	280473	2	AC068823	Homo sapi
36.7	397	11	G71414	721672031FM
36.7	414	11	G70470	721672031FB
36.7	66005	9	AP005435	Homo sapi
36.7	75416	9	AP004833	Homo sapi
36.7	87667	10	AL845546	Mouse DNA
36.7	160683	9	AP004607	Homo sapi
36.7	166287	2	AC060830	Homo sapi
36.7	231256	2	AC119554	Rattus no
36.7	238723	2	AC106476	Rattus no
36.7	242640	2	AC111232	Rattus no
36.7	247231	2	AC106295	Rattus no
36.7	258201	2	AC125910	Rattus no
36.4	633	6	AX242002	Sequence
36.4	634	9	U86300	Homo sapien
36.4	1791	6	CQ739826	Sequence
36.4	3302	9	AY186997	Homo sapi
36.4	3459	6	BD183247	Marker fo
36.4	3763	9	AY040324	Homo sapi
36.4	5419	9	AB058722	Homo sapi
36.4	5419	9	AY040322	Homo sapi
36.4	10658	2	AC013049	Drosophill
36.4	60747	6	CQ593675	Sequence
36.4	66984	9	AL606753	Human DNA
36.4	91658	2	AC005645	Drosophill
36.4	102813	2	AC136544	Rattus no
36.4	130445	9	AC116648	Homo sapi
36.4	134011	9	AC005886	b240g16,
36.4	137718	9	AL137218	Human DNA
36.4	139665	2	AP000865	Homo sapi
36.4	144014	2	AC111685	Homo sapi
36.4	150742	9	AC147649	Homo sapi
36.4	160889	9	AC136535	Human DNA
36.4	161193	2	AC011033	Homo sapi
36.4	168738	2	AC023462	Homo sapi
36.4	169689	3	AC008306	Drosophill
36.4	170772	2	AC016454	Homo sapi
36.4	172917	3	AC007836	Drosophill
36.4	176286	2	AL391234	Homo sapi

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26.6 36.4 179060 2 AC074382
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26.6 36.4 179310 9 AC006160
95 AC011842 Homo sapi
26.6 36.4 189631 2 AC011842
c 96 26.6 36.4 196606 9 AP000779
26.6 36.4 196606 9 AP000779
c 97 26.6 36.4 199230 2 AC048360
26.6 36.4 199230 2 AC048360
98 AC048360 Homo sapi
26.6 36.4 216800 10 AL599744
99 AL599744 Mouse DNA
c 100 26.6 36.4 239237 2 AC094621
AC094621 Rattus no

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ALIGNMENTS

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RESULT 1
AL845354/c
LOCUS
DEFINITION Mouse DNA sequence from clone RP23-318L10 on chromosome 2, complete
sequence.
ACCESSION AL845354
VERSION AL845354.13 GI:32187955
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 178468)
AUTHORS Tracey.A.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 24 2003 this sequence version replaced gi:321311063.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----

```

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-318L10 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBAC3.6.

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FEATURES
source
1. .178468
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/Chromosomes="2"
/clone="RP23-318L10"
/clone_lib="RPCI-23"

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ORIGIN

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Query Match 43.6%; Score 31.8; DB 10; Length 178468;
Best Local Similarity 67.2%; Pred.No.2.9; 22; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 0;

QY 1 TTGGCAGGAGATAGGTAACTCTTGAAGCTTGACGAGTGGTAAATCTATCTCTG 60
Db 48646 TTGGCAGGAGACACAGTAACCTACTTATTAAAGTTCAACAGGAGGTTCTCTTACCTG 48587

QY 61 CTAAACAG 67
Db 48586 CAAAGAG 48580

RESULT 2
AC122277
LOCUS
DEFINITION Mus musculus chromosome UNK clone RP23-231N7, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
ACCESSION AC122277
VERSION AC122277.2 GI:22004622
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 233378)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 233378)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 233378)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Jul 30, 2002 this sequence version replaced gi:21105133.
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```

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M BA0231N07
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 229423 bases at least Q40
Consensus quality: 230099 bases at least Q30
Consensus quality: 230466 bases at least Q20
Insert size: 170000; agarose-ff
Insert size: 232778; sum-of-contigs
Quality coverage: 13.22 in Q20 bases; agarose-ff
Quality coverage: 10.03 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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```

* 1 71720: contig of 71720 bp in length
* 71721 71820: gap of unknown length
* 71821 134774: contig of 62954 bp in length
* 134775 134875: gap of unknown length
* 134876 136238: contig of 1364 bp in length
* 136239 136339: gap of unknown length
* 136340 138393: contig of 2055 bp in length
* 138394 138494: gap of unknown length
* 138495 140771: contig of 2278 bp in length
* 140772 140871: gap of unknown length
* 140872 182344: contig of 41473 bp in length
* 182345 182445: gap of unknown length
* 182446 233378: contig of 50934 bp in length.

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FEATURES

source

Location/Qualifiers

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1. .233378
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-231N7"

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misc_feature

1. .71720

/note="assembly_name:Contig10"

misc_feature

71821..134774

/note="assembly_name:Contig11"

misc_feature

134875..136238

/note="assembly_name:Contig5"

misc_feature

136339..138393

/note="assembly_name:Contig6"

misc_feature

138494..140771

/note="assembly_name:Contig7"

misc_feature

140872..182344

/note="assembly_name:Contig8"

misc_feature

182445..233378

/note="assembly_name:Contig9"

ORIGIN

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Query Match 43.6%; Score 31.8; DB 2; Length 233378;
Best Local Similarity 67.2%; Pred. No. 2.9;
Matches 45; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TTGGCAGGAGATAGGTTAACTACTGTTGAAGCTTGAGCGAGGTTGTTAATCTATCTCTG 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 218932 TTGGCAGGAGCAACAGTAAGTACTTTATTAAGTTCAACAGAGGTTCTTCATCCCTG 218991
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 CTAACAG 67
| | | | |
Db 218992 CAAAGAG 218998

```

RESULT 3

AL845354

LOCUS

Mouse DNA sequence from clone RP23-318L10 on chromosome 2, complete sequence.

ACCESSION

AL845354

VERSION

AL845354.13

KEYWORDS

HTG.

SOURCE

Mus musculus

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (24-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 On Jun 24, 2003 this sequence version replaced gi:32131063.
 Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information

on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-318L10 is

from the RPCI-23 Mouse BAC Library

constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBac3.6.

FEATURES

source

Location/Qualifiers

1. .178468

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="2"

/clone="RP23-318L10"

/clone_lib="RPCI-23"

ORIGIN

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Query Match 41.4%; Score 30.2; DB 10; Length 178468;
Best Local Similarity 65.7%; Pred. No. 10;
Matches 44; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 TTGGCAGGAGATAGGTTAACTACTGTTGAAGCTTGAGCGAGGTTGTTAATCTATCTCTG 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 48583 TTTCAGGGTATCAAGGAACTCTCTTGAACCTTAATAAGTAGTTACTGTGCTTCTG 48642
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 CTAACAG 67
| | | | |
Db 48643 CCAAAAG 48649

```

RESULT 4

AC122277/c

LOCUS

DEFINITION

Mus musculus chromosome UNK clone RP23-231N7, WORKING DRAFT

SEQUENCE, 7 unordered pieces.

ACCESSION

AC122277

VERSION

AC122277.2

KEYWORDS

HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE

Mus musculus

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

3 (bases 1 to 233378)

AUTHORS
TITLE
JOURNAL
COMMENT

McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (30-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Jul 30, 2002 this sequence version replaced gi:21105133.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: M_BA0231N07

----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-terminator; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 229423 bases at least Q40
Consensus quality: 230099 bases at least Q30
Consensus quality: 230466 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 232778; sum-of-contigs
Quality coverage: 13.22 in Q20 bases; agarose-fp
Quality coverage: 10.03 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 71720: contig of 71720 bp in length
* 71721 71820: gap of unknown length
* 71821 134774: contig of 62954 bp in length
* 134775 134874: gap of unknown length
* 134875 136238: contig of 1364 bp in length
* 136239 136338: gap of unknown length
* 136339 138393: contig of 2055 bp in length
* 138394 138493: gap of unknown length
* 138494 140771: contig of 2278 bp in length
* 140772 140871: gap of unknown length
* 140872 182344: contig of 41473 bp in length
* 182345 182444: gap of unknown length
* 182445 233378: contig of 50934 bp in length.

FEATURES
source

1..233378
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
/clone="RP23-231N7"

misc_feature

1..71720
/note="assembly_name:Contig10"
71821..134774
/note="assembly_name:Contig11"
134875..136238
/note="assembly_name:Contigs"
136339..138393
/note="assembly_name:Contig6"
138494..140771
/note="assembly_name:Contig7"
140872..182344
/note="assembly_name:Contig8"
182445..233378
/note="assembly_name:Contig9"

ORIGIN

Query Match 41.4%; Score 30.2; DB 2; Length 233378;

Best Local Similarity 65.7%; Pred. No. 10;
Matches 44; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 1 TTGCGAGGATAGGTAACTACCTGTTGAAGCTTGACGAGGTGTTAATCTATCTCTG 60
Db 218995 TTTGCGAGGATAGGAGCACTCTCTGTTGAACCTTAATGAAGTAGTACTGTTGCTTCTG 218936
Qy 61 CTAACAG 67
Db 218935 CCAAAAG 218929

RESULT 5

AC151668 107660 bp DNA linear HTG 12-OCT-2004
LOCUS Medicago truncatula clone mth2-6e22, WORKING DRAFT SEQUENCE, 3
DEFINITION ordered pieces.
AC151668
VERSION AC151668.8 GI:54035640
KEYWORDS HTG; HTGS PHASR2; HTGS DRAFT.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE

1 (bases 1 to 107660)
Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.
and Roe, B.A.

TITLE
JOURNAL

REFERENCE

2 (bases 1 to 107660)
Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.
and Roe, B.A.
Direct Submission

TITLE
JOURNAL

Submitted (23-SEP-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

REFERENCE

3 (bases 1 to 107660)
Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D.
and Roe, B.A.

TITLE
JOURNAL

Submitted (12-OCT-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA

COMMENT

On Oct 12, 2004 this sequence version replaced gi:53984532.

----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code: UOKNOR

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 3048: contig of 3048 bp in length
* 3049 3148: gap of unknown length
* 3149 38700: contig of 35552 bp in length
* 38701 38800: gap of unknown length
* 38801 107660: contig of 68860 bp in length.

FEATURES
source

1..107660
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/db_xref="taxon:3880"
/clone="mth2-6e22"
/clone_lib="Medicago truncatula BAC library H2"

ORIGIN

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Query Match      40.5%; Score 29.6; DB 2; Length 107660;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACCTGTTGAAGCTTCAGCAGGTTGTTAATCTATCTCTCTGCTTAACA 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 17664 GGAATAAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCCTTCTTAACA 17723

RESULT 6
AC139709/c
LOCUS      AC139709
DEFINITION Medicago truncatula clone mth2-22d18, complete sequence.
ACCESSION  AC139709
VERSION     AC139709.17 GI:50872504
KEYWORDS   HTG.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1 (bases 1 to 116983)
AUTHORS    Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE      Medicago truncatula BAC Clone mth2-22d18
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 116983)
AUTHORS    Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (11-FEB-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE   3 (bases 1 to 116983)
AUTHORS    Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (15-JUN-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE   4 (bases 1 to 116983)
AUTHORS    Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (31-JUL-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On Jul 31, 2004 this sequence version replaced gi:48717554.
            ----- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR

FEATURES             source
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Location/Qualifiers
1. .116983
   /organism="Medicago truncatula"
   /mol_type="genomic DNA"
   /db_xref="taxon:3880"
   /clone="mth2-22d18"
   /notes="This is one of two clones in the same well from
            mth2-22d18"

ORIGIN
Query Match      40.5%; Score 29.6; DB 8; Length 116983;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACCTGTTGAAGCTTCAGCAGGTTGTTAATCTATCTCTCTGCTTAACA 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 103089 GGAATAAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCCTTCTTAACA 103030

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RESULT 7
AC141364/c
LOCUS      AC141364
DEFINITION Medicago truncatula clone mth2-8a2, WORKING DRAFT SEQUENCE, 2
            ordered pieces.
ACCESSION  AC141364
VERSION     AC141364.13 GI:53793745
KEYWORDS   HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1 (bases 1 to 120033)
AUTHORS    Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE      Medicago truncatula BAC Clone mth2-8a2
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 120033)
AUTHORS    Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (13-MAR-2003) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE   3 (bases 1 to 120033)
AUTHORS    Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (05-OCT-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On Oct 5, 2004 this sequence version replaced gi:47174786.
            ----- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR

FEATURES             source
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Location/Qualifiers
1. .120033
   /organism="Medicago truncatula"
   /mol_type="genomic DNA"
   /db_xref="taxon:3880"
   /clone="mth2-8a2"
   /clone_lib="Medicago truncatula BAC library H2"

ORIGIN
Query Match      40.5%; Score 29.6; DB 2; Length 120033;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACCTGTTGAAGCTTCAGCAGGTTGTTAATCTATCTCTCTGCTTAACA 66
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DB 103131 GGAATAAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCCTTCTTAACA 103072

RESULT 8
AC137835/c

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LOCUS      AC137835      122355 bp      DNA      linear      HTG 06-AUG-2004
DEFINITION Medicago truncatula clone mth2-29b14, WORKING DRAFT SEQUENCE, 2
AC137835
VERSION    AC137835.41  GI:51011171
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 122355)
AUTHORS    Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE      Medicago truncatula BAC Clone mth2-29b14
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 122355)
AUTHORS    Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (04-DEC-2002) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  3 (bases 1 to 122355)
AUTHORS    Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
            Cook,D., Kim,D. and Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (06-AUG-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT    On Aug 6, 2004 this sequence version replaced gi:50950328.
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            Center: Department Of Chemistry And Biochemistry
            Genome Center
            The University Of Oklahoma
            Center code:UOKNOR
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1 3645: contig of 3645 bp in length
            * 3646 3745: gap of unknown length
            * 3746 122355: contig of 118610 bp in length.
            *
            * Location/Qualifiers
            *   1..122355
            *     /organism="Medicago truncatula"
            *     /mol_type="genomic DNA"
            *     /db_xref="taxon:3880"
            *     /clone="mth2-29b14"
            *     /clone_lib="Medicago truncatula BAC library H2"
ORIGIN
Query Match      40.5%; Score 29.6; DB 2; Length 122355;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 7 GGAGATAGGTTAACTACCTGTTGAAGCTTGACGAGGTGGTTAACTATCTCTCTAACA 66
|||||
Db 107426 GGAAATAGGTAATTAGGTGGTATAGCATCTTATATGCTTAATCGATCTCTCTAACA 107367
|||||

RESULT 9
AC093544/c
LOCUS      AC093544      124033 bp      DNA      linear      PLN 11-MAR-2003
DEFINITION Medicago truncatula chloroplast, complete genome, complete
            sequence.
ACCESSION  AC093544
VERSION    AC093544.8  GI:17149410

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KEYWORDS    HTG.
SOURCE      Medicago truncatula (barrel medic)
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 124033)
AUTHORS    Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE      Medicago truncatula Variety Jema Long A-17 Chloroplast, Complete
            Sequence
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 124033)
AUTHORS    Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (31-AUG-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  3 (bases 1 to 124033)
AUTHORS    Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (19-SEP-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  4 (bases 1 to 124033)
AUTHORS    Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (19-OCT-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  5 (bases 1 to 124033)
AUTHORS    Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (03-NOV-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  6 (bases 1 to 124033)
AUTHORS    Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (07-NOV-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  7 (bases 1 to 124033)
AUTHORS    Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (29-NOV-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  8 (bases 1 to 124033)
AUTHORS    Lin,S., Wu,H., Jia,H., Zhang,P., Dixon,R., May,G., Gonzales,R. and
            Roe,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (11-MAR-2003) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT    On Nov 29, 2001 this sequence version replaced gi:16756257.
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            Center: Department Of Chemistry
            Genome Center
            The University Of Oklahoma
            Center code:UOKNOR
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            * Location/Qualifiers
            *   1..124033
            *     /organism="Medicago truncatula"
            *     /mol_type="genomic DNA"
            *     /strain="Variety Jema Long A-17"
FEATURES
source

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/db_xref="taxon:3880"
/clon="chloroplast"

ORIGIN
Query Match      40.5%; Score 29.6; DB 8; Length 124033;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCTGCTAAACA 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6449 GGAATAAGGTAATTAGGTGGTATAGCATTTCTATATGCTTATATCGATCTCTCTTCTAAACA 6390

RESULT 10
AC142142/c      124158 bp DNA linear HTG 06-OCT-2004
LOCUS Medicago truncatula clone mth2-31e20, WORKING DRAFT SEQUENCE, 4
DEFINITION ordered pieces.
ACCESSION AC142142 GI:53828773
VERSION HTG; HTGS PHASE2; HTGS DRAFT.
KEYWORDS Medicago truncatula (barrel medic)
SOURCE Medicago truncatula
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 124158)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Medicago truncatula BAC Clone mth2-31e20
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 124158)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 3 (bases 1 to 124158)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Oct 6, 2004 this sequence version replaced gi:53793750.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 104141: contig of 104141 bp in length
* 104142 104241: gap of unknown length
* 107242 107695: contig of 3454 bp in length
* 107596 107795: gap of unknown length
* 121926 121925: contig of 14130 bp in length
* 121926 122025: gap of unknown length
* 122026 124158: contig of 2133 bp in length.
* Location/Qualifiers
FEATURES
source
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/db_xref="taxon:3880"

/clon="mth2-31e20"
/clon_lib="Medicago truncatula BAC library H2"
/notes="This is one of two clones in the same well from
mth2-31e20"

ORIGIN
Query Match      40.5%; Score 29.6; DB 2; Length 124158;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTCTGCTAAACA 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 89560 GGAATAAGGTAATTAGGTGGTATAGCATTTCTATATGCTTATATCGATCTCTCTTCTAAACA 89501

RESULT 11
AC126018/c      124977 bp DNA linear HTG 28-SEP-2004
LOCUS Medicago truncatula clone mth2-14h13, WORKING DRAFT SEQUENCE, 4
DEFINITION unordered pieces.
ACCESSION AC126018 GI:52346226
VERSION HTG; HTGS PHASE1; HTGS DRAFT.
KEYWORDS Medicago truncatula (barrel medic)
SOURCE Medicago truncatula
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 124977)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Medicago truncatula BAC Clone mth2-14h13
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 124977)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 3 (bases 1 to 124977)
AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Sep 19, 2004 this sequence version replaced gi:52318767.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2357: contig of 2357 bp in length
* 2358 2457: gap of unknown length
* 2458 4533: contig of 2076 bp in length
* 4534 4633: gap of unknown length
* 4634 6932: contig of 2299 bp in length
* 6933 7032: gap of unknown length
* 7033 124977: contig of 117945 bp in length.
* Location/Qualifiers
FEATURES
source
/organism="Medicago truncatula"
/mol_type="genomic DNA"

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/db_xref="taxon:3880"
/clones="mth2-14h13"
/clone_lib="Medicago truncatula BAC library H2"

ORIGIN
    Query Match      40.5%; Score 29.6; DB 2; Length 124977;
    Best Local Similarity 68.3%; Pred. No. 17;
    Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 7 GGAGATAGTTAACTACCTGTTGAAGCTTGAGCAGGTTGTTAACTATCTCTCTCTAACA 66
    |||||
Db 110414 GGAAATAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCTTCTAACA 110355

RESULT 12
AC149573/c
LOCUS      AC149573          320731 bp      DNA      linear      HTG 06-OCT-2004
DEFINITION Medicago truncatula clone mth2-11994, WORKING DRAFT SEQUENCE, 52
            unordered pieces.
ACCESSION  AC149573
VERSION    AC149573.8 GI:53828780
KEYWORDS   HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE     Medicago truncatula (barrel medic)
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 320731)
            Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D.
            and Roe,B.A.
            Medicago truncatula BAC Clone mth2-11994
            Unpublished
REFERENCE  2 (bases 1 to 320731)
            Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D.
            and Roe,B.A.
            Direct Submission
            Submitted (08-JUN-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE  3 (bases 1 to 320731)
            Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D.
            and Roe,B.A.
            Direct Submission
            Submitted (06-OCT-2004) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT    On Oct 6, 2004 this sequence version replaced gi:53793764.
            ----- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 52 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1
            * 2120: contig of 2120 bp in length
            * 2220: gap of unknown length
            * 2221: 4377: contig of 2157 bp in length
            * 4478: 4477: gap of unknown length
            * 4478: 6499: contig of 2022 bp in length
            * 6500: 6599: gap of unknown length
            * 6600: 8658: contig of 2059 bp in length
            * 8659: 8758: gap of unknown length
            * 8759: 11276: contig of 2518 bp in length
            * 11277: 11376: gap of unknown length
            * 11377: 13990: contig of 2614 bp in length
            * 13991: 14090: gap of unknown length
            *
            * 14091: contig of 2242 bp in length
            * 16332: gap of unknown length
            * 16333: contig of 2068 bp in length
            * 18500: gap of unknown length
            * 18600: gap of unknown length
            * 18601: contig of 2551 bp in length
            * 21151: gap of unknown length
            * 21152: contig of 2238 bp in length
            * 23489: gap of unknown length
            * 23490: contig of 3118 bp in length
            * 26707: gap of unknown length
            * 26807: contig of 3218 bp in length
            * 30025: gap of unknown length
            * 30026: contig of 3008 bp in length
            * 30125: gap of unknown length
            * 30126: contig of 2163 bp in length
            * 33233: gap of unknown length
            * 33234: contig of 2163 bp in length
            * 35397: gap of unknown length
            * 35497: contig of 2789 bp in length
            * 38286: gap of unknown length
            * 38386: contig of 3832 bp in length
            * 42217: gap of unknown length
            * 42318: contig of 2615 bp in length
            * 44932: gap of unknown length
            * 45032: contig of 3023 bp in length
            * 48055: gap of unknown length
            * 48155: contig of 2416 bp in length
            * 50571: gap of unknown length
            * 50671: contig of 2115 bp in length
            * 52786: gap of unknown length
            * 52887: contig of 2128 bp in length
            * 55014: gap of unknown length
            * 55114: contig of 3342 bp in length
            * 55115: gap of unknown length
            * 58457: contig of 2018 bp in length
            * 58557: gap of unknown length
            * 60575: contig of 4259 bp in length
            * 60674: gap of unknown length
            * 64933: contig of 3589 bp in length
            * 65033: gap of unknown length
            * 68622: contig of 4768 bp in length
            * 68722: gap of unknown length
            * 73490: contig of 3688 bp in length
            * 73491: gap of unknown length
            * 77379: contig of 3341 bp in length
            * 77379: gap of unknown length
            * 80720: gap of unknown length
            * 80820: contig of 4458 bp in length
            * 85278: gap of unknown length
            * 85377: contig of 6929 bp in length
            * 92306: gap of unknown length
            * 92307: contig of 4830 bp in length
            * 92407: gap of unknown length
            * 97237: contig of 5225 bp in length
            * 97337: gap of unknown length
            * 102562: contig of 4226 bp in length
            * 102562: gap of unknown length
            * 106888: contig of 5026 bp in length
            * 106988: gap of unknown length
            * 112013: contig of 4849 bp in length
            * 112014: gap of unknown length
            * 112114: contig of 5181 bp in length
            * 116963: gap of unknown length
            * 117063: contig of 9312 bp in length
            * 122244: gap of unknown length
            * 122344: contig of 9312 bp in length
            * 131556: gap of unknown length
            * 131756: contig of 6082 bp in length
            * 137838: gap of unknown length
            * 137938: contig of 6174 bp in length
            * 144111: gap of unknown length
            * 144112: contig of 9300 bp in length
            * 153512: gap of unknown length
            * 153612: contig of 5872 bp in length
            * 159484: gap of unknown length
            * 159584: contig of 9115 bp in length
            * 168699: gap of unknown length
            * 168798: contig of 9662 bp in length
            * 178460: contig of 9662 bp in length

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```

* 178461 178560: gap of unknown length
* 178561 189146: contig of 10586 bp in length
* 189147 189246: gap of unknown length
* 189247 205996: contig of 16750 bp in length
* 205997 206096: gap of unknown length
* 206097 221512: contig of 15416 bp in length
* 221513 221612: gap of unknown length
* 221613 235904: contig of 14292 bp in length
* 235905 236004: gap of unknown length
* 236005 248142: contig of 12138 bp in length
* 248143 248242: gap of unknown length
* 248243 263641: contig of 15399 bp in length
* 263642 263741: gap of unknown length
* 263742 280695: contig of 16954 bp in length
* 280696 280796: gap of unknown length
* 280797 301898: contig of 21103 bp in length
* 301899 301999: gap of unknown length
* 301999 320731: contig of 18733 bp in length.

FEATURES
    source
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    /organism="Medicago truncatula"
    /mol_type="genomic DNA"
    /db_xref="taxon:3880"
    /clone_lib="Medicago truncatula BAC library H2"

ORIGIN
Query Match      40.5%; Score 29.6; DB 2; Length 320731;
Best Local Similarity 68.3%; Pred. No. 17;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 7 GGAGATAGGTTAACTACCTTGAAGCTTGAGCAGGTGGTAACTATCTATCTCTGCTAACA 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 85884 GGAATAAGGTAATTAGGTGGTATAGCATTTCTATATGCTTAACTCGATCTCTCTTAACA 85825

RESULT 13
AC019298
LOCUS
DEFINITION Homo sapiens clone RP11-30H20, WORKING DRAFT SEQUENCE, 24 unordered
            pieces.
AC019298
VERSION AC019298.3 GI:7382219
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Birren,B., Linton,L., Nusbaum,C., Lander,E., Aldrich,E., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bida,F.,
            Boguslavsky,L., Bouckgeer,B., Brown,A., Burkett,G., Castle,A.,
            Choquel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
            DeArrellano,K., Dewar,K., Domino,M., Doyle,M., Fenesstor,J.,
            Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,
            Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
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            McPheeters,R., Meldrum,J., Meneus,L., Morrow,J., Navlor,J.,
            Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,
            Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
            Roy,A., Santos,R., Severi,P., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Tirrell,A., Vassiliou,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
            Zimmer,A., and Zody,M.
            Direct Submission
            Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA

```

COMMENT

On Apr 1, 2000 this sequence version replaced gi:6721285.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center.
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L4878
 Center Clone name: 30_H_20
 ----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 134743 bases at least Q40
 Consensus quality: 140753 bases at least Q30
 Consensus quality: 142882 bases at least Q20
 Insert size: 150000; agarose-fp
 Insert size: 145252; sum-of-contigs
 Quality coverage: 3.6 in Q20 bases; agarose-fp
 Quality coverage: 3.8 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
 consists of 24 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence.
 as soon as it is available and the accession number will
 be preserved.

1 1112: contig of 1112 bp in length
 * 1113 1212: gap of 100 bp
 * 1213 2733: contig of 1521 bp in length
 * 2734 2833: gap of 100 bp
 * 2834 4679: contig of 1846 bp in length
 * 4680 4779: gap of 100 bp
 * 4780 7239: contig of 2460 bp in length
 * 7240 7339: gap of 100 bp
 * 7340 9564: contig of 2225 bp in length
 * 9565 9665: contig of 4032 bp in length
 * 9666 13697: gap of 100 bp
 * 13698 17531: contig of 3735 bp in length
 * 17532 17631: gap of 100 bp
 * 17632 21288: contig of 3657 bp in length
 * 21289 21388: gap of 100 bp
 * 21389 25895: contig of 4507 bp in length
 * 25896 25995: gap of 100 bp
 * 25996 31062: contig of 5067 bp in length
 * 31063 31162: gap of 100 bp
 * 31163 33753: contig of 2591 bp in length
 * 33754 33854: gap of 100 bp
 * 33855 38963: contig of 5110 bp in length
 * 38964 39063: gap of 100 bp
 * 39064 45761: contig of 6698 bp in length
 * 45762 45861: gap of 100 bp
 * 45862 52769: contig of 6908 bp in length
 * 52770 52869: gap of 100 bp
 * 52870 60905: contig of 8036 bp in length
 * 60906 61005: gap of 100 bp
 * 61006 69111: contig of 5906 bp in length
 * 69112 76011: gap of 100 bp
 * 76012 73602: contig of 6591 bp in length
 * 73603 73702: gap of 100 bp
 * 73703 80372: contig of 6670 bp in length
 * 80373 80472: gap of 100 bp
 * 80473 91073: contig of 10601 bp in length
 * 91074 91173: gap of 100 bp
 * 91174 99031: contig of 7858 bp in length
 * 99032 99331: gap of 100 bp
 * 99332 110237: contig of 11106 bp in length

SEQUENCE, 4 ordered pieces.

AC079965 GI:14547792
VERSION HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS Homo sapiens (human)
SOURCE

ORGANISM
Homo sapiens
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 154866)
TITLE Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 154866)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavskiy,L.,
Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArnellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
FitZHugh,W., Gage,D., Galagan,J., Gardyna,S., Glinde,S., Goyette,M.,
Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L.,
Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., LaRocque,K.,
Llamaras,R., Landers,T., Lehoczyk,J., Levine,R., Liu,C., Liu,G.,
Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrum,J., Menushkin,L., Mihova,T., Miengua,V.,
Morrow,J., Murphy,T., Naylor,J.T., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J.J., Tesfaye,S., Theodore,J.,
Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,A. and Zody,M.

DIRECT SUBMISSION
Submitted (20-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 25, 2001 this sequence version replaced gi:14336470.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: Li0817
Center clone name: 2649 A_9
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 153320 bases at least Q40
Consensus quality: 154086 bases at least Q30
Consensus quality: 154389 bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 154566; sum-of-contigs
Quality coverage: 9.9 in Q20 bases; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 873: contig of 873 bp in length
* 874 973: gap of 100 bp
* 974 2323: contig of 1350 bp in length
* 2324 2423: gap of 100 bp

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2005, 19:23:31 ; Search time 3242 Seconds
(without alignments)
857.092 Million cell updates/sec

Title: US-10-698-070-2
Perfect score: 73
Sequence: 1 ttggcaggagataggttaac.....tctctgctaacagttttt 73

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	42.5	944	8	AZ673840
2	30.4	41.6	768	5	BU333082
3	29.6	40.5	358	2	BE323297
4	29.6	40.5	390	4	EG456980
5	29.6	40.5	590	9	CR312921
6	29.6	40.5	696	9	CR342420
7	29.4	40.3	530	8	BH615508
8	29	39.7	559	8	BH765778
9	28.6	39.2	861	7	CK418262
10	28.4	38.9	662	8	BH462209
11	28	38.4	248	8	EA04037
12	28	38.4	552	5	EX476471
13	27.6	37.8	662	9	AG177371
14	27.6	37.8	722	5	BU476113
15	27.6	37.8	775	7	CK312407
16	27.4	37.5	660	4	BM682169
17	27.4	37.5	673	4	BM683036
18	27.2	37.3	456	9	CC689926
19	27.2	37.3	682	9	CE706471
20	27	37.0	485	7	CK751301
21	27	37.0	595	8	AQ259536
22	27	37.0	759	9	CC869050
23	26.8	36.7	360	9	CL900263
24	26.8	36.7	415	2	AW327602

C 98 25.8 35.3 425 2 AW450084 UT-H-BI3-
C 99 25.8 35.3 447 4 BM126223
C 100 25.8 35.3 448 1 AI609071 tw29g01.x

ALIGNMENTS

RESULT 1
AZ673840
LOCUS
DEFINITION
ENTIV66TR Entamoeba histolytica Sheared DNA linear GSS 14-DEC-2000
genomic, genomic survey sequence.
ACCESSION
AZ673840
VERSION
AZ673840.1 GI:11810986
KEYWORDS
GSS.
SOURCE
Entamoeba histolytica
ORGANISM
Entamoeba histolytica
Eukaryota; Entamebidae; Entamoeba.
REFERENCE
1 (bases 1 to 944)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
TITLE
HMI:IMSS sheared DNA library
JOURNAL
Unpublished (2000)
COMMENT
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library

FEATURES
source
1..944
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOS1; Site 1: Bat 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

ORIGIN
Query Match 42.5%; Score 31; DB 8; Length 944;
Best Local Similarity 68.3%; Pred. No. 5;
Matches 43; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 10 GATAGGTTACTACCTGGTTGAGCTTGAGCGTGGTTAATCTATCTCTGCTAACAGTT 69
Db 19 GTTAGGTTAGTTTTTTTTTGGCTGTGCTGCTAGATAGTCTAATCTCTGCTACAGAT 78
QY 70 TTT 72
Db 79 TGT 81

RESULT 2

BU333082
LOCUS
DEFINITION

ACCESSION
BU333082
VERSION
BU333082.1 GI:25841083
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE
AUTHORS
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
1..768
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, HiseX"
/db_xref="taxon:9031"
/clone="ChEST418m1"
/tissue_type="whole embryo"
/dev_stage="10"
/lab_host="DH10B"
/clone_lib="CSEQCHM65"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN
Query Match 41.6%; Score 30.4; DB 5; Length 768;
Best Local Similarity 63.9%; Pred. No. 7.9;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 1 TTGGCAGGAGATAGGTTAACTACCTGTGAGCTTGAGCGTGGTTAATCTATCTCTG 60
Db 378 TTGGCAAGGGCTATATTGCTCCCTGTTACCTCTGGAACCTGGTAATGTCACCTG 437
QY 61 CTAACAGTTTTT 72
Db 438 GTCACCGGTGTT 449

RESULT 3
BE323297
LOCUS
DEFINITION
NF005E03PL1F1019 Phosphate starved leaf Medicago truncatula cDNA
clone NF005E03PL 5', mRNA sequence.
ACCESSION
BE323297

```

VERSION BE323297.2 GI:11966701
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 358)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Iman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula phosphate-starved leaf library
COMMENT On Jul 14, 2000 this sequence version replaced gi:9197074.
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Medicago Genome Initiative accession: MGI:S:19485
Insert Length: 808 Std Error: 0.00
Plate: 005 row: E column: 03
Seq primer: TCACACAGGAACAGCTATGAC.
FEATURES
source
1..358
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF005E03PL"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/clone_lib="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."
ORIGIN
Query Match 40.5%; Score 29.6; DB 2; Length 358;
Best Local Similarity 68.3%; Pred. No. 13;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 7 GGAGATAGGTTAACTACCTGTTGAGCTTGACGAGGTGTTATCTATCTATCTCTCTTAACA 66
Db 150 GGAATAAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCTCTTAACA 209

RESULT 4
CR312921/c
LOCUS CR312921 390 bp mRNA linear EST 19-MAR-2001
DEFINITION Medicago truncatula phosphate starved leaf Medicago truncatula cDNA
clone NF098G09PL 5', mRNA sequence.
ACCESSION BG456980
VERSION BG456980
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 390)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Iman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula phosphate-starved leaf library
COMMENT Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Medicago Genome Initiative accession: MGI:S:19485
Insert Length: 808 Std Error: 0.00
Plate: 005 row: E column: 03
Seq primer: TCACACAGGAACAGCTATGAC.
FEATURES
source
1..358
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF005E03PL"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/clone_lib="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."
ORIGIN
Query Match 40.5%; Score 29.6; DB 2; Length 358;
Best Local Similarity 68.3%; Pred. No. 13;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 7 GGAGATAGGTTAACTACCTGTTGAGCTTGACGAGGTGTTATCTATCTATCTCTCTTAACA 66
Db 150 GGAATAAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCTCTTAACA 209

RESULT 5
CR312921/c
LOCUS CR312921 590 bp DNA linear GSS 01-MAR-2004
DEFINITION Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
truncatula, genomic survey sequence.
ACCESSION CR312921
VERSION CR312921.1 GI:44859065
KEYWORDS GSS.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 590)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :
BP 9191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
FEATURES
source
1..590
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="Jemalong A17"
/db_xref="taxon:3880"
/clone_lib="MTE1"
/note="Vector: pIndigoBAC ; Site 1: EcoRI ; Site 2: EcoRI
; Debelle F. and Chalhoub B.-Genoscope sequence ID :
mtel-35B18FM1"
ORIGIN
Query Match 40.5%; Score 29.6; DB 9; Length 590;
Best Local Similarity 68.3%; Pred. No. 15;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 7 GGAGATAGGTTAACTACCTGTTGAGCTTGACGAGGTGTTATCTATCTATCTCTCTTAACA 66

```

```

Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 390 Std Error: 0.00
Plate: 098 row: G column: 09
Seq primer: TCACACAGGAACAGCTATGAC.
FEATURES
Location/Qualifiers
1..390
/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF098G09PL"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/clone_lib="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."
ORIGIN
Query Match 40.5%; Score 29.6; DB 4; Length 390;
Best Local Similarity 68.3%; Pred. No. 14;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 7 GGAGATAGGTTAACTACCTGTTGAGCTTGACGAGGTGTTATCTATCTCTCTTAACA 66
Db 150 GGAATAAGGTAATTAGTGGTATAGCATTTCTATATGCTTAATCGATCTCTCTTAACA 209

RESULT 5
CR312921/c
LOCUS CR312921 590 bp DNA linear GSS 01-MAR-2004
DEFINITION Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
truncatula, genomic survey sequence.
ACCESSION CR312921
VERSION CR312921.1 GI:44859065
KEYWORDS GSS.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 590)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :
BP 9191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
FEATURES
Location/Qualifiers
1..590
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="Jemalong A17"
/db_xref="taxon:3880"
/clone_lib="MTE1"
/note="Vector: pIndigoBAC ; Site 1: EcoRI ; Site 2: EcoRI
; Debelle F. and Chalhoub B.-Genoscope sequence ID :
mtel-35B18FM1"
ORIGIN
Query Match 40.5%; Score 29.6; DB 9; Length 590;
Best Local Similarity 68.3%; Pred. No. 15;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 7 GGAGATAGGTTAACTACCTGTTGAGCTTGACGAGGTGTTATCTATCTCTCTTAACA 66

```

Db 478 GGAAATAGGTAATAGGTGGTATAGCATTTCTATATGATTAATCGATCTCTCTTAACA 419

RESULT 6
CR342420/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

CR342420
Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago truncatula, genomic survey sequence.
CR342420
GSS.
CR342420.1 GI:44912755
Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Trioliteae; Medicago.
1 (bases 1 to 696)
Genoscope.
Direct Submission
Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

FEATURES
source
Location/Qualifiers
1..696
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="Jemalong A17"
/db_xref="taxon:3880"
/clone_lib="MTE1"
/note="Vector: pIndigoBAC ; Site_1: EcoRI ; Site_2: EcoRI ; DeBelle F. and Chalhou B.-Genoscope sequence ID : mte1-75K21FM1"

ORIGIN
Query Match 40.5%; Score 29.6; DB 9; Length 696;
Best Local Similarity 68.3%; Pred. No. 15;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 7 GGAGTAGGTAACCTACCTGTTGAGCTTGAGCGGTGTAATCTATCTCTCTTAACA 66
Db 481 GGAAATAGGTAATAGGTGGTATAGCATTTCTATATGATTAATCGATCTCTCTTAACA 422

RESULT 7
BH615508/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BH615508
BMBAC303A02T7_P5U Brugia malayi Genomic Bac Library 3 Brugia malayi genomic, genomic survey sequence.
BH615508
GSS.
BH615508.1 GI:18380196
Brugia malayi
Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Brugia.
1 (bases 1 to 530)
Whitton, C., Daub, J., Quail, M., Hall, N., Foster, J., Ware, J., Ganatra, M., Slatko, B., Barrell, B. and Blaxter, M.
A genome sequence survey of the filarial nematode Brugia malayi: repeats, gene discovery, and comparative genomics
Mol. Biochem. Parasitol. 137 (2), 215-227 (2004)
Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9 3JT, UK
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK.

collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK.
Seq primer: T7 (TAATACGACTCACTATAGG)
Class: BAC ends.
Location/Qualifiers
1..530
/organism="Brugia malayi"
/mol_type="genomic DNA"
/strain="TRS"
/db_xref="taxon:6279"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"

collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK.
Seq primer: T7 (TAATACGACTCACTATAGG)
Class: BAC ends.
Location/Qualifiers
1..530
/organism="Brugia malayi"
/mol_type="genomic DNA"
/strain="TRS"
/db_xref="taxon:6279"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"

/dev_stage="microfilaria (L1)"
 /clone lib="Brugia malayi Genomic Bac Library 3"
 /notes="Vector: pBACE3.6; Site 1: BamH I; Brugia malayi
 genomic DNA was partially cleaved with Sau3A I and size
 fractionated. 7,392 clones were generated with mean insert
 size ~48 kbp. The library was constructed by Claire
 Whitton, Blaxter Nematode Genetics Lab, University of
 Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
 Unit, The Sanger Centre, Cambridge, UK."

ORIGIN

Query Match 39.7%; Score 29; DB 8; Length 559;
 Best Local Similarity 71.7%; Pred. No. 24;
 Matches 38; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 21 TACCTGTTGAAGCTTGAGCAGGTGGTTAATCTATCTCTGCTAACAAGTCTTTT 73
 |||||
 Db 232 TACCTCTTGACGTTGGCTGGTAGTTAATTTATTACTGACAGAGTCTTTT 180
 |||||

RESULT 9

CK418262/c
 LOCUS 861 bp mRNA linear EST 05-JAN-2004
 DEFINITION AUF_ipint_58_m01 Intestine cDNA library Ictalurus punctatus cDNA
 5', mRNA sequence.

ACCESSION CK418262

VERSION CK418262

KEYWORDS EST.

SOURCE Ictalurus punctatus (channel catfish)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 Ictaluridae; Ictalurus.

REFERENCE

1 (bases 1 to 861)

AUTHORS

Liu, Z., Li, P., Liu, L., He, C., Kucuktas, H., Peng, J., Chen, L.,
 Featman, E., Baoprasertkul, P., Simmons, M., Muir, W., Grizzle, J.,
 Dunham, R., and Brady, Y.

30,000 new catfish ESTs: new resources for functional analysis of
 genes involved in aquaculture performance traits

TITLE

Unpublished (2004)

JOURNAL

Contact: Liu ZJ

COMMENT

The Fish Molecular Genetics and Biotechnology Laboratory,
 Department of Fisheries and Allied Aquacultures and Program of Cell
 and Molecular Biosciences

Auburn University

203 Swingle Hall, Auburn University, Auburn, AL 36849, USA

Tel: 334 844 4054

Fax: 334 844 9208

Email: zliu@acesag.auburn.edu

Seq primer: T7.

FEATURES

source

1..861 Location/Qualifiers

/organism="Ictalurus punctatus"

/mol_type="mRNA"

/db_xref="taxon:7998"

/clone lib="Intestine cDNA library"

/notes="Organ: Intestine; Vector: pSport1; Site_1: NotI;
 Site_2: SalI"

ORIGIN

Query Match 39.2%; Score 28.6; DB 7; Length 861;
 Best Local Similarity 64.2%; Pred. No. 35;
 Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 6 AGAGATAGTTTAACTACCTGTTGAGCTTGAGCTTGAGCAGGTGTTTAACTATCTCTGCTAAC 65
 |||||
 Db 222 AGCGATACAGAACCTACCTGTTGTTCTTGAGCTCCCTGCTCTCTTCTGCTAAC 163
 |||||

QY 66 AGTTTTT 72

Db 162 TGTTTTT 156

RESULT 10

BH462209

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 662)

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Other_GSSs: BOHAI25TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..662

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOHAI25"

/clone lib="BOHA"

/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOS1 using BstXI linkers"

Query Match 38.9%; Score 28.4; DB 8; Length 662;
 Best Local Similarity 66.1%; Pred. No. 40;
 Matches 41; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 5 CAGGAGATAGTTAACTACCTGTTGAGCTTGAGCAGGTGGTGAATCTATCTCTCTAA 64
 |||||
 Db 265 CAGGAGTGGGATTACAATCTGTTGAGCTTGAGCAGATGGGTATTGATATTCTGCGAA 324
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QY 65 CA 66

Db 325 GA 326

RESULT 11

B04037/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 248)

Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M.,
 Jones, D., Ward, T., Gillian, E., Schagemann, J., Probst, S.,
 Harris, J., DeFord, J., McFarland, J., Burzinski, K., Khan, M.,
 Kupfer, K. and Garner, H.R.

Genomic Sequence Sampled Map of Chromosome 11

Unpublished (1996)

Contact: Evans GA, Shane Probst

McDermott Center for Human Growth and Development

BH462209 662 bp DNA linear GSS 13-DEC-2001
 BOHAI25TF BOHA Brassica oleracea genomic clone BOHAI25, genomic
 survey sequence.

BH462209

BH462209.1 GI:17653553

GSS.

Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 662)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Other_GSSs: BOHAI25TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..662

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOHAI25"

/clone lib="BOHA"

/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOS1 using BstXI linkers"


```

RESULT 14
BU476113
LOCUS
DEFINITION BU476113 722 bp mRNA linear EST 30-NOV-2002
603842214f1 CSEQBN22 Gallus gallus cdna clone CHEST82514 5', mRNA
sequence.
ACCESSION BU476113
VERSION BU476113.1 GI:25969690
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 722)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
source
1..722
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST82514"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate
cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQBN22"
/note="Vector: Bluescript II KS(+); Site_1: EcoRI;
Site_2: NotI; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction double-stranded cDNA was blunted, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."
ORIGIN
Query Match 37.8%; Score 27.6; DB 5; Length 722;
Best Local Similarity 78.6%; Pred. No. 77;
Matches 33; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 5 CAGGAGATAGGTTAACTACCTGTTGAAGCTTGAGCAGGTGGT 46
|||||
DB 24 CAGGAGACAGGTTAACTACAGGTTTAGGCATCAGCAGGAGGT 65
|||||

RESULT 15
CK312407/c
LOCUS
DEFINITION CK312407 775 bp mRNA linear EST 01-MAR-2004
SB02011B2D06.f1 normalized Keck-Tagu Library SB02 Taeniopygia
guttata cdna clone SB02011B2D06.f1 5, mRNA sequence.
ACCESSION CK312407
VERSION CK312407.1 GI:44821981

```

KEYWORDS

SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENTFEATURES
source

ORIGIN

Query Match 37.8%; Score 27.6; DB 7; Length 775;
Best Local Similarity 72.0%; Pred. No. 78;
Matches 36; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 16 TTAACCTACCTGTTGAAGCTTGAGCAGGTGGTGAATCTATCTCTGCTAAC 65
|||||

DB 723 TTAATACCTCTTGAAGCTTTATCATCTGCTTAACTGTACCATGATATC 674
|||||

Search completed: August 14, 2005, 21:48:05
Job time : 3257 secs

EST.

Taeniopygia guttata
Taeniopygia guttata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.

1 (bases 1 to 775)

Clayton,D.F., Arnold,A.P., Ball,G.F., Brenowitz,E., George,J.M.,
Mello,C.V., Wade,J., Replogle,K., Lewin,H., Band,M., Hernandez,A.
and Liu,L.

The Songbird Neurogenomics Initiative: An Evolving Public Resource
for Study of Genes, Brain, and Behavior
Unpublished (2004)

Contact: David F. Clayton

University of Illinois

B107 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA

Tel: 217 244 3668

Fax: 217 244 1648

Email: dclayton@uiuc.edu

Base Calling/Quality Scores: PHRED from Washington University
Genome Center.

Vector Trimming: Cross match from Washington University Genome
Center PHRAP suite. Low quality bases (Phred score < 20) were
trimmed from both ends of the sequence by an in-house script.

This sequence is vector free and at least 200 bp in length. Funded
by PHS grant # RO1 NS045264, 'Songbird Neurogenomics Initiative,'
PCR Primers

FORWARD: TAATACGACTCACTATAGGG(T7)

BACKWARD: ATTAACCTCTACTTAAG(T3)

Insert length: 775 Std Error: 0.00

Plate: SB02011B2 row: D column: 06

Seq primer: TAATACGACTCACTATAGGG (T7)

High quality sequence stop: 775.

Location/Qualifiers

1..775

/organism="Taeniopygia guttata"

/mol_type="mRNA"

/db_xref="taxon:59729"

/clone="SB02011B2D06.f1"

/tissue_type="brain"

/dev_stage="late embryo, post-hatch days 1, 10, 20, 45,

and adult (pooled)"

/lab_host="DH10B"

/clone_lib="normalized Keck-Tagu Library SB02"

/note="Organ: brain; Vector: pBS II SK(+); Site 1:

EcoRI(5' side of insert); Site 2: NotI (3' side of

insert); The library was constructed and normalized as

described by Bonaldo, M.F., Lennon, G. and Soares, M.B.

(1996), Genome Research 6(9): 791-806. An identifying tag

was added at the 3'during cDNA synthesis:

insertAAAAAAAAAAAAAAAAAATCGCA."

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